

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:36:05 ; Search time 92.97 Seconds  
(without alignments)  
663.819 Million cell updates/sec

Title: US-09-397-548-15  
Perfect score: 5346  
Sequence: 1 MAACLLALTLFQSLIG.....TNLFIMVESKGTCPDTRL 1018

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
1: /cgnl\_9/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /cgnl\_9/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /cgnl\_9/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /cgnl\_9/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
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11: /cgnl\_9/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
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19: /cgnl\_9/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /cgnl\_9/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /cgnl\_9/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /cgnl\_9/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	DB ID	Description
1	5346	100.0	1091	16	AAR71011	Human neuronal cal
2	5346	100.0	1091	16	AAW63145	Human calcium chan
3	5346	100.0	1091	21	AAW63151	Human calcium chan
4	5342	99.9	1091	19	AAW63154	Human calcium chan
5	5340	99.9	1091	14	AAW63158	Sequence of the al
6	5326.5	99.6	1100	16	AAW63148	Human calcium chan
7	5306.5	99.3	1086	16	AAW63153	Human neuronal cal
8	5306.5	99.3	1086	21	AAW63158	Human calcium chan
9	5306.5	99.3	1086	21	AAW63158	Human calcium chan
10	5289.5	98.9	1084	16	AAR71015	Human neuronal cal
11	5289.5	98.9	1084	19	AAW63155	Human calcium chan

12	5289.5	98.9	1084	21	AAW63158	Human calcium chan
13	5270	98.6	1103	16	AAR71012	Human neuronal cal
14	5270	98.6	1103	19	AAW63151	Human calcium chan
15	5270	98.6	1103	21	AAW63158	Human calcium chan
16	5250	98.2	1079	19	AAW63154	Human calcium chan
17	5250	98.2	1079	21	AAW63158	Human calcium chan
18	5244	98.1	1079	16	AAR71014	Human neuronal cal
19	5137.5	96.1	1106	18	AAW37712	Rabbit skeletal ca
20	5137.5	96.1	1106	18	AAW18389	Rabbit skeletal ca
21	5137.5	96.1	1106	21	AAW77545	Rabbit skeletal ca
22	5116.5	95.7	1106	16	AAW73056	Rabbit skeletal ca
23	5009.5	93.7	1100	10	AAW95644	Rabbit skeletal mus
24	2872.5	53.7	1145	21	AAW92322	Human alpha-2-delt
25	2581.5	48.3	508	19	AAW42032	Human skeletal cal
26	2581.5	48.3	508	21	AAW77546	Human alpha-2-delt
27	1087	20.3	1085	21	AAW92320	Human alpha-2-delt
28	1065.5	19.9	1120	21	AAW92321	Human alpha-2-delt
29	1035.5	19.4	1096	21	AAW92324	Human alpha-2-delt
30	992.5	18.6	1096	21	AAW92323	Human alpha-2-delt
31	733.5	13.7	519	21	AAW70460	Human membrane cha
32	161	3.0	1829	18	AAW29322	DNA polymerase wit
33	158.5	3.0	894	20	AAW00133	Enterococcus faeca
34	158.5	3.0	962	20	AAW00244	Enterococcus faeca
35	158.5	3.0	962	20	AAW00246	Enterococcus faeca
36	158.5	3.0	962	20	AAW00248	Enterococcus faeca
37	158.5	3.0	962	20	AAW00132	Enterococcus faeca
38	158.5	3.0	962	20	AAW00134	Enterococcus faeca
39	158.5	3.0	962	20	AAW00136	Enterococcus faeca
40	155	2.9	1516	21	AAW18195	Plasmodium falcipa
41	154.5	2.9	946	21	AAW29100	Human inter-alpha-
42	154.5	2.9	1315	20	AAW08642	S. aureus SdrD pro
43	154	2.9	903	15	AAW60183	PA(1-725)-----Huma
44	152.5	2.9	789	17	AAW91244	B. thuringiensis V
45	152.5	2.9	789	18	AAW19515	B. cereus VIP3A(b)

ALIGNMENTS

RESULT 1  
AAR71011  
ID AAR71011 standard; Protein; 1091 AA.  
XX AAR71011;  
AC AAR71011;  
XX  
DT 01-DEC-1995 (first entry)  
XX  
DE Human neuronal calcium channel subunit alpha 2b.  
XX  
KW Calcium channel subunit; antagonist; agonist; diagnosis;  
KW Lambert Eaton Syndrome.  
XX  
OS Homo sapiens.  
XX  
PN W09504822-A.  
XX  
PD 16-FEB-1995.  
XX  
PF 11-AUG-1994; 94WO-US09230.  
XX  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
XX  
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;  
XX WPI; 1995-090900/12.  
XX N-PSDB; AAQ84664.  
XX  
XX DNA encoding human calcium channel sub-unit(s) - used for  
XX developing prods. for studying calcium channels, e.g. for  
XX obtaining agonists and antagonists

XX PS Disclosure; Page 166-171; 285pp; English.

XX CC Human neuronal alpha 2 coding sequence (AA084664) transcript is

CC differentially processed in skeletal muscle, aorta, and CNS in

CC the region corresp. to nt 1995-1942 of AA084664 in each of the

CC tissues. Five alternatively spliced variant transcripts that differ

CC in the presence or absence of one to three different portions of

CC this region. There are three sequences involved (see AA084664, FT

CC and AA084665 FT), sequence 1, sequence 2 and sequence 3. The five

CC alpha 2 encoding transcripts from the different tissues include

CC different combinations of the three sequences, except for one of

CC the alpha 2 transcripts expressed in aorta which lacks all three

CC sequences. The five alpha 2 forms identified are (1) a form that

CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle

CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS

CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in

CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,

CC expressed in aorta and (5) one that lacks sequences 1 and 3

CC called alpha 2e.

XX CC Sequence 1091 AA;

XX QY Query Match 100.0%; Score 5346; DB 16; Length 1091;

XX QY Best Local Similarity 100.0%; Pred. No. 0;

XX QY Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLALTLTQSLIGPSSSEPPPSAVTIKSWVDKMOEDLVTLAKTASGVNOLVDI 60

DB 1 maagclaltltlqsligpsssepppsavtikswvdkmqedlvtlaktasgvnqlvdi 60

QY 61 YEKYQDLYTEPNARQLVEIARDTEKLSNRSKALVSLALEAEKVQAARHQRDFASN 120

DB 61 yekyqdytvepnarqlveiaardteklksnrskalvslaleaekvqaahqrdfasn 120

QY 121 EVVYNAKDDLPEKNDSPGSRQIKPVFTEDANFGROIQSYQAAVHIPDIYEGSTIVL 180

DB 121 evvyynakddlpekdndspgsrqikpvftedanfgrqisqyqaaahvipcdiyegstivl 180

QY 181 NELNWTALDEVFKNREEDPSLLQVFGSATGLARYTPASPVDNSRTPNKIDLDVRR 240

DB 181 nelnwtaldevfknnreedpsllqvfgsatglarytpaspvwdnsrtpnkldlydrr 240

QY 241 RPWYIQAASPDKMLILVDVSGVSGITLKLRTSVSEMLETSSDDDFVNVASFNSNAQD 300

DB 241 rpwyiqgaaspdkmllilvdvsgvsgitlklrtsvsemletssdddfvnvasfnasnaqd 300

QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEOILLNYSRANCNKIIML 360

DB 301 vscfqlhvganvrnkkvldkavnnitakgtdykgkgsfafeqllnynvsrancnkliiml 360

QY 361 FTDCGEERAQEIFNKNKRRVFRFSVQGHYVERGPIQWACENKGYIYEIPSGAIR 420

DB 361 ftdggeeraqeifnknkrrvfrfsvqghyvergpiqwmacenkgyyieipsigair 420

QY 421 INTQEYLDVLGRPMVLADGAKAQVQWNTNVLDALEGLVITGLPVPNTITGQFENKTNLK 480

DB 421 intqeyldvlgpmvmladgkakqvqwntnvnldaleglvitglpvpnitgqfenktnlk 480

QY 481 NQTLGVGMVDVSLDKRLTPRTLCPCNGYYPADPNQVYLLHPLNLPKNPKSQEPVTL 540

DB 481 nqtlgvgmvdvsldkrltprtlcpngyyypadpnqvyllhplnlpknpsqepvtil 540

QY 541 DFLDAELNDIKVIRNKMIDGESGETFTFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600

DB 541 dfldaeendikveirnkmidgesgetftflvksqderydkgnrtytwtvpvngtdysl 600

QY 601 ALVLPYTSFYVIKAKLBETITQARSKGKMKDSTLKPDPFESGYTFIAPRDYCNDLKI 660

DB 601 alvlpysfyvikakleetitqarskkgmkdsetlkdndfreesgytftiaprdyendlki 660

QY 661 SDNTEFLNFEINIDRTPNPNPCNADLNRLVLDAGFTNQLVQWSKQKNKIKGVKAR 720

DB 661 sdnteflnfnefidrktcpnpscnadlnrvlldagftnelvqnywskgnikgvkar 720

QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780

DB 721 fvtvdggitrvypkeagenwqenpetyedsfykrsildndnyvftapyfnksgpgayesgi 780

QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840

DB 781 myskaveiyiogkllkllpavvgiikidvnswienvtktksirpcagpycdckrnsdvmdcvi 840

QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPILMRHLVNIISVYAFNKSVDYOSVCEPGAAPKQ 900

DB 841 lddggfllmanhddytngqgrffgeidpslmrhlvnisvyafnksydyosvcepgaapkq 900

QY 901 GAGHRSAVPSVADILQIGWATAAASIILOQLLSLTPRLLAEVEMEDDDFTASLSKQ 960

DB 901 gaghrsavpsvadilqigwataaasilqllsltprrlleavemedddftaslskq 960

QY 961 SCTTEQTYFFDNDKSFSGVLDCGNCRIFFHCEKLMNTNLIIFIMVESKGTCPCDTRL 1018

DB 961 sciteqtqyffndndksfsgvlcdgncsriffhceklmntnliifimveskgtcpcdtrl 1018

RESULT 2

AAW63145

ID AAW63145 standard; Protein; 1091 AA.

XX AC AAW63145;

XX DT 12-OCT-1998 (first entry)

XX DE Human calcium channel alpha-2 subunit.

XX KW Alpha-2 subunit; human; calcium channel; assay; detection;

XX KW Characterisation; Lambert Eaton Syndrome; LES; diagnosis.

XX OS Homo sapiens.

XX PN US5792846-A.

XX PD 11-AUG-1998.

XX PF 31-MAY-1995; 95US-0455543.

XX PR 04-APR-1994; 94US-0223305.

XX PR 04-APR-1988; 88US-0176899.

XX PR 04-APR-1989; 89US-0603751.

XX PR 04-APR-1989; 89WO-US01408.

XX PR 20-FEB-1990; 90US-0482384.

XX PR 30-NOV-1990; 90US-0620250.

XX PR 15-AUG-1991; 91US-0745206.

XX PR 31-MAY-1995; 95US-0455543.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;

XX PI Williams ME;

XX WPI; 1998-456192/39.

XX N-PSDB; AAV42689.

XX DNA encoding human calcium channel alpha 1B subunit protein -

XX useful for recombinant production of the channel for screening of

XX its modulators, and diagnosis of Lambert Eaton Syndrome

XX Claim 4; Columns 283-288; 166pp; English.

XX The present sequence represents the alpha-2 subunit of a human calcium

XX channel. Calcium channels are membrane-spanning, multi-subunit proteins

XX that allow controlled entry of calcium ions into cells. This leads

XX to depolarisation events required for muscle contraction. The recombinant

XX subunit, when expressed with nucleic acids encoding the complete calcium





CC described in the method of the invention.

XX  
SQ Sequence 1091 AA;

Query Match 100.0%; Score 5346; DB 21; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
DB 1 maagcllalttlfoslilgppsseppfsavtikswdkmqedlvtlaktasgvnqlvdi 60

QY 61 YEKYQDLYTEPNNAQOLVEIAARDIEKLLSNRSLKALVSLALEAEKVOAAHQWREDEASN 120  
DB 61 yekyqdltytepnnaqlveiaardieklslnrslkalvslaleaekevooahqwrdeasn 120

QY 121 EYVYNKADDDLPENKNDSEPSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
DB 121 evvynakddldpenkndsepsqrikpvfiedanfgroisqyhaavhiptdiyegstivl 180

QY 181 NELNWTSSALDEVFKKRRNEDPSLLWQVGSATGLARYTPASPVDNSRTPNKIDLYDVR 240  
DB 181 nelnwtssaldevfkknredpsllwqvgstglarytpaspvwnsrtpnkdilydvrr 240

QY 241 RPWYIQAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASFNSAQD 300  
DB 241 rpyylqgaaspkdmlilvdvsgvsgltglkirtsvesmleclsdvfvnvasfnasqd 300

QY 301 VSCFOHLYVOANVRNKKVLKADVNNITAKGITDYKKGFSAFEPQLLYNVSRANCKIIML 360  
DB 301 vscfqlhvganvrnkvlkadvnnitakgitdykkgfsafepqllnvsrancnkiiiml 360

QY 361 FIDGGEERAQELFNKYNKDKKVRFRFSVQGNHYRGPQIOMACENKYYEIPSGAIR 420  
DB 361 ftdggeeaeqlfnkynkdkkvrfrfsvqgnhyrpgpiomacenkyyeipsigair 420

QY 421 INTQYLDVLRGPMVLAGDKAQOVWTVYLDALBGLVITGTLFVFNITGOFENKTLK 480  
DB 421 intqeyldvlgpmvlagdkaqovwtnvylldalbglvitgtlfpvfnitgofenktlk 480

QY 481 NQLILGVNGVDSLEDKRLPRFTLCPNGYFFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
DB 481 nqlilgvngvdsledkrlprftlcpngyffaidpngyvlhlpnlqpnkpsqepvtl 540

QY 541 DFLDAELENDIKVEIRNMKIDGSEKFTFRILVKSQDRYIDKGNRTTWPVNGTDSL 600  
DB 541 dfldaelendikveirnmkidgesektfrtlvksqderyidkgnrtwtvpngtdysl 600

QY 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSFTLKPDPNFEEGTYTFIAPRDYCNLKI 660  
DB 601 alvlpftyfyiykakleetitqarskkgmkdsetlkdpnfneesgytftiaprdocnlki 660

QY 661 SDNTEFLNFEIDRTPNPNNSADLIRNLVLDAGFTNELVQYVWSKOKNKGVKAR 720  
DB 661 sdnntefllnfeidrtpnnpnsadlirnlvldagftnelvqyvwskoknkgvkar 720

QY 721 FVWTDGGITRYVPKEAGNENQENPTYEDSYKRSKLDNDNVFAPYFNKSGPAYESGI 780  
DB 721 fvwtddgitryvpkeagenenqenptyedsykrskldndnvfapynksgpayesgi 780

QY 781 MYSKAVEIYIOCKLLKPAVVGKIDVNSWENFTKTSIRDCAGVPDCRKNSDVMDCVI 840  
DB 781 mvskaveiyiockllkpaavgkiddvnswnenftktsirdcagvpdcckrnsdvmdcvi 840

QY 841 LDDGFLMANHDDYTNIGRFFGEIDPSLMRHLNIVSYAFNKSYSQYCEGPAAPKQ 900  
DB 841 lddgflmanhddytngirffgeidpslmrhlvnsyafnksydsqycegpaapkq 900

QY 901 GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFFPRLLEAVENEDDDFTASLSKQ 960  
DB 901 gaghsayvpsvadilqigwataaasilqofllsltfprrlleavenedddftaslskq 960

QY 961 SCITEOTOYFFDNDKSPSGVLDGNCGRIPHEKXLMNTNLIIFIMVESKGTCPDCTRL 1018  
DB 961 sciteqtocyffndksksfsgvldcgnscrfhgeklmtnliffimveskgtcpdctrl 1018

## RESULT 4

AAW37879  
ID AAW37879 standard; Protein; 1091 AA.

AC AAW37879;

DT 28-AUG-1998 (first entry)

DE Human calcium channel a2d subunit.

KW Calcium channel; human; central nervous system disorder;  
Lambert-Eaton syndrome; diagnosis; therapy.

OS Homo sapiens.

PN WO98111131-A2.

PD 19-MAR-1998.

PF 11-SEP-1997; 97WO-US16146.

PR 16-SEP-1996; 96US-0713118.

PA (AMHP ) AMERICAN HOME PROD CORP.

PI Chen ARS, Franco R, Shuey DJ;

DR WPI; 1998-207325/18.

DR N-PSDB; AAV29060.

PT DNA encoding human neuronal calcium channel subunit(s) - useful for  
diagnosis of and treatment of central nervous system disorders, e.g.  
Lambert-Eaton syndrome

PS Disclosure; Fig 2; 89pp; English.

XX This polypeptide comprises the a2d subunit of the human neuronal  
calcium channel. cDNA clones (see AAV29059-61) encoding the a1b  
subunit (see AAW37878), the a2d subunit and a b3 subunit (see AAW37880)  
have been isolated. These have been inserted into expression  
vectors and are stably expressed in transformed cell lines. The  
transformed cells show omega-conotoxin GVIA binding activity,  
and omega-conotoxin GVIA toxin sensitive potassium-stimulated  
calcium uptake, indicating that the proteins expressed by the  
clones are capable of forming a functioning calcium channel.  
Nucleic acids encoding the 3 subunits, as well as vectors, host  
cells and methods of isolating nucleic acids encoding related  
calcium channels are disclosed. Fusion proteins incorporating the  
subunit proteins, antibodies, and assays for identifying agents  
that modulate calcium channel activity are also provided. Such  
agents can be used to treat certain central nervous system  
disorders by altering calcium channel activity. Methods of  
diagnosing diseases associated with particular calcium channels,  
such as Lambert-Eaton syndrome, are disclosed.

SQ Sequence 1091 AA;

Query Match 99.9%; Score 5342; DB 19; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
DB 1 maagcllalttlfoslilgppsseppfsavtikswdkmqedlvtlaktasgvnqlvdi 60

QY 61 YEKYQDLYTEPNNAQOLVEIAARDIEKLLSNRSLKALVSLALEAEKVOAAHQWREDEASN 120  
DB 61 yekyqdltytepnnaqlveiaardieklslnrslkalvslaleaekevooahqwrdeasn 120

Db 61 yekyqdytvepnnaqlveiaardleklslsrskalsvlsaleaekvqaahqwfesfn 120  
QY 121 EVYYNAKDDLDPEKNDSEPGSORIKPVFTEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 evyyynakddldpekndsepgsgrikpvfiedanfgqisyqhaavhptdiyegstivl 180  
QY 181 NELNWTSALEDVEFKKNEEDPSLLMQVFGSATGLARYYPASPVWVDSRTPNKKIDLDVRR 240  
Db 181 nelnwtlsaldevfkknreedsllwqvfsgatglaryypaspvwvdsrtpnkldldvrr 240  
QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTIKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
Db 241 rpywiggaaspkdmlilvdvsgsvsgltiklirtsvsemletisdddfvnvasfnasqd 300  
QY 301 VSCFQHLVQANVRNKKVLDAVNNTAKGITYDKGFSFAFEOQLLNNVSRANCKIIML 360  
Db 301 vscfqlhqvsnvrnkkvldavnnitakgitydkgfsfafeqllnnvsvrancnkiml 360  
QY 361 FTGGERAQEIPNKYNKKKRVFRFSVQGHNYERGPIQWACENKGYIYEIPSGAIR 420  
Db 361 ftggeeadeifnknynkkkvrfrfsvqghnyergpiqwmacenkgyyieipsigair 420  
QY 421 INTQEVLDVLGRPMVLGAKAKOVQNTNYLDALGLGLVITGTLPVFNITGQFENKTNL 480  
Db 421 intqevldvlgrpmvlgakakovqntnyldaleglglvitgtlpvfnitgqfenktnl 480  
QY 481 NQILGVMGVDSLEDIKRLTFRFTLCPNGYYPFAIDPNGVLLHPLNLPKNKPSQBPVTL 540  
Db 481 nqilgvmgvdsleedikrltfrftlcpngyypfaidpngvllhplnlpknpsqbpvltl 540  
QY 541 DFLDALENDIKVEIRNMKIDGSGEKTFTLVKSDERYDKGNRTYTPVNGTDYSL 600  
Db 541 dfldaelendikveirnmkidgsgektftlvksqerydkgnrtypvngtdysl 600  
QY 601 ALVLPYSFYIYKAKLEETITQARSKKGMKDSKTELKPDNFESGYTFIAPRDCYNDLKI 660  
Db 601 alvlpysfyiykakeetitqarskkgmkdselkpdnfesgytfiaprdcndlki 660  
QY 661 SDNNTFELNFNFIKRPNNPNCNADLNIRVLLDAGFTNELVQNYWSKQNKIKGVYKAR 720  
Db 661 sdntefllnfnfirkpnnpncnadlnirvlldagftnelvqnywskqknkigvykar 720  
QY 721 FVYTDGTRVYPKRAGENQENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
Db 721 fvtydgtrvypkragenqenpeyedsfykrsldndnyftapyfnksgpgayesgi 780  
QY 781 MVSKEYEITQGLKPAVVGIKIDVNSWIENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
Db 781 mvskaveiytqglkpvavvgikidvnswieftktsirpcagpvcdckrnsdvmdcvi 840  
QY 841 LDGGLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSXYDQSVCEPFGAPKQ 900  
Db 841 ldggglmanhddytngqigrffgeidpslmrhlvnsyafnksydyqsvcepgaapkq 900  
QY 901 GAGHSAVPSVADIQIGWATAAASWILQOFLSLTTPRLEAVEMEDDDFTASLSKQ 960  
Db 901 gadhsavpsvadiqigwataaaswllqofllsttprleavemedddftaslskq 960  
QY 961 SCITEQTYFFDNDKSFSGVLDCGNCRFFHGEKLMNTNLIIFIMVESKGTCTPCDTRL 1018  
Db 961 sciteqtyffndksfsgvlcgcncrffhgekmlmntnliifimveskgtcpcdtrl 1018

RESULT 5

AAR33553

ID AAR33553 standard; Protein; 1091 AA.

XX

AC AAR33553;

XX

DT 30-JUN-1993 (first entry)

XX

DE Sequence of the alpha 2 human calcium channel subunit.

XX

KW Human calcium channel subunit; diagnosis; agonist; antagonist;  
KW Lambert Eaton syndrome.  
OS Homo sapiens.  
PN WO9304083-A.  
XX  
PD 04-MAR-1993.  
XX  
PF 14-AUG-1992; 92WO-US06903.  
XX  
PR 15-AUG-1991; 91US-0745206.  
PR 10-APR-1992; 92US-0868354.  
XX  
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
PI Williams ME;  
XX  
DR WPI; 1993-093936/11.  
DR N-PSDB; AAQ37821.  
XX  
PT DNA encoding specific human calcium channel sub-units - used for  
PT identifying calcium channel agonists and antagonists and  
PT diagnosing Lambert Eaton syndrome  
XX  
PS Disclosure; Page 134-138; 150pp; English.  
XX  
CC DNA encoding a human neuronal calcium channel alpha 2 subunit was  
CC isolated from a human genomic DNA library probed under low and high  
CC stringency conditions with a fragment of DNA encoding the rabbit  
CC skeletal muscle calcium channel alpha 2 subunit. The fragment  
CC included nucleotides having a sequence corresponding to the  
CC nucleotide sequence between nucleotides 43 and 272 inclusive of  
CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.  
CC PCR analysis identified splice variants of the human calcium alpha  
CC 2 subunit transcript. In particularly preferred embodiments, the  
CC DNA encoding the alpha 2 subunit is produced by alternative  
CC processing of a primary transcript that includes DNA encoding the  
CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted  
CC between nucleotides 1624 and 1625 of AAQ37821.  
XX  
SQ Sequence 1091 AA;

Query Match 99.9%; Score 5340; DB 14; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCCLALTLTFLQSLIGPSSSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60  
Db 1 magcclaltltlfgslilgppsseepfpsavtikswdkmqedlvtlaktasvnglvd 60  
QY 61 YEKYQDYTVEPNNAQLVEIAARDIEKLKLSNRKALVLSALEAEKVQAAHQRDFASN 120  
Db 61 yekyqdytvepnnaqlveiaardieklklsnrskalsvlsaleaekvqaahqrdfasn 120  
QY 121 EVYYNAKDDLDPEKNDSEPGSORIKPVFTEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 evyyynakddldpekndsepgsgrikpvfiedanfgqisyqhaavhptdiyegstivl 180  
QY 181 NELNWTSALEDVEFKKNEEDPSLLMQVFGSATGLARYYPASPVWVDSRTPNKKIDLDVRR 240  
Db 181 nelnwtlsaldevfkknreedsllwqvfsgatglaryypaspvwvdsrtpnkldldvrr 240  
QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTIKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
Db 241 rpywiggaaspkdmlilvdvsgsvsgltiklirtsvsemletisdddfvnvasfnasqd 300  
QY 301 VSCFQHLVQANVRNKKVLDAVNNTAKGITYDKGFSFAFEOQLLNNVSRANCKIIML 360  
Db 301 vscfqlhqvsnvrnkkvldavnnitakgitydkgfsfafeqllnnvsvrancnkiml 360

QY 361 FTDGGERAQELFNKYNKDKVVRERFSGOHNRYERGPQIOWMACENKGYVEIPISGAI 420  
Db 361 fdg9geeraqelfnkynkdkkvrirfsvghnyergpqlwmacenkgyveipisgair 420  
QY 421 INTQYLDVLGRPMVLADKAKQVQWNTVYLDALGLVITGLPVFNITGOFENKTNLK 480  
Db 421 intqeyldvlgrpmvladkakqvqwtvnyldaleglvitgltpvfnitgofenktalk 480  
QY 481 NQILIGVMGVDSLEDEIKRLTPRFTLCPNGYYFAIDPNGYVLLHNLQPNKPKSQEPVTL 540  
Db 481 nqililgvmgvdslesedikrltprftlcpngyyfaidpngyvlhnlqpnkpkseqpvtl 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTPLVKSODERYIDKGNRTYTWTVPNGTDSL 600  
Db 541 dfldaeelndikveirnmidgesgkftplvksqderidkgnrtwtvtpngtdysl 600  
QY 601 ALVLPYSFYIKAKLEETITQARSKGKMDSETLKPDPNFESGYTFIAPRDYCNLKI 660  
Db 601 alvlpysfyyikakleetitqarskkgmdsetlkdnpnfesgytfiaprdydcndlki 660  
QY 661 SONTEFLNFEIDRKTTPNPNSCNADLINRVLLDAGTNELVQYWSKQKNIGVKAR 720  
Db 661 sdnteflnfnedrkttpnpnsnadlinrvlldagtnelvgqywsqknikgvkar 720  
QY 721 FVYTDGIGTRVYPKEAGENQENPETYEDSFYKRSILDNDNVYFTAPYFNKSGPGAYESGI 780  
Db 721 fvytdgigtrvypkeagenqenpetyedsfyrksildndnyvftapyfnksgpgayesgi 780  
QY 781 MYSKAVEIYIOGLKLPVAVGKIDVNSHNIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
Db 781 mvskaivelyiogllkpvavgikidvnsnienftktsirdpcagpvcdcrnsdvmdcvi 840  
QY 841 LDGGFLLMANHDDTYNQIGRFGEDIDPSLMRHLVNSIVYAKNSYDYQSVCEPGAAPKQ 900  
Db 841 ldggfllmanhddytngigrfgedidpslmrhlvnsivayaknsydyqsvcepgaapkq 900  
QY 901 GAGHSAYVPSVADIIQIGWATAAASWTLQOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960  
Db 901 gaghsayvpsvadiiqigwataaawsllqofllsltprrlleavemedddftaslskq 960  
QY 961 SCITEQTYFFNDKSKFSVGLDCGNCRSIFRFGKIMNTNLNLFIMVESKGTGCPCTR 1018  
Db 961 sciteqtyffndkksfsgvldcncrsifrgkikmntnlfnimveskgtgpcctr 1018  
RESULT 6  
AAW63148  
ID AAW63148 standard; Protein; 1110 AA.  
XX AC AAW63148;  
XX DT 12-OCT-1998 (first entry)  
XX DE Human calcium channel alpha-2 subunit.  
XX KW Alpha-2 subunit; human; calcium channel; assay; detection;  
XX characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
XX OS Homo sapiens.  
XX PN US5792846-A.  
XX PD 11-AUG-1998.  
XX PF 31-MAY-1995; 95US-0455543.  
XX PR 04-APR-1994; 94US-0223305.  
XX PR 04-APR-1988; 88US-0176899.  
XX PR 04-APR-1989; 89US-0603751.  
XX PR 04-APR-1989; 89WO-0501408.  
XX PR 20-FEB-1990; 90US-0482384.  
XX PR 30-NOV-1990; 90US-0620250.  
XX PR 15-AUG-1991; 91US-0745206.

PR 31-MAY-1995; 95US-0455543.  
XX (STBI-) SIBIA NEUROSCIENCES INC.  
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
XX Williams ME;  
XX WPI; 1998-456192/39.  
XX N-PSDB; AAV42694.  
PT DNA encoding human calcium channel alpha 1B subunit protein -  
PT useful for recombinant production of the channel for screening of  
PT its modulators, and diagnosis of Lambert Eaton Syndrome  
XX PS Disclosure; Columns 131-138; 166pp; English.  
XX The present sequence represents the alpha-2 subunit of a human calcium  
XX channel. Calcium channels are membrane-spanning, multi-subunit proteins  
XX that allow controlled entry of calcium ions into cells. This leads  
XX to depolarisation events required for muscle contraction. The recombinant  
XX subunit, when expressed with nucleic acids encoding the complete calcium  
XX channel, can be used in assays for the detection and characterisation of  
XX compounds that modulate the channel. The DNA encoding the subunits can  
XX be alternatively spliced when transcribed, giving more than one form of  
XX the protein from the same transcript, each having slightly different  
XX properties. In addition, the reactivity of the alpha 1 subunit with IgG  
XX molecules from the serum of an individual with Lambert Eaton Syndrome  
XX (LES) can be used as a diagnostic for the disease.  
XX Sequence 1110 AA;  
QY

Query Match 99.6%; Score 5326.5; DB 19; Length 1110;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 19; Gaps 1;  
QY 1 MAAGCLLALTTLTFLFOSLIGPSSPEPEPSAVTIKSWDKMQEDVLTLAKTAGSVNQLVDI 60  
Db 1 maagcllalttlfloslilgppspepfpsavticwskwvdkmqedvltlaktasgvnqlvdi 60  
QY 61 YEKYODLYTFEPNNAQLVEIAARDIEKLLSNRSLVSLALEAEKVQAHOHQWEDFASN 120  
Db 61 yekyodlytvepnnarqlveiaardieklslsrslvslaleaeekvqaahqhwedfasn 120  
QY 121 EVVYNAKDDLDPEKNSEPGSQRIKPVFIEDANFGRQISYOHAAVHIPTDIYESTIVL 180  
Db 121 evvynakddldpeknsepgsqrikpvfiedanfgrqisyqhaavhiptdiyestivl 180  
QY 181 NELNWTLSALDEVFKKNREEDPSLLHQVFGSATGLARYYPASVPWDSNRPKNKIDLYDVR 240  
Db 181 nelnwtlsaldevfkknreedpsllhwvfgsatglaryypasvpwdsnrtpknkidlydvr 240  
QY 241 RPWYIQTGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLETSDDDFYNVASFNSNAQ 300  
Db 241 rpwyiqgaaspkdmililvdvsgsvsgltklirtsvsemletisdddfynvasfnasnaq 300  
QY 301 VSCFOHLYQAVNRNKKVLKDAYNNITAKGITYKKGFSAFQOLLNINVSRRANCKNIML 360  
Db 301 vscfqlhlyqanvrnkvlkdavnnitakgitykkgfsafqollnynvsrrancnkilm 360  
QY 361 FTDGEEERAQELFNKYNKDKVVRERFSGOHNRYERGPQIOWMACENKGYVEIPISGAI 420  
Db 361 ftdggeeraqelfnkynkdkkvrirfsvghnyergpqlwmacenkgyveipisgair 420  
QY 421 INTQYLDVLGRPMVLADKAKQVQWNTVYLDALGLVITGLPVFNITGOFENKTNLK 480  
Db 421 intqeyldvlgrpmvladkakqvqwtvnyldaleglvitgltpvfnitgofenktalk 480  
QY 481 NQILIGVMGVDSLEDEIKRLTPRFTLCPNGYYFAIDPNGYVLLHNLQPNKPKSQEPVTL 530  
Db 481 nqililgvmgvdslesedikrltprftlcpngyyfaidpngyvlhnlqpnkpkseqpvtin 540  
QY 531 -----NPKSQEPVTLDFDLDALENDIKVEIRNKMIDGESGKFTPLVKSQDERYI 581

Db 541 lrkrrpniqpkseqpvtidflaeldendkveirnkmdgesgektfrtlvksqeryl 600  
 QY 582 DKGNNRYTWPVNGTYSIALVPTYSFYIYKAKLEETITQARSKGKMKDSETLKPDNF 641  
 Db 601 dkgntytwpvngtysialvptysfyiyakleetitqarskkgkmdsetlkpdnf 660  
 QY 642 EESGYTFIAPRDYCNOLKISDNNTELLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTN 701  
 Db 661 eesgytfiaprdycnolkisdnnnteflnfnefidrktppnpscnadlinrvldagftn 720  
 QY 702 ELVQNTWSQKNIKGVKARFVVDGITTIVYPKEAGENWOENPETYEDSFYKRSLDNDY 761  
 Db 721 elvqnywskgnikgvkarfvvtdgittivypkeagenwqenpetyedsfykrsldndy 780  
 QY 762 VFTAPFNKSGPGAYESGIMVSKAVIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 821  
 Db 781 vftapyfnksgpgayesgimvskaveiyiqgkllkpvvgkikdvnswiensfctksirp 840  
 QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSPMLRHLVNSVYA 881  
 Db 841 cagpvcdcrnsdvmcviiddggfllmanhddytnoigrffgeidpssmlrhlvnsyva 900  
 QY 882 FNKSYDYQVCBPAGAPKQAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPR 941  
 Db 901 fnksydyqvcbpagapkgaghrsayvpsvadilqigwataaawslilqflsltfpr 960  
 QY 942 LLEAVEMEDDDFTASLSKQSCITEQYQFFDNDKSFSGVLDGNGSRIFHGEKLMNTNL 1001  
 Db 961 lleavemedddftaslskqsciteqyqffndksfsgvldcngsrifhgeklmntnl 1020  
 QY 1002 IFIMVESKTCPCDREL 1018  
 Db 1021 ifimvesktpcdrel 1037

## RESULT 7

ID AAR71013 standard; Protein; 1086 AA.  
 XX AC AAR71013;  
 XX DT 01-DEC-1995 (first entry)  
 XX DE Human neuronal calcium channel subunit alpha 2c.  
 XX KW Calcium channel subunit; antagonist; agonist; diagnosis;  
 XX KW Lambert Eaton Syndrome.  
 XX OS Homo sapiens.  
 XX PN W09504822-A.  
 XX PD 16-FEB-1995.  
 XX PF 11-AUG-1994; 94WO-US09230.  
 XX PR 11-AUG-1993; 93US-0105536.  
 XX PR 05-NOV-1993; 93US-0149097.  
 XX PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 XX PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
 XX WPI; 1995-090900/12.  
 XX DR N-PSDB; AAQ84667.  
 XX PT DNA encoding human calcium channel sub-unit(s) - used for  
 XX PT developing prods. for studying calcium channels, e.g. for  
 XX PT obtaining agonists and antagonists  
 XX PS Disclosure; Page 237-242; 285pp; English.

CC Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
 CC differentially processed in skeletal muscle, aorta, and CNS in  
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
 CC tissues. Five alternatively spliced variant transcripts that differ  
 CC in the presence or absence of one to three different portions of  
 CC this region. There are three sequences involved (see AAQ84664 FT  
 CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
 CC alpha 2 encoding transcripts from the different tissues include  
 CC different combinations of the three sequences, except for one of  
 CC the alpha 2 transcripts expressed in aorta which lacks all three  
 CC sequences. The five alpha 2 forms identified are (1) a form that  
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
 CC expressed in aorta and (5) one that lacks sequences 1 and 3  
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
 CC are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.  
 XX XX Sequence 1086 AA;  
 SQ

Query Match 99.3%; Score 5306.5; DB 16; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1013; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCCLLALTTLFQSLIGSPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
 Db 1 maagccllalttlfqslligspseepfpaavtikswdkmqedlvtlaktasgvnldi 60  
 QY 61 YEKYQDLTVPENNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREFASN 120  
 Db 61 yekyqdltyvepnnarqlveiaardiekllsnrskalvslaleaeqvgaahqwfrefasn 120  
 QY 121 EVVYVNAKDDLPEKNDSEPPGSRQIKPVFIEDANFGROIYSQHAAVHITDIVEGFTVL 180  
 Db 121 evvyynakddlpeknndseppgsrqlkpvfiedanfgroisqhaaahvhitdivegstvl 180  
 QY 181 NEINWTSALDEVFKKNREEDPSLLQVFGSATGLARYYPASPVDNRSRPNKIDLDVRR 240  
 Db 181 neinwtsaldevfkknreedpsllqvfgsatglaryypaspvwnsrtpnkldydvrr 240  
 QY 241 RPWYIGGAASPKDMLILDVSGSVSGLTILKLRISVSEMLETISDDDFVNVASFNSNAQD 300  
 Db 241 rpwyiggaaspkdmlilvdsgsvsgltlklirtsvsemletlssdddfvnvasfnasnaqd 300  
 QY 301 VSCFOHLYQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360  
 Db 301 vscfghlyqanvrnkvlkdavnnitakgitykkgfsfafqollnysrancnkilml 360  
 QY 361 FTDGGEERAQEIFKNYKDKKVRFRFSYGOHNYERGPQWMACENKGYIYIPISGAIR 420  
 Db 361 ftdggeeraqeifknykdkkvrfrfsyvgqhnyergpqiwmacenkgyyieipsigair 420  
 QY 421 INTQEYLDVLRPMVLGADKAKQVQNTNYYLDALGLVITGTLVPVFNITGFENKTNLK 480  
 Db 421 intqeyldvlgrpmvlgadkakvqntnnyldaleglvitgtlvpvfnitgfenktnlk 480  
 QY 481 NOLILGVMGVDVSLIEDIKELTPFTLCPNGYVFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540  
 Db 481 nqllilgvmgvdvsliedikeltprftlcpngyvfaidpnyvllhpnlpknpsqepvltl 540  
 QY 541 DFLDAELENDIKVEIRNKNMIDGESGEKFTLVKQSDERYIDKGNRTYTWTVPNGDYSL 600  
 Db 536 dfldaelendikveirnkndmidesgektfrtlvksqeryidkgnrtywtvpngtdysl 595  
 QY 601 ALVLPYFYFYIKAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYCNLDKI 660  
 Db 596 alvlpysfyiyikakleetitqarskkgkmdsetlkpdnfeesgytflaprdydcndlki 655  
 QY 661 SDNNTFEFLNPFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQNKIGVVAR 720  
 Db 656 sdnntefllnfnfnefidrktppnpscnadlinrvllldagftnelvqnywskqngkvkar 715



QY 901 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db |||||||  
 QY 961 SCITEQTYFFDNDKSFSGVLDGNGCSRIFFHGKLMNTNLIFFTWESKGCPCDTRL 1018  
 Db |||||||  
 QY 956 SCITEQTYFFDNDKSFSGVLDGNGCSRIFFHGKLMNTNLIFFTWESKGCPCDTRL 1013  
 Db |||||||

RESULT 9  
 AAB10587  
 ID AAB10587 standard; Protein; 1086 AA.  
 XX  
 AC AAB10587;  
 XX  
 DT 22-DEC-2000 (first entry)  
 XX  
 DE Human calcium channel alpha-2c subunit protein.  
 XX  
 KW Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2c.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US6096514-A.  
 PN  
 XX 01-AUG-2000.  
 PD  
 XX 25-MAY-1995; 95US-0450562.  
 XX  
 XX 04-APR-1988; 88US-0176899.  
 PR  
 XX 02-FEB-1990; 90US-0482384.  
 PR  
 XX 08-NOV-1990; 90US-0603751.  
 PR  
 XX 30-NOV-1990; 90US-0620250.  
 PR  
 XX 15-AUG-1991; 91US-0745206.  
 PR  
 XX 10-APR-1992; 92US-0868354.  
 PR  
 XX 13-JUL-1992; 92US-0914231.  
 PR  
 XX 11-AUG-1993; 93US-0105536.  
 PR  
 XX 05-NOV-1993; 93US-0149097.  
 PR  
 XX 07-FEB-1994; 94US-0193078.  
 PR  
 XX 04-APR-1994; 94US-0223305.  
 PR  
 XX 11-AUG-1994; 94US-0290012.  
 PR  
 XX 23-SEP-1994; 94US-0311363.  
 PR  
 XX 28-SEP-1994; 94US-0314083.  
 PR  
 XX 07-NOV-1994; 94US-0336257.  
 PR  
 XX 13-MAR-1995; 95US-0404950.  
 XX  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX  
 XX Ellis SB, Williams ME, McCue AF, Harpold MW;  
 PI N-PSDB; AAA71725.  
 XX  
 XX WPI; 2000-548230/50.  
 DR  
 XX N-PSDB; AAA71725.  
 XX  
 XX Human calcium channel beta subunit polynucleotides, useful for  
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
 PT Syndrome -  
 XX  
 XX Disclosure; Column 237-244; 153pp; English.  
 PS  
 XX  
 XX This invention describes a novel isolated DNA molecule (I) comprising a  
 CC sequence encoding a beta3-1 subunit of a human calcium channel.  
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
 CC beta3 subunit encoding DNA are useful for isolation and cloning of  
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 CC express heterologous calcium channel are useful for identifying compounds  
 CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit or eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2c subunit which is  
 CC described in the method of the invention.

SO Sequence 1086 AA;  
 Query Match 99.3%; Score 5306.5; DB 21; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1013; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
 QY 1 MAAGCLLALTLTFLQSLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGSNQNLVDI 60  
 Db |||||||  
 QY 1 MAAGCLLALTLTFLQSLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGSNQNLVDI 60  
 Db |||||||  
 QY 61 YEKYQDLYTVEPNNAARQLVEIAARDIEKLNSRKALVSLALEAEKVQAHQWEDFASN 120  
 Db |||||||  
 QY 61 YEKYQDLYTVEPNNAARQLVEIAARDIEKLNSRKALVSLALEAEKVQAHQWEDFASN 120  
 Db |||||||  
 QY 121 EVVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
 Db |||||||  
 QY 121 EVVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
 Db |||||||  
 QY 181 NELNWTSALEDEVFKKNEEDPSLLWQVFGSATGLARYYPASWPVDNSRTPNKIDLYDVR 240  
 Db |||||||  
 QY 181 NELNWTSALEDEVFKKNEEDPSLLWQVFGSATGLARYYPASWPVDNSRTPNKIDLYDVR 240  
 Db |||||||  
 QY 241 RPWYIQGAAPKMDLILVDYSGSVGLTLKLIRTSVSEMLETLDSDDFVNVASNSNAQD 300  
 Db |||||||  
 QY 241 RPWYIQGAAPKMDLILVDYSGSVGLTLKLIRTSVSEMLETLDSDDFVNVASNSNAQD 300  
 Db |||||||  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSFAFEQLLNVSRANCKIIML 360  
 Db |||||||  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGSFAFEQLLNVSRANCKIIML 360  
 Db |||||||  
 QY 361 FTDGGEERAQEIFNKYKDKKVRFRFSVGHNYERGPIONMACENKGYEIPISGAIR 420  
 Db |||||||  
 QY 361 FTDGGEERAQEIFNKYKDKKVRFRFSVGHNYERGPIONMACENKGYEIPISGAIR 420  
 Db |||||||  
 QY 421 INTOEYLDVLGRPMVLAGDKAKOVQWTVNLDLELGLVITGTLPVNTIGOFENKLNK 480  
 Db |||||||  
 QY 421 INTOEYLDVLGRPMVLAGDKAKOVQWTVNLDLELGLVITGTLPVNTIGOFENKLNK 480  
 Db |||||||  
 QY 481 NQLTLGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
 Db |||||||  
 QY 481 NQLTLGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
 Db |||||||  
 QY 541 DFLDAELENDIKVEIRNKMIDGSEKFTFLVKSQDERYIDKGNRTYTTPVNGTDSL 600  
 Db |||||||  
 QY 536 DFLDAELENDIKVEIRNKMIDGSEKFTFLVKSQDERYIDKGNRTYTTPVNGTDSL 595  
 Db |||||||  
 QY 601 ALVLPYTSFYIIRAKLEETITQARSKKGMKDSLETLPDNEFESGYTFIAPRDYCNLKI 660  
 Db |||||||  
 QY 596 ALVLPYTSFYIIRAKLEETITQARSKKGMKDSLETLPDNEFESGYTFIAPRDYCNLKI 655  
 Db |||||||  
 QY 661 SDNTEFLNFEFIDRKTNNPNSCNADLNRLVLDAGFTNELVQYWSKQNKIKGVKAR 720  
 Db |||||||  
 QY 656 SDNTEFLNFEFIDRKTNNPNSCNADLNRLVLDAGFTNELVQYWSKQNKIKGVKAR 715  
 Db |||||||  
 QY 721 FVYTDGGRITRVYKREAGENQENPETYEDSFYKSLDNDNYFTAPYFNKSGPGAYESGI 780  
 Db |||||||  
 QY 716 FVYTDGGRITRVYKREAGENQENPETYEDSFYKSLDNDNYFTAPYFNKSGPGAYESGI 775  
 Db |||||||  
 QY 781 MVSXKAVIYIYQGLLKPAAVVGKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840  
 Db |||||||  
 QY 776 MVSXKAVIYIYQGLLKPAAVVGKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 835  
 Db |||||||  
 QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRLHVNISVYAFNKSVDYQSVCEPAAAPKQ 900  
 Db |||||||  
 QY 836 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRLHVNISVYAFNKSVDYQSVCEPAAAPKQ 895  
 Db |||||||  
 QY 901 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db |||||||  
 QY 896 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 955  
 Db |||||||  
 QY 961 SCITEQTYFFDNDKSFSGVLDGNGCSRIFFHGKLMNTNLIFFTWESKGCPCDTRL 1018  
 Db |||||||



Db 956 sciteqtqyffndsksfsgvldcgnscsrfhgeklmtnlifimveskgtcpcdtrl 1013

RESULT 10  
AAR71015  
ID AAR71015 standard; Protein; 1084 AA.

AC AAR71015;  
XX  
DT 01-DEC-1995 (first entry)  
XX  
DE Human neuronal calcium channel subunit alpha 2e.  
XX  
KW Calcium channel subunit; antagonist; agonist; diagnosis;  
KW Lambert Eaton Syndrome.  
XX  
OS Homo sapiens.  
XX  
FN W09504822-A.  
XX  
PD 16-FEB-1995.  
XX  
XX 11-AUG-1994; 94WO-0609230.  
XX  
PF 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
XX  
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

XX Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;  
XX WPI; 1995-090900/12.  
DR N-PSDB; AAQ84669.  
XX  
XX DNA encoding human calcium channel sub-unit(s) - used for  
XX developing prods. for studying calcium channels, e.g. for  
XX obtaining agonists and antagonists  
XX  
XX Disclosure; Page 248-253; 285pp; English.  
XX  
XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
XX differentially processed in skeletal muscle, aorta, and CNS in  
XX the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
XX tissues. Five alternatively spliced variant transcripts that differ  
XX in the presence or absence of one to three different portions of  
XX this region. There are three sequences involved (see AAQ84664 FT  
XX and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
XX alpha 2 encoding transcripts from the different tissues include  
XX different combinations of the three sequences, except for one of  
XX the alpha 2 transcripts expressed in aorta which lacks all three  
XX sequences. The five alpha 2 forms identified are (1) a form that  
XX lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
XX (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
XX (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
XX aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
XX expressed in aorta and (5) one that lacks sequences 1 and 3  
XX called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
XX are set forth in AAQ84666-084669 and AAR71012-R71015 respectively.  
XX Sequence 1084 AA;

Query Match 98.9%; Score 5289.5; DB 16; Length 1084;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCILLALTTLFOSLILGPSSEPEPPSAVTIKSVDKMQEDLVTLAKTAGVGNOLYDI 60  
DB 1 maagcillaltlcfslilgpsseepfsvtiksvdkmqedlvtlaktasgvnqlvdi 60  
QY 61 YEKYQDLYTVEPNARQLVEAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120  
DB 61 yekyqdytvepnarqlveaardieklslsrskalvslaleaeqvaaqhwredfasn 120

QY 121 EVVYNAKDDLDPEKNDSEPSQSRIKPVFIETDANFGQISYQHAHVHPTDIYEGSTIVL 180  
DB 121 evvynakddldpekndsepsqsrirkpvfiedanfgqisyqhaavhptdiyegstivl 180  
QY 181 NELNWTSALEDEVEKKNREEDPSLIMQVFGSATGLARYYPASPWWVDSNRTPNKIDLYDVR 240  
DB 181 nelnwtosaldevfkknreedpsllwvfgsatglaryypaspwwvdsnrtpnkidlydvr 240  
QY 241 RPWYIOGAASPKDMLILVDVSGSVSGTLTKLIRTSVEMLETLSDDDFVNVASNSNAQD 300  
DB 241 rpywiggaaspkdmlilvdvsgsvsgitlklirtsvemletlsdddfvnvasnsnaqd 300  
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTDYKKGSEFAEQLNLYNVRANCKIIML 360  
DB 301 vscfghlvqanvrnkkvldkavnnitakgtdykkgsefafedqlnlynvrancnkiml 360  
QY 361 FTGGEERAQEIFNKYNKDKKRVFRFVSQGHNYERGIQWACENKGYIYEIPISGAIR 420  
DB 361 ftggeeraqeifnknkdkkrrvfrfsvqghnyerqipwmacenkgyiyeipisgaair 420  
QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPVFNITQCFENKTNLK 480  
DB 421 intqeyldvlgpmvlagdkakqvgwntnvyldalelgvltgtlvpfnitqcfenknlnk 480  
QY 481 NQLILGVMGVDSLEDIKRLTPREFTLCPNGYFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540  
DB 481 nqlilgvmgvdsledikrltpreflcpngyfaidpngyvvllhpnlpknkpsqepvtl 540  
QY 541 DFLDAELENDIKVEIRNMIDGESGKTFRTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
DB 541 dfldaelendikveirnmidgesgktrftlvksqderydkgntytwtpvngtdysl 600  
QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSFTLPDNFEESGYTFIAPRDYCNDLKI 660  
DB 601 alvlpysfyiykakleetitqary-----setlkpndfeesgytftiaprdocndlki 660  
QY 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720  
DB 661 sdntefllnfeefdirktpnpncnadlinrvlldagftnelvqnywskknkgvkar 720  
QY 721 FVVTDDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNTYFTAPYFNKSGPGAYESGI 780  
DB 721 fvtddggitrvypkeagenwqenpetyedsfykrsldndnyvftapyfnksgpgayesgi 780  
QY 781 MVSRAVEIYIOGKLLKPAVGIKIDVNSWIENFTKSTRDPCAGPCVDCCKNSVMDCVI 840  
DB 781 mvskavelyioqgkllkpavvikidvnswieftkstrdpcagpcvdccknsdvmdevi 840  
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900  
DB 841 lddggflmanhddytnoigrffgeidpslmrhlvniisvyafnksidyqsvcepgaapkq 900  
QY 901 GAGHRSAYVPSVADILQIGWATAAAMSILQOFLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
DB 901 gaghrsayvpsvadilqigwataaawsilqgflsltfprlleavemedddftaslskq 960  
QY 961 SCITEQTYQFPDNDKSPFSGVLDGNCNCSRFHGEKLMNTLIFIMVESKGTCPDTRL 1018  
DB 961 sciteqtqyffndsksfsgvldcgnscsrfhgeklmtnlifimveskgtcpcdtrl 1018  
DB 954 sciteqtqyffndsksfsgvldcgnscsrfhgeklmtnlifimveskgtcpcdtrl 1011

RESULT 11  
AAW63155  
ID AAW63155 standard; Protein; 1084 AA.  
XX  
AC AAW63155;  
XX  
DT 12-OCT-1998 (first entry)  
XX  
DE Human calcium channel alpha-2e subunit.  
XX  
KW Alpha-2 subunit; human; calcium channel; assay; detection;

characterisation; Lambert Eaton Syndrome; LES; diagnosis.

Homo sapiens.

US5792846-A.

11-AUG-1998.

31-MAY-1995; 95US-0455543.

04-APR-1994; 94US-0223305.

04-APR-1988; 88US-0176899.

04-APR-1989; 89US-0603751.

04-APR-1989; 89WO-0501408.

20-FEB-1990; 90US-0482384.

30-NOV-1990; 90US-0620250.

15-AUG-1991; 91US-0745206.

31-MAY-1995; 95US-0455543.

(SIBI-) SIBIA NEUROSCIENCES INC.

Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;

Williams ME;

WPI: 1998-456192/39.

N-PSDB; AAV42704.

DNA encoding human calcium channel alpha 1B subunit protein -

useful for recombinant production of the channel for screening of

its modulators, and diagnosis of Lambert Eaton Syndrome

Claim 3; Columns 305-310; 166pp; English.

The present sequence represents the alpha-2e subunit of a human calcium

channel. Calcium channels are membrane-spanning, multi-subunit proteins

that allow controlled entry of calcium ions into cells. This leads

to depolarisation events required for muscle contraction. The recombinant

subunit, when expressed with nucleic acids encoding the complete calcium

channel, can be used in assays for the detection and characterisation of

compounds that modulate the channel. The DNA encoding the subunits can

be alternatively spliced when transcribed, giving more than one form of

the protein from the same transcript, each having slightly different

properties. In addition, the reactivity of the alpha 1 subunit with IgG

molecules from the serum of an individual with Lambert Eaton Syndrome

(LES) can be used as a diagnostic for the disease.

Sequence 1084 AA;

Query Match 98.9%; Score 5289.5; DB 19; Length 1084;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCILLATLTLFQSLIGPSEPPFPFAVTKSWDKMQEDLVTLAKTAGVNLVDI 60

Db 1 maagcillaatlflgsligpseepfpfaavtkswdkmqedlvtlaktasvnglvd 60

QY 61 YEKYQDLYTVEPNNAOLVEIAARDTEKLSNRKALVSLALEAEKVQAAHQRDFASN 120

Db 61 yekyqdytvepnnarqlveiaardteklslsrkalvslaleaeakvqaahqrdfasn 120

QY 121 EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGRIQSYQHAAPHIPTDIYEGSTIVL 180

Db 121 evvynakddldpeknsepgsqrikpvfiedanfgriqsyqhaaphiptdiyegstivl 180

QY 181 NELNWTLSALDEVFKKNREDDPSLLNQVGSATGLARYTPASPWVNSRTPNPKIDLYDVR 240

Db 181 nelnwtlsaldevfkknreedpsllnwqfsgatglarytpaspwvnsrtpnknidlydvr 240

QY 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLSDDDFVNVASFNSNAQD 300

Db 241 rpwyiqgaaspkdmlilvdvsgsvsgltklirtsvsemletlsdldfnnvasfnnaqd 300

QY 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKITDYKKGFSAFEQLLNNVSRANCKIIML 360

Db 301 vscfqlhvqanvrnkkvylkdavnnitakitdykkgfsafeqllnynvarancnkiiiml 360

QY 361 FTGGGERAQEIENKYNKDKKRVFRFVSGQHNTERPIQWACENKGYIYEIPIGAI 420

Db 361 ftdggeeraqeiefnkynkdkkvrfrfsvsgqhnterpqiwmacenkgyyeipisigair 420

QY 421 INTQEYLDVLGRPMYLAGDKAKOVQWNTNVYLDALGLVITGTLPVFNITGQFENKTNLK 480

Db 421 intqeyldvlgrpmvlagdkakqvqwcenvyldaleglvltgtlplvfnitgqfenkcnlk 480

QY 481 NQLILGYMGVDVSLIEDIKRLTPRFTLCPCNGYIFAIDPNGYVLLHPNLQPNKPSQEPVTL 540

Db 481 nqlilgvmgvdvsledikrltpftlcpngyyifaidpngyvvllhpnlpknpsqepvtl 540

QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERIDKGNRTYTWTPVNGTDYSL 600

Db 541 dfldaeelendikveirnkmidgesgktrtlvksqderiydkgnrtytwtvpngtdysl 600

QY 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDMFEESGYTFIAPRDYCNDLKI 660

Db 601 alvlptysfyirakleetitqary-----setlkpdmfeesgytfiaprdycndiki 660

QY 661 SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNTWSKQNKIKGYKAR 720

Db 661 sdntefllnfnefidrktpnpnpscnadlinrvlldagftnelvqntwsqknikgykar 720

QY 721 FVYTDGGITRVYKPEAGENQENPEYEDSFYKRSLDNDNYFTAPYFNKSGGAYESGI 780

Db 721 fvytdggitrvykpeagenqenpetyedsfyrslndndnyftapyfnksggayesgi 780

QY 781 MVSQAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDPACAGVCDCKRNSDVMDCVI 840

Db 781 mvsqaveiyiqgllkpavvgikidvnswieftktsirpcagpvcddckrnsdvmdcvi 840

QY 841 LDGSGFLMANHDDYTNQIGRFFGEIDPISLMRHLVNIISYAFNKSXDYQVCEPFGAAPKQ 900

Db 841 ldgsgflmanhdytnqigrffgeidpslmrhlvnisvafnksydyqvccepfgaapq 900

QY 901 GAGHRAVYVPSVADIIQIGWATAAASLIQQLLSLTTPRLLAEVEMEDDDFTASLSKQ 960

Db 901 gaghravypsavadliqigwataaasliqqllsltprrlleavemedddftaslskq 960

QY 961 SCITEQTYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIIFIMVESKGTCPCDTRL 1018

Db 961 sciteqtyffndksfsfsgvldcgncsrifhgeklnmtnlifimveskgtcpcdtrl 1018

RESULT 12

AAB10589

ID AAB10589 standard; Protein; 1084 AA.

XX AAB10589;

XX 22-DEC-2000 (first entry)

XX Human calcium channel alpha-2e subunit protein.

XX Human; calcium channel; calcium channel subunit; diagnosis;

XX Lambert Eaton Syndrome; calcium channel subunit alpha-2e.

XX Homo sapiens.

XX US6096514-A.

XX 01-AUG-2000.

XX 25-MAY-1995; 95US-0450562.

XX 04-APR-1988; 88US-0176899.

XX 02-FEB-1990; 90US-0482384.

XX 08-NOV-1990; 90US-0603751.

PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 10-APR-1992; 92US-0868354.  
 PR 13-JUL-1992; 92US-0914231.  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 PR 07-FEB-1994; 94US-0193078.  
 PR 04-APR-1994; 94US-0223305.  
 PR 11-AUG-1994; 94US-0290012.  
 PR 23-SEP-1994; 94US-0311363.  
 PR 28-SEP-1994; 94US-0314083.  
 PR 07-NOV-1994; 94US-0336257.  
 PR 13-MAR-1995; 95US-0404950.  
 XX  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX  
 FI Ellis SB, Williams ME, McCue AF, Harpold MM;  
 XX  
 DR WPI; 2000-548230/50.  
 DR N-PSDB; RAA71727.  
 XX  
 PT Human calcium channel beta subunit polynucleotides, useful for  
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
 PT Syndrome.  
 XX  
 PS Disclosure; Column 253-260; 153pp; English.  
 XX  
 CC This invention describes a novel isolated DNA molecule (I) comprising a  
 CC sequence encoding a beta3-1 subunit of a human calcium channel.  
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
 CC beta-3 subunit encoding DNA are useful for isolation and cloning of  
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 CC express heterologous calcium channel are useful for identifying compounds  
 CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit or eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2e subunit which is  
 CC described in the method of the invention.  
 XX  
 SQ Sequence 1084 AA;  
 Query Match 98.9%; Score 5289.5; DB 21; Length 1084;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;  
 QY 1 MAAGCLLALTTLFQSLTIGPSSSEPPSPSAVTIKSWVDKMOEDLVTLAKTAGVGNQLYDI 60  
 DB 1 maagclaltltlfgsligpsseppfsavtikawvdkmqedltlaktasgvnqlvdi 60  
 QY 61 YEKYQDLTYTEPNNAQRLVEIAARDEIKLLNSRKALVSLALEAEKVQAAHQWRDFASN 120  
 DB 61 yekyqdltytepnnaqriveiaardiekllnsrkalsvslaleaeqvqaahqwrdfasn 120  
 QY 121 EVVYNNAKDDLPEKNDSEPSQRIKPFVIEDANGRISYQHAHVHPTDIYEGSTIVL 180  
 DB 121 evvyynakddlpeknsepsqrikpfviedangrisyqhaahvhtptdiyegstivl 180  
 QY 181 NELNWTSDALDEYFKKRNREDPSLLMQVFGSATGLARYYPASVPWDSNRTPNKKIDLYDVR 240  
 DB 181 nelnwtalsaldevfkknredpsllmqvfgsatglaryypasvpwdsnrtpnkkidlydvr 240  
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGGLTKLIRTSVSEMLEFTLSDDDDFNVASFNSNAQD 300  
 DB 241 rpwyiqgaaspkdmlilvdvsgvsggltklirtsvsemlfetlstdddfnvvasfnasnaqd 300  
 QY 301 VSCFOHLVQANVRNKKYLKDVANNITAKGIDYKKGFSFAPEQLLNYNVSRANCNKIIML 360  
 DB 301 vscfghlvqanvrnkylkdvannitakgidtykkgfsfafeqllnynvsrancnkilml 360  
 QY 361 FTDGGERAQEIFNKNYKDKKVRFRFVSQHNRYERGPIONMACENKGYIYEPSIGAIR 420  
 DB 361 ftdggeeraqeifnknynkdkkvrfrfvsqghnyergpionmacenkgyyielpsigaair 420

Db 361 ftdggeeraqeifnknynkdkkvrfrfvsqghnyergpionmacenkgyyielpsigaair 420  
 QY 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTVYLDALGLVITGTLPVENITGQFENKTNLK 480  
 Db 421 intqeyldvigrpmvlagdkakqvqwnvtyldaleglvigtltlpvniitgqfenktnlk 480  
 QY 481 NOLITGVMGVDVLEDIKRLTPRETLPNGYFFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540  
 Db 481 nolitgvmgvdvleedikrltprtlcpngyffaidpnyvllhpnlpknpkseqeptvl 540  
 QY 541 DFLDAELNDIKVEIRNMIDGESGETFTLVKSQDERYIDKGNRYITWTVPVNGTDSL 600  
 Db 541 dfldaelendikveirnmidgesgetftrlvksqderydkgnrtyitwtvpvngtdysl 600  
 QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSLETLPDNEESGYTFIARPDVCNDLKI 660  
 Db 601 alvlpysfyiykakleetitqary-----setlcpdneesgytffiardvcndlki 653  
 QY 661 SDNTEFLNFEIDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKOKNKGVKAR 720  
 Db 661 sdntefllnfnfidrktppnpscnadlinrvlldagftnelvqnywskknkgvkar 713  
 QY 721 FVWTDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780  
 Db 721 fvtddggitrvypkeagenwqenpetyedsfyrslndnnyvftapyfnksgpgayesgi 773  
 QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCCKNSDVMDCVI 840  
 Db 774 mvskaveiyiogkllkpaavgikidvnswieftktsirdpcagpvcdccknsdvmdcvi 833  
 QY 841 LDDGGFLIMANHHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900  
 Db 834 lddggflimanhddytngirffgeidpslmrhlvnisvafnksydyqsvcepgaapq 893  
 QY 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLSLTFPRLLLEAVENEDDDFTASLSKQ 960  
 Db 894 gaghsayvpsvadilqigwataaawsilqgflsltfprlleavenedddftaslskq 953  
 QY 961 SCITEQTOYFFDNDSKSPSGVLDGNCSCRIPIHGEKLMNTLIFIMVESKGTCPDTRL 1018  
 Db 954 sciteqtqyffdnksksfsgvldcncsrifhgeklnmtliffimveskgtcpcdtrl 1011  
 RESULT 13  
 RAR71012  
 ID AAR71012 standard; Protein; 1103 AA.  
 XX  
 AC AAR71012;  
 DF 01-DEC-1995 (first entry)  
 XX  
 DE Human neuronal calcium channel subunit alpha 2a.  
 XX  
 KW Calcium channel subunit; antagonist; agonist; diagnosis;  
 KW Lambert Eaton Syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9504822-A.  
 XX  
 PD 16-FEB-1995.  
 XX  
 PF 11-AUG-1994; 94WO-US09230.  
 XX  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 XX  
 PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 XX  
 PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
 XX  
 DR WPI; 1995-090900/12.  
 DR N-PSDB; AAQ84666.

XX DNA encoding human calcium channel sub-unit(s) - used for  
 PT developing prods. for studying calcium channels, e.g. for  
 PT obtaining agonists and antagonists

PS Disclosure; Page 231-236; 285pp; English.

XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
 CC differentially processed in skeletal muscle, aorta, and CNS in  
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
 CC tissues. Five alternatively spliced variant transcripts that differ  
 CC in the presence or absence of one to three different portions of  
 CC this region. There are three sequences involved (see AAQ84664 FT  
 CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
 CC alpha 2 encoding transcripts from the different tissues include  
 CC different combinations of the three sequences, except for one of  
 CC the alpha 2 transcripts expressed in aorta which lacks all three  
 CC sequences. The five alpha 2 forms identified are (1) a form that  
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
 CC expressed in aorta and (5) one that lacks sequences 1 and 3  
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
 CC are set forth in AAQ84666-Q84669 and AAR1012-R1015 respectively.

XX Sequence 1103 AA;

Query Match 98.6%; Score 5270; DB 16; Length 1103;

Best Local Similarity 97.4%; Pred. No. 0;

Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCILLALTILFQSLGIPSEEPFSAVITKSWDKMQEDLVTLAKTAGVGNOLVDI 60  
 DB 1 maagcillaaltliffqslgipseepfpaavtikswdkmqedlvltaktasyvnlvdi 60  
 QY 61 YEKYQDLVTEPNNAQVLEIARDIEKLKLSNRKALVLALEAEKVQAHOHREDFASN 120  
 DB 61 yekyqdlvtepnnaqlveiaardiekilnsrkalvslaleaeekvqaahwredfasn 120  
 QY 121 EVVYNAKDDLPKNDSPGSGRIKPVIEDANFGROISYQAAVHIPTDIYEGSTIVL 180  
 DB 121 evvynakddlpkndspgsgrikpviedanfgroisqyhaavhiptdiyegstivl 180  
 QY 181 NELNWTSAIDVFKKNEEDPSLLWQVFGSATGLARYYPASPVWDNSRTPNKKIDLYDVR 240  
 DB 181 nelnwtaldevfkknreedpsllwqvfgsatglaryypaspvwdnsrtpnkkidlydvr 240  
 QY 241 RPWYIQAASPKDMLILVDVSGVSGLTLLKLRITSVSEMLETSLDDDFVNVASFNSNAQD 300  
 DB 241 rpwyiqgaaspkdmlilvdvsgvsgltllkirtssemlletlsdddfvnvasfnsnaqd 300  
 QY 301 VSCFOHLVQANVRNKKVLDAVNNTAKGTDYKKGFSFAFEOPLLNVNVRANCNIIML 360  
 DB 301 vscfqlvqanvrnkvldavnntakgtdykkgfsfafepollnvnvrancnkilm 360  
 QY 361 FTDGGEERAQEIFNKYNDKVRFRFSVQGHNYERGPIQWACENKGYIYETPSIGAIR 420  
 DB 361 ftdggeeraqeifnkyndkvrfrfsvqghnyergpqlwacenkgyiypsigair 420  
 QY 421 INTQEYDLVGRPVLAGOKAQOVQNTVYLDALLEGVLITGTPVFNITGOFENKTNLK 480  
 DB 421 intqeydlvgrpmvlagkakqvntvyldalelgvlitgtlvpfnitgofenknk 480  
 QY 481 NOLILGVMGVDSLEDIKRLTFRFTLCPNGYFAIDPNGYVILLHPNLQPK----- 530  
 DB 481 nolilgvmgvdsledikrltfrftlcpngyfaidpngyvilhpnlpkpgvgvigtin 540  
 QY 531 -----NPKSQEPVTLDFDALELNDIKVEIRNKMIDGESGEKTFRTLVKSOQERYI 581  
 DB 541 lkrkrrpnqpkseqvptldfidaelndikveirnkmidgesgektftrtlvksqderyi 600

QY 582 DKGNRTYTWTPVNGTDYSALVLPTYSFYIKAKLEETITQARSKKGMKDSKPDNF 641  
 DB 601 dkgnrtytwtpvngtdysalvlptysfyikakleetitgar-----setlkpndf 653  
 QY 642 EESGYTFIAPRDYCNLKDSDNTEFLNENETDRTPNPNPCNADLINRVLLDAGFTN 701  
 DB 654 eesgytfiaprdycndlkisdntefllnnefdrktpnpscnadlinrvlldagftn 713  
 QY 702 ELYQNTWSKQNKIKGVKAREVVTGGITRYVPKEAGENWQENPETYEDSYKSLDNDNY 761  
 DB 714 elqnywskqknkigvkarfvtdggitrvyypkeagenwqenpetyedsfksldndny 773  
 QY 762 VFTAPFNKSGPCAYESGIMVSKAVELIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 821  
 DB 774 vftapyfngskpgayesgimvskavelylqgkllkpavvgikidvnswieenftktsirdp 833  
 QY 822 CAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMHLVNSVYA 881  
 DB 834 cagpvcdckrnsdvmcviiddggfllmanhddytnoigrffgeidpslmhlvnsvya 893  
 QY 882 FNKSYDQSYCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAASILQOFLSLTFPR 941  
 DB 894 fnksydyqsvcepgaapkgaghrrsayvpsvadilqigwwataaawilqfllstfpr 953  
 QY 942 LLEAVEMEDDDFTASLSKOSCITEQTYFPDNDKSKFSFVLDGCGNCSRIHPHGEKLMNTNL 1001  
 DB 954 lleavemedddftaslsksciteqtyffndndsksfvldcgcncsrifhgeklmntnl 1013  
 QY 1002 IFIMVESKGTCPGCDTRL 1018  
 DB 1014 ifimveskgtcpcdtrl 1030  
 RESULT 14  
 ID AAW63151 standard; Protein; 1103 AA.  
 XX AC AAW63151;  
 XX DT 12-OCT-1998 (first entry)  
 XX DE Human calcium channel alpha-2a subunit.  
 XX KW Alpha-2 subunit; human; calcium channel; assay; detection;  
 XX OS Homo sapiens.  
 XX PN US5792846-A.  
 XX PD 11-AUG-1998.  
 XX PF 31-MAY-1995; 95US-0455543.  
 XX PR 04-APR-1994; 94US-0223305.  
 XX PR 04-APR-1988; 88US-0176899.  
 XX PR 04-APR-1989; 89US-0603751.  
 XX PR 04-APR-1989; 89WO-US01408.  
 XX PR 20-FEB-1990; 90US-0482384.  
 XX PR 30-NOV-1990; 90US-0620250.  
 XX PR 15-AUG-1991; 91US-0745206.  
 XX PR 31-MAY-1995; 95US-0455543.  
 XX PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 XX PI Williams ME;  
 XX DR WPI; 1998-456192/39.  
 XX DR N-PSDB; AAV42700.  
 XX PT DNA encoding human calcium channel alpha 1B subunit protein -  
 XX PT useful for recombinant production of the channel for screening of

its modulators, and diagnosis of Lambert Eaton Syndrome  
Claim 3; Columns 287-294; 166pp; English.

The present sequence represents the alpha-2a subunit of a human calcium channel. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha 1 subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.

Sequence 1103 AA;

Query Match 98.6%; Score 5270; DB 19; Length 1103;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLTFLGSLIGPSSEPPFSAVTKSWDKMOEDLVTLAKTASGVNQLVDI 60  
DB 1 maagcllaltltflgsligpsseppfsavtikswdkmqedlvtlaktasgvnqlvdi 60  
QY 61 YEKYQDLYTVEPNNAQLVEIARIEKLLSNRSKALVSLALEAEKVQAQHWREDFASN 120  
DB 61 yekyqdytvepnnaqlveiaardiekllsnrskalvslaleaekvqaahqwedfasn 120  
QY 121 EVVYNAKDLDPKNDSPGSGQRKPVFIEDANGRQISYQHAHVHPTDIYEGSTIVL 180  
DB 121 evvynakddlpeknndspgsgqrkpvfiedanfrqisyqhaavhptdiyegstivl 180  
QY 181 NELNWTLSALDEVFKKREDEPSLLMQVFGSATGLARYYPASPWVDNRRTPNKIDLYDVR 240  
DB 181 nelnwtsaldevfkkredepssllmqvfgsatglaryypaspwvdnrrtpnkidlydvrr 240  
QY 241 RPWYIGGAASPKDMLILVDVSGVSLTLKILRTSYSEMLETLSDDDFYNVASFNSNAQD 300  
DB 241 rpwyiggaaspkdmlilvdvsgvsgltklilrtsysemletlsdddfynvasfnsgnqd 300  
QY 301 VSCFQHLVQANVRNKKVLKDVANNITAKITDYKGFSAFQQLNLYNVSRANCNKIIML 360  
DB 301 vscfghlvqanvrnkkvlkdavnnitakitdykgyfsafqqlnlynvsnrncnkilm 360  
QY 361 FTDGGEARQAEIFNKYKDKKVRVFRFSVQHNRYERGPIQWACENKGYEYIPTSIGAIR 420  
DB 361 ftdggearaeifnkykdkkvrfrfsvqhnryergpiqwmacenkgyyeipsgair 420  
QY 421 INTQEYLDVLRPMVLGAKAKQVQNTVYLDALGLVITGTPVFNITGQFENKTNLK 480  
DB 421 intqeyldvlrpmvlgakakqvqntvnyldaleglvitgtplvfnitgqfenktnlk 480  
QY 481 NQILGVMGVDVSLDIKRLTPRTLCPCNGYFAIDPNGYVLLHPNLQPK-----530  
DB 481 nqilgvmgvdsleldikrltprtlpcngyfaidpngyvllhpnlpk-----530  
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERVI 581  
DB 541 lrkrpniqnksqepvtldfdaelendikveirnmkidgesgektftrtlvksqderyi 600  
QY 582 DKGNNRYTTPVNGTDYSLALVLPYTSFYIYAKLEETITOARSKKGMKDSSETLKPQDNF 641  
DB 601 dkgnrtytvpngtdyslalvlpysfyiyakleetitqary-----setlkdndf 653  
QY 642 EESGYTFIAPRDYCNLDKISDNNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTN 701  
DB 654 eesgytfiaprdydcndlkisdnnnteflnfneidrktnpnpscnadlinrvlldagftn 713  
QY 702 ELVQYWSKQKNIKVKARVTVTDGGITRVYPKEAGENQENPETYEDSFYKSLDNQY 761

DB 714 ELVQYWSKQKNIKVKARVTVTDGGITRVYPKEAGENQENPETYEDSFYKSLDNQY 773  
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 821  
DB 774 vftapyfnksgpgayesgimvskaveilyioqkllkpvavvgikidvnswnlenfkttsird 833  
QY 822 CAGPYCDCKRNSDVNDCVILDDGFLMANHDDYTNQIGRFFGEIDPSSLRHLVNIISVYA 881  
DB 834 cagpycdckrnsdvndcvilddggflmanhddytngqgrffgeidpslmlrlhvnisvya 893  
QY 882 FNKSYDYOSVCEPGAAPKOGAGHRSAYVPSVADIIQIGWATAAAMSIIQQFLLSLTFPR 941  
DB 894 fnksydyosvcepgaapkgaghrsayvpsvadilqigwwataaawslilqgllsltfpr 953  
QY 942 LLEAVEMEDDDFTASLSKSCITEQTEQYFFEDNDKSFSGVLDCGNCSTRIFHGEKLMNTNL 1001  
DB 954 lleavemedddftaslsksciteqteqyffndndksfsgvlcgcncsrifhgeklmntnl 1013  
QY 1002 IFIMVESKGTCPDTRL 1018  
DB 1014 ifimveskgtcpdtrl 1030  
RESULT 15  
AAB10586  
ID AAB10586 standard; Protein; 1103 AA.  
XX AC AAB10586;  
XX DT 22-DEC-2000 (first entry)  
XX DE Human calcium channel alpha-2a subunit protein.  
XX KW Human; calcium channel; calcium channel subunit; diagnosis; Lambert Eaton Syndrome; calcium channel subunit alpha-2a.  
XX OS Homo sapiens.  
XX PN US6096514-A.  
XX PD 01-AUG-2000.  
XX PF 25-MAY-1995; 95US-0450562.  
XX PR 04-APR-1988; 88US-0176899.  
XX PR 02-FEB-1990; 90US-0482384.  
XX PR 08-NOV-1990; 90US-0603751.  
XX PR 30-NOV-1990; 90US-0620250.  
XX PR 15-AUG-1991; 91US-0745206.  
XX PR 10-APR-1992; 92US-0868354.  
XX PR 13-JUL-1992; 92US-0914231.  
XX PR 11-AUG-1993; 93US-0105536.  
XX PR 05-NOV-1993; 93US-0149097.  
XX PR 07-FEB-1994; 94US-0193078.  
XX PR 04-APR-1994; 94US-0223305.  
XX PR 11-AUG-1994; 94US-0290012.  
XX PR 23-SEP-1994; 94US-0311363.  
XX PR 28-SEP-1994; 94US-0314083.  
XX PR 07-NOV-1994; 94US-0336257.  
XX PR 13-MAR-1995; 95US-0404950.  
XX PA (SIBI-) SIBIA NEUROSCIENCES INC.  
XX PI Ellis SB, Williams ME, McCue AF, Harpold MM;  
XX DR WPI: 2000-548230/50.  
XX DR N-PSDB; AAA71724.  
XX PT Human calcium channel beta subunit polynucleotides, useful for producing recombinant eukaryotic cells and for diagnosing Lambert Eaton Syndrome

PS Disclosure; Column 229-236; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a  
CC sequence encoding a beta3-1 subunit of a human calcium channel.  
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
CC beta3 subunit encoding DNA are useful for isolation and cloning of  
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
CC express heterologous calcium channel and in assays for identifying compounds  
CC that modulate calcium channel activity and in assays for identifying  
CC agonists and antagonists of calcium channel activity in humans. Human  
CC calcium channel subunit or eukaryotic cells expressing the channel are  
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
CC sequence represents the human calcium channel alpha-2a subunit which is  
CC described in the method of the invention.

XX Sequence 1103 AA;

Query Match 98.6%; Score 5270; DB 21; Length 1103;

Best Local Similarity 97.4%; Pred. No. 0;

Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY	1	MAAGCLLALTTLFQSLIGPSEEPFSAVTKSWDKMQEDLVTLAKTAGVNOLVDI	60
Db	1	maagcllaltltlfgsligpseepfpsavtikswdkmqedlvtlaktasgvnlvdi	60
QY	61	YEKYQDLYTVEPNNAQOLVEIAARDIEKLNSRKALVSLALEAEKVAQAHHOWREDFASN	120
Db	61	yekyqdltyvepnnaarqlveiaardieklnsrkalvslaleaeakvqaahqwredfasn	120
QY	121	EVVYVNAKDDLDPEKNDSPGQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL	180
Db	121	evvyvnaakddlpeknndsepgsqrikpviedanfgrqisyqhaavhiptdiyegstivl	180
QY	181	NELNWTSSALDEVFKNREDDPSLLWQVFGSAGTLARYYPASPMVDNSRTPNKTIDLYDVR	240
Db	181	nelnwtssaldevfknreedpsllwqvfgsagtlaryypaspmvdnsrtpnktidlydvrr	240
QY	241	RPWYIGGAASPKDMLILVDVSGSVSLTKLIRTSVSEMLETLSDDDFVNVASFNSNAQD	300
Db	241	rpywiggaaspkdmliilvdvsgsvsgltklirtsvsemletlsdddffnvvasfnnaqd	300
QY	301	VSCFQHLVQANVRNKKVLDAVNNITAKITDYKGFSAFAPQOLLNYSRANCNKIIML	360
Db	301	vscfqlhvdanvrnkkvlkdvannitakitdykgsfafefagfqlnynvsrancnkilm	360
QY	361	FTDGGEEAQAEIFNKYNKDKVVRPFVSQHNRYERGPIQWACENKGYEYIEPSIGAIR	420
Db	361	fdgggeeraqeifnknkdkvvrpfvsqhnryergpiqwmacenkgyyeiepsigair	420
QY	421	INTQEYLDVLRPMVLGADKAKQVQNTVYLDALGLVITGTLPVFNITGOFENKTNLK	480
Db	421	intqeyldvlgprmvlagdakqgvntvyldaleglvitgtlpvfnitgofenktnlk	480
QY	481	NQLIGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNCYVLLHPNLQPK-----530	
Db	481	nqliigvmgvdvsledikrltpftlcpngyyfaidpncyvllhpnlpkpgvgvptin	540
QY	531	-----NPKSOEPTVTLDELDAELENDIKVEIRNKMIDGESGEKTFRTLKSDQERYI	581
Db	541	lkrkrpnlgnpksgqepvtldfdaelendikveirnkmidgesgektftrlvksqderyi	600
QY	582	DKGNRTYTWTPVNGDYSIALVLPYTSFYIIRAKLEETITQARSKKGMKDSSETLKPDNF	641
Db	601	dkgnrttytwtpvngtdysialvlpysfyiakleetitqary-----setlkpdnf	653
QY	642	EESGYTFIAPROYCNLDKISDNNTPELLNFIEDIRKTPNPNSCNADLINRVLLDAGFTN	701
Db	654	eesgytfiaprdycndlkisdntefilnfefidrktpnpnscnadlinrvllldagftn	713
QY	702	ELVONTWSKQNKIKGVKARFVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY	761
Db	714	elvqnywskqknkigvkarfvvtddggitrvypkeagenqenpetyedsfykrslndndy	773

QY	762	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRD	821
Db	774	vftapyfnksgpgayesgimvskaveiyiqgkllkpavvgikidvnswieenftktsird	833
QY	822	CAGPVCDCCKRNSDVMDCVILLDDGGFTLLMANHDDYTNOIGRFFGCEIDPSSLMRHLVNI	881
Db	834	cagpvcddckrnsdvmcvcvllddggfllmanhddytngigrfgceidpslmrhlvnisvya	893
QY	882	FNKSYDYQSVCEPGAAPKOGACGHRSAVPSVADILQIGWATAAAWSILQQFLLSLTFPR	941
Db	894	fnksydyqsvcepgaapkgaghrsayvpsvadilqigwataaawsilqqfllsltfpr	953
QY	942	LLEAVEMEDDDFTASLSKOSCITEQYQYFDDNDSKSFSGVLDGCGNCSRFHGEKLMNTNL	1001
Db	954	lleavemedddftaslsksciteqyqyffddndsksfsgvldcgncsrifhgeklmntnl	1013
QY	1002	IFIMVESKGTGCPDTRL	1018
Db	1014	ifimveskgtcpodtrl	1030

Search completed: July 23, 2001, 07:36:25  
Job time: 466 sec

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QY 61 YEKYODLTVBPNARQLVEAARDIEKLSNRKALVSLALEAEKVAQAHHQWREDFASN 120  
DB 61 YEKYODLTVBPNARQLVEAARDIEKLSNRKALVSLALEAEKVAQAHHQWREDFASN 120  
QY 121 EYVYNKADDDPEKNDSEPSQRIKPVFIEDANFGROISQHAHVHPTDIYEGSIYL 180  
DB 121 EYVYNKADDDPEKNDSEPSQRIKPVFIEDANFGROISQHAHVHPTDIYEGSIYL 180  
QY 181 NELNWTSSALDEVFKNREDDPSLLMOVFGSGTLGARYYPASPDWVNSRTPNKIDLYDVR 240  
DB 181 NELNWTSSALDEVFKNREDDPSLLMOVFGSGTLGARYYPASPDWVNSRTPNKIDLYDVR 240  
QY 241 RPWYIQAASPKDMLILYDVSGVSGTLKLIIRTSVSEMLETLSDDDDFVNVASFNSNAQD 300  
DB 241 RPWYIQAASPKDMLILYDVSGVSGTLKLIIRTSVSEMLETLSDDDDFVNVASFNSNAQD 300  
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCKIIML 360  
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCKIIML 360  
QY 361 FTDGGEERAQEIFNKYNDKKVRFVRSVGOHNYERGPIOMACENKGYEIPISGAIR 420  
DB 361 FTDGGEERAQEIFNKYNDKKVRFVRSVGOHNYERGPIOMACENKGYEIPISGAIR 420  
QY 421 INTQYLDVLRPMVLAGDKAQVQWTVNYLDALGLVITGTLVPVFNITQGFENKTNLK 480  
DB 421 INTQYLDVLRPMVLAGDKAQVQWTVNYLDALGLVITGTLVPVFNITQGFENKTNLK 480  
QY 481 NOLILGVNGVDVSLIEDIRLTPRETLCPNGYFAIDPNGYVLLHPNLPKPKSOEPTVL 540  
DB 481 NOLILGVNGVDVSLIEDIRLTPRETLCPNGYFAIDPNGYVLLHPNLPKPKSOEPTVL 540  
QY 541 DFLDALENDIKVEIRNMIDGSEKFTRLVKQSDERYIDKGNRTYTWTPVNGTDYSL 600  
DB 541 DFLDALENDIKVEIRNMIDGSEKFTRLVKQSDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIYKALEETITQARSKKGMKDSFELKPDNFEESGYTFIAPRDYCNLDKI 660  
DB 601 ALVLPYTFYIYKALEETITQARSKKGMKDSFELKPDNFEESGYTFIAPRDYCNLDKI 660  
QY 661 SONTEFLNFEETDRTPNPNPCNADLINRVLLDAGFTNELVQVNSKOKNKGVAR 720  
DB 661 SONTEFLNFEETDRTPNPNPCNADLINRVLLDAGFTNELVQVNSKOKNKGVAR 720  
QY 721 FVYTDGGITRVYKPEAGENWQENPTYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780  
DB 721 FVYTDGGITRVYKPEAGENWQENPTYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPGAGVPCDKRNSDVMDCVI 840  
DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPGAGVPCDKRNSDVMDCVI 840  
QY 841 LDGGLFLLMANHDDYTNQIGRFGGIDPSLMRHLNIVSYAFNKSVDYQSVCEPAAKPK 900  
DB 841 LDGGLFLLMANHDDYTNQIGRFGGIDPSLMRHLNIVSYAFNKSVDYQSVCEPAAKPK 900  
QY 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLFPRLLEAVENEDDDFTASLSQK 960  
DB 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLFPRLLEAVENEDDDFTASLSQK 960  
QY 961 SCITEQTYFFNDKSKFSGVLDGNCNCRIFHGEKLMNTNLIIFIMVESKGTGCPDTRL 1018  
DB 961 SCITEQTYFFNDKSKFSGVLDGNCNCRIFHGEKLMNTNLIIFIMVESKGTGCPDTRL 1018

RESULT 2

US-08-455-543A-52  
; Sequence 52, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; Ellis, Steven

APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-52

Query Match 100.0%; Score 5346; DB 1; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLTIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVGNQYDI 60  
DB 1 MAAGCLLALTTLTFLQSLTIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVGNQYDI 60  
QY 61 YEKYODLTVBPNARQLVEAARDIEKLSNRKALVSLALEAEKVAQAHHQWREDFASN 120

Db	61	YKYO	DLTY	EP	NARQ	LV	ET	AA	RD	IE	KL	SN	KS	KALV	SLLA	EA	EKV	QA	HW	RE	FA	SN	120	
Qy	121	EV	YNA	KD	LD	PK	ND	SE	PG	SQ	RI	K	P	V	F	E	D	A	N	F	G	R	Q	180
Db	121	EV	YNA	KD	LD	PK	ND	SE	PG	SQ	RI	K	P	V	F	E	D	A	N	F	G	R	Q	180
Qy	181	NEL	NWT	SAL	D	VF	V	K	K	NE	E	D	P	S	L	L	Q	V	G	S	A	T	GL	240
Db	181	NEL	NWT	SAL	D	VF	V	K	K	NE	E	D	P	S	L	L	Q	V	G	S	A	T	GL	240
Qy	241	RP	W	I	Q	G	A	S	P	K	M	L	I	V	D	S	G	S	G	L	T	L	I	300
Db	241	RP	W	I	Q	G	A	S	P	K	M	L	I	V	D	S	G	S	G	L	T	L	I	300
Qy	301	V	S	C	F	H	L	V	Q	A	N	R	N	K	K	V	L	K	D	A	V	N	I	360
Db	301	V	S	C	F	H	L	V	Q	A	N	R	N	K	K	V	L	K	D	A	V	N	I	360
Qy	361	F	T	D	G	E	R	A	E	I	E	N	K	N	K	K	V	F	R	F	S	V	G	420
Db	361	F	T	D	G	E	R	A	E	I	E	N	K	N	K	K	V	F	R	F	S	V	G	420
Qy	421	I	N	T	O	E	Y	L	D	L	G	R	P	M	V	L	A	G	R	A	K	O	V	480
Db	421	I	N	T	O	E	Y	L	D	L	G	R	P	M	V	L	A	G	R	A	K	O	V	480
Qy	481	N	O	L	I	L	G	V	M	G	V	D	S	L	E	I	K	R	L	T	P	R	T	540
Db	481	N	O	L	I	L	G	V	M	G	V	D	S	L	E	I	K	R	L	T	P	R	T	540
Qy	541	D	F	L	D	A	E	L	E	N	D	I	K	V	E	I	R	N	K	M	I	D	G	600
Db	541	D	F	L	D	A	E	L	E	N	D	I	K	V	E	I	R	N	K	M	I	D	G	600
Qy	601	A	L	V	L	P	T	S	F	F	Y	I	K	A	L	E	E	T	I	Q	A	R	S	660
Db	601	A	L	V	L	P	T	S	F	F	Y	I	K	A	L	E	E	T	I	Q	A	R	S	660
Qy	661	S	D	N	T	E	F	L	N	F	E	I	D	R	K	T	P	N	P	S	C	N	A	720
Db	661	S	D	N	T	E	F	L	N	F	E	I	D	R	K	T	P	N	P	S	C	N	A	720
Qy	721	F	V	T	D	G	I	T	R	V	P	K	E	A	G	E	N	K	O	E	N	P	E	780
Db	721	F	V	T	D	G	I	T	R	V	P	K	E	A	G	E	N	K	O	E	N	P	E	780
Qy	781	M	S	K	A	V	E	I	I	Q	G	L	L	K	P	A	V	G	I	D	V	N	S	840
Db	781	M	S	K	A	V	E	I	I	Q	G	L	L	K	P	A	V	G	I	D	V	N	S	840
Qy	841	L	D	D	G	F	L	L	M	A	N	H	D	D	T	N	O	I	G	R	F	F	E	900
Db	841	L	D	D	G	F	L	L	M	A	N	H	D	D	T	N	O	I	G	R	F	F	E	900
Qy	901	G	A	G	H	R	S	A	Y	P	S	V	A	D	I	L	I	Q	I	G	W	A	T	960
Db	901	G	A	G	H	R	S	A	Y	P	S	V	A	D	I	L	I	Q	I	G	W	A	T	960
Qy	961	S	C	I	T	E	O	T	O</															

APPLICANT: McCue, Ann  
 APPLICANT: Brenner, Robert  
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1650 Union Street  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/223.305C  
 FILING DATE: April 4, 1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/868,354  
 FILING DATE: April 10, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/745,206  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/620,250  
 FILING DATE: 30-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/482,384  
 FILING DATE: 20-FEB-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/603,751  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US89/01408  
 FILING DATE: 04-APR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/176,899  
 FILING DATE: 04-APR-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 52516 (P519739)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)238-0999  
 TELEFAX: (619)238-0062  
 INFORMATION FOR SEQ ID NO: 52:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1091 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-223-305C-52

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Query Match      100.0%; Score 5346; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Qy	1	MAACCLALALITLTFQSLIGSSEEPSPS	AVTTKSWVDKMQEDLVTLAKTASGV	NDVI	60
Db	1	MAACCLALALITLTFQSLIGSSEEPSPS	AVTTKSWVDKMQEDLVTLAKTASGV	NDVI	60
Qy	61	YEQDLYTYEPNNARQLVIAARDTEKLS	NKSALVSLAEAKVQAAHQWREDFAS	N	120
Db	61	YEQDLYTYEPNNARQLVIAARDTEKLS	NKSALVSLAEAKVQAAHQWREDFAS	N	120
Qy	121	EVVYNAKDDLDPKNDSEPGSQRIPVFT	EDANFGRQISYCHAAVHIPTDIYEG	STYL	180

RESULT 3  
US-08-2233-30SC-52  
; Sequence 52, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel

Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIHQAAVHIPTDIYEGSTIVL 180  
Qy 181 NELNWTSSALDEVEFKKNEEDSLWQVFGSATGLARYYPASPWVDSNTPNKIDLYDVR 240  
Db 181 NELNWTSSALDEVEFKKNEEDSLWQVFGSATGLARYYPASPWVDSNTPNKIDLYDVR 240  
Qy 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLIKRTSVSEMLETSLDDDFVNVASFNNAQD 300  
Db 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLIKRTSVSEMLETSLDDDFVNVASFNNAQD 300  
Qy 301 VSCFQHLVQANVRNKKVUKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVUKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360  
Qy 361 FTDGGEERAQAEIFNKYNKDKKVRFRFVSGQHNRYERGIQWACENKGYEIPISGAIR 420  
Db 361 FTDGGEERAQAEIFNKYNKDKKVRFRFVSGQHNRYERGIQWACENKGYEIPISGAIR 420  
Qy 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKTNL 480  
Db 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKTNL 480  
Qy 481 NOLILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
Db 481 NOLILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
Qy 541 DFLDALENDIKVEIRNKMIDGESKFTFLVKSQDRIYDKGNRTYTWTVPNGTDYSL 600  
Db 541 DFLDALENDIKVEIRNKMIDGESKFTFLVKSQDRIYDKGNRTYTWTVPNGTDYSL 600  
Qy 601 ALVLPYTFYIKAKLETITQARSKKMKMDSEYLPKPDNFEESGYTFIAPRDCNDLKI 660  
Db 601 ALVLPYTFYIKAKLETITQARSKKMKMDSEYLPKPDNFEESGYTFIAPRDCNDLKI 660  
Qy 661 SDNTEFLNFEIDRTPNPNNSCNADLNRLVLDAGFTNELVQYWSKQKNKGVKAR 720  
Db 661 SDNTEFLNFEIDRTPNPNNSCNADLNRLVLDAGFTNELVQYWSKQKNKGVKAR 720  
Qy 721 FVVTGGITRVYPRKAGENQWENPTYEDSYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780  
Db 721 FVVTGGITRVYPRKAGENQWENPTYEDSYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780  
Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDCAGVPCCKNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDCAGVPCCKNSDVMDCVI 840  
Qy 841 LDGQFLMANHDDYTNQIGRFFGIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDGQFLMANHDDYTNQIGRFFGIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
Qy 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTPRLLLEAVEMDDDFASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTPRLLLEAVEMDDDFASLSKQ 960  
Qy 961 SCITETQYFFONDKSFSGVLDGNCNCRIFHGEKLMNTNIFIMVESKGCPCDTRL 1018  
Db 961 SCITETQYFFONDKSFSGVLDGNCNCRIFHGEKLMNTNIFIMVESKGCPCDTRL 1018

RESULT 4

US-08-311-363-25  
; Sequence 25, Application US/08311363  
; Patent No. 5876958  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: Human Calcium Channel Compositions and  
; METHODS  
; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311.363  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-51506  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-311-363-25

Query Match 100.0%; Score 5346; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTITLQSLIGPSSSEPPFSVATIKSWDKMQEDLVTLAKTAGVNLVDI 60  
Db 1 MAAGCLLALTITLQSLIGPSSSEPPFSVATIKSWDKMQEDLVTLAKTAGVNLVDI 60  
Qy 61 YEKQDLYTVEPNARQLVEIARADIEKLLSNRSKALVSLAEAEKQAAHQRREDFASN 120  
Db 61 YEKQDLYTVEPNARQLVEIARADIEKLLSNRSKALVSLAEAEKQAAHQRREDFASN 120  
Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIHQAAVHIPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIHQAAVHIPTDIYEGSTIVL 180  
Qy 181 NELNWTSSALDEVEFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNTPNKIDLYDVR 240  
Db 181 NELNWTSSALDEVEFKKNEEDPSLLWQVFGSATGLARYYPASPWVDSNTPNKIDLYDVR 240  
Qy 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLIKRTSVSEMLETSLDDDFVNVASFNNAQD 300  
Db 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLIKRTSVSEMLETSLDDDFVNVASFNNAQD 300  
Qy 301 VSCFQHLVQANVRNKKVUKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVUKDAVNNTAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360  
Qy 361 FTDGGEERAQAEIFNKYNKDKKVRFRFVSGQHNRYERGIQWACENKGYEIPISGAIR 420  
Db 361 FTDGGEERAQAEIFNKYNKDKKVRFRFVSGQHNRYERGIQWACENKGYEIPISGAIR 420  
Qy 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKTNL 480  
Db 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKTNL 480  
Qy 481 NOLILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
Db 481 NOLILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540

541 DFLDAELNDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660  
QY 661 SDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKVYKAR 720  
Db 661 SDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKVYKAR 720  
QY 721 FVYTDGGITRVYKKEAGENQWENPETEYDSFYKRSIDNDNYVETAFYFNKSGPAYESGI 780  
Db 721 FVYTDGGITRVYKKEAGENQWENPETEYDSFYKRSIDNDNYVETAFYFNKSGPAYESGI 780  
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840  
QY 841 LDGGFLLMANHDDYTNQIGRFEGEIDPSLMRHLVNI SYAFNKSVDYOSVCEPGAAPKQ 900  
Db 841 LDGGFLLMANHDDYTNQIGRFEGEIDPSLMRHLVNI SYAFNKSVDYOSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAAWSILQOFLSLTTPRLLAEVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAAWSILQOFLSLTTPRLLAEVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTOYFFNDNDSKFSFGLDCGNCRSIFHGEKLMNTNLFIMVESKGTCTCDTRL 1018  
Db 961 SCITEQTOYFFNDNDSKFSFGLDCGNCRSIFHGEKLMNTNLFIMVESKGTCTCDTRL 1018

## RESULT 5

US-08-713-118-4  
; Sequence 4, Application US/08713118  
; Patent No. 6040436  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suey, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713.118  
; FILING DATE: 16-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

## ; MOLECULE TYPE: protein

US-08-713-118-4

Query Match 99.9%; Score 5342; DB 3; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCCLALTLTQLFOSLLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCCLALTLTQLFOSLLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYODLYTEPNNAQOLVEIARADIEKLKLSNRSKALVSLAEAEKVQAAHQREDPASN 120  
Db 61 YEKYODLYTEPNNAQOLVEIARADIEKLKLSNRSKALVSLAEAEKVQAAHQREDPASN 120  
QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFRQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFRQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSAIDVEFKKNEEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
Db 181 NELNWTSAIDVEFKKNEEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
QY 241 RPYIIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPYIIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETSLDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVNKKVLDKAVNNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360  
Db 301 VSCFQHLVQANVNKKVLDKAVNNITAKGTDYKKGFSFAFQOLLNYSRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKYKNDKKVRFVRSVQGHNYERGIOMMACENKNGYYEIPSGAIR 420  
Db 361 FTDGGEERAQEIFNKYKNDKKVRFVRSVQGHNYERGIOMMACENKNGYYEIPSGAIR 420  
QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGTLPVFNITGQENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGTLPVFNITGQENKTNLK 480  
QY 481 NQLILGVMGVDSLEDIKRLTPRTILCPNGYYPADIPNGYVLLHPLNLPKNPKSQBPVTL 540  
Db 481 NQLILGVMGVDSLEDIKRLTPRTILCPNGYYPADIPNGYVLLHPLNLPKNPKSQBPVTL 540  
QY 541 DFLDAELNDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIIKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFIAPRDYCNLDKI 660  
QY 661 SDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKVYKAR 720  
Db 661 SDNNTFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKVYKAR 720  
QY 721 FVYTDGGITRVYKKEAGENQWENPETEYDSFYKRSIDNDNYVETAFYFNKSGPAYESGI 780  
Db 721 FVYTDGGITRVYKKEAGENQWENPETEYDSFYKRSIDNDNYVETAFYFNKSGPAYESGI 780  
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPACAGPYCDCKRNSDVMDCVI 840  
QY 841 LDGGFLLMANHDDYTNQIGRFEGEIDPSLMRHLVNI SYAFNKSVDYOSVCEPGAAPKQ 900  
Db 841 LDGGFLLMANHDDYTNQIGRFEGEIDPSLMRHLVNI SYAFNKSVDYOSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAAWSILQOFLSLTTPRLLAEVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAAWSILQOFLSLTTPRLLAEVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTOYFFNDNDSKFSFGLDCGNCRSIFHGEKLMNTNLFIMVESKGTCTCDTRL 1018

Db 961 SCITEQYFFDNDKSFSGVLDGNCNRSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018

RESULT 6  
US-09-452-007-4  
; Sequence 4, Application US/09452007  
; Patent No. 6140485  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suet, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/452.007  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713.118  
; FILING DATE: 16-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-452-007-4

Query Match 99.9%; Score 5342; DB 4; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1017; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTTLFSLIGLSPSSSEPPFSATYIKSWDKMQEDLVTLAKTAGVYNQLVDI 60  
DB 1 MAAGCLLALTTLFSLIGLSPSSSEPPFSATYIKSWDKMQEDLVTLAKTAGVYNQLVDI 60  
QY 61 YKYQDLYTVEPNNAQLVETAAARIEKLLNSRKALYSALAEKVOAAHQWREDFASN 120  
DB 61 YKYQDLYTVEPNNAQLVETAAARIEKLLNSRKALYSALAEKVOAAHQWREDFASN 120  
QY 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180  
DB 121 EYVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTALDEVFKKNREDEPSLLMQVFGSATGLARYYPASFPWDNSTRTPNKIDLYDVR 240  
DB 181 NELNWTALDEVFKKNREDEPSLLMQVFGSATGLARYYPASFPWDNSTRTPNKIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
DB 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300

QY 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKGITYDKKGSFAFEQLLNYNVSRANCKIIML 360  
DB 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKGITYDKKGSFAFEQLLNYNVSRANCKIIML 360  
QY 361 FTGGERAQEIEFNKYNKDKKRVFRFESVGOHNYERGIQWMACENKGYIYFISGAIR 420  
DB 361 FTGGERAQEIEFNKYNKDKKRVFRFESVGOHNYERGIQWMACENKGYIYFISGAIR 420  
QY 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNVLDALEGLVITGTLVPFNITGQFENKLNK 480  
DB 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNVLDALEGLVITGTLVPFNITGQFENKLNK 480  
QY 481 NQLILGVMGVDVSLDIKRLTPRETLCPNGYIFAIIDNGVYLLHPNLPKNPKSQEPVTL 540  
DB 481 NQLILGVMGVDVSLDIKRLTPRETLCPNGYIFAIIDNGVYLLHPNLPKNPKSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
DB 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYSFYIYKAKLEETITQARSKGKMKDSTLKPDPNFEESGYTFIAPRDYCNDLKI 660  
DB 601 ALVLPYSFYIYKAKLEETITQARSKGKMKDSTLKPDPNFEESGYTFIAPRDYCNDLKI 660  
QY 661 SDNTEFLANFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSKOKNKGVKAR 720  
DB 661 SDNTEFLANFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSKOKNKGVKAR 720  
QY 721 FVTDGGITRVYPKEAGENMOENPETYEDSFYKRSKLDNDNTVFTAFYFNKSGPGAYESGI 780  
DB 721 FVTDGGITRVYPKEAGENMOENPETYEDSFYKRSKLDNDNTVFTAFYFNKSGPGAYESGI 780  
QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCCKRNSVMDCVI 840  
DB 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCCKRNSVMDCVI 840  
QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPISLMRHLVNSVYAFNKSIDYQSVCEPGAAPKQ 900  
DB 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPISLMRHLVNSVYAFNKSIDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGMWATAAAMSILQOFLSLTFFPRLEAEMEDDDFTASLSKQ 960  
DB 901 GAGHSAYVPSVADILQIGMWATAAAMSILQOFLSLTFFPRLEAEMEDDDFTASLSKQ 960  
QY 961 SCITEQYFFDNDKSFSGVLDGNCNRSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018  
DB 961 SCITEQYFFDNDKSFSGVLDGNCNRSRIFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018

RESULT 7  
US-08-455-543A-54  
; Sequence 54, Application US/0845543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette

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;;
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/455,543A
;; FILING DATE: May 31, 1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/223,305
;; FILING DATE: April 4, 1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/868,354
;; FILING DATE: April 10, 1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/745,206
;; FILING DATE: 15-AUG-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/620,250
;; FILING DATE: 30-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/482,384
;; FILING DATE: 20-FEB-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/603,751
;; FILING DATE: 04-APR-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US89/01408
;; FILING DATE: 04-APR-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/176,899
;; FILING DATE: 04-APR-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seigman, Stephanie L.
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 6362-52517
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619)238-0999
;; TELEFAX: (619)238-0062
;; INFORMATION FOR SEQ ID NO: 54:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1086 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
;; US-08-455-543A-54
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Query Match 99.3%; Score 5306.5; DB 1; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1013; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

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DB 1 MAAGCLLATLTLFOSLLIGPSEPPFSAVTKSWVDKMQEDLVTLAKTASGVNOLVDI 60
QY 61 YEKYQDYLVTPENNAQLVEIARDIEKLLSNRKALYSALAEAKVQAAHQWREDFASN 120
DB 61 YEKYQDYLVTPENNAQLVEIARDIEKLLSNRKALYSALAEAKVQAAHQWREDFASN 120
QY 121 EVVYVNAKDDLPENKREDDPSSGSRIPKPIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180
DB 121 EVVYVNAKDDLPENKREDDPSSGSRIPKPIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTALDEYFKKNREDDPSSGSRIPKPIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 240
DB 181 NELNWTALDEYFKKNREDDPSSGSRIPKPIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 240
QY 241 RPWYIOGAASPKDMLTLDVDSVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
DB 241 RPWYIOGAASPKDMLTLDVDSVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVNNKVKLVDAVNNITAKGITYKKGFSFAFEOQLLNNVSRANCKIIML 360
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DB 301 VSCFQHLVQANVNNKVKLVDAVNNITAKGITYKKGFSFAFEOQLLNNVSRANCKIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVVFRFSVQGHNYERPIQWACENKGYIYEIPSGAIR 420
DB 361 FTDGGEERAQEIFNKYNKDKKVVFRFSVQGHNYERPIQWACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLGRPMVLADKAKOVQWNTNYLDALGLVITGTLPVFNITGQFENKTLK 480
DB 421 INTQEYLDVLGRPMVLADKAKOVQWNTNYLDALGLVITGTLPVFNITGQFENKTLK 480
QY 481 NQILGVMGVDSLEDIKRLTPRETLCPNGYYFAIDPNQVLLHPNLPKNPKSQBPVTL 540
DB 481 NQILGVMGVDSLEDIKRLTPRETLCPNGYYFAIDPNQVLLHPNLPKNPKSQBPVTL 540
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTFRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
DB 541 DFLDAELNDIKVEIRNKMIDGESGKFTFRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYISFYIYKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFTAPRDYCNDLKI 660
DB 601 ALVLPYISFYIYKAKLEETITQARSKKGMKDSSETLKPONFEESGYTFTAPRDYCNDLKI 660
QY 661 SDNNTFLLNENEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNVWSKQNIKGVKAR 720
DB 661 SDNNTFLLNENEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNVWSKQNIKGVKAR 720
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DB 721 FVVTGGITRVYPKEAGENKQENPETEYDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
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DB 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840
QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPISLMRHLVNSVYAFNKSVDYQSVCPGGAAPKQ 900
DB 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPISLMRHLVNSVYAFNKSVDYQSVCPGGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAASILQFLLSITFPRLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHSAYVPSVADILQIGWATAAASILQFLLSITFPRLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRL 1018
DB 961 SCITEQTYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRL 1018
QY 996 SCITEQTYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRL 1013
DB 996 SCITEQTYFFDNDKSFSGVLDCGNCGRIFHGEKLMNTNLIIFIMVESKGTCTCDTRL 1013

RESULT 8
US-08-223-305C-54
; Sequence 54, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA: US/08/223.305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1086 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-54

Query Match 99.3%; Score 5306.5; DB 2; Length 1086;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1013; Conservative 0; Mismatches 0; Gaps 1;  
QY 1 MAAGCLLALTTLFQSLTIGPSSPEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLFQSLTIGPSSPEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSLVSLALEAEKVQAAHQWREDFASN 120  
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QY 121 EVVYNAKDDLPKNDSPGSGQRKPFIEDANFGRIYSYQHAHVHTDIYEGSTIVL 180  
DB 121 EVVYNAKDDLPKNDSPGSGQRKPFIEDANFGRIYSYQHAHVHTDIYEGSTIVL 180  
QY 181 NELNWTSALEDFKKNREDPDLWQVFGSATGLARYYPASFPWDSNRPKNIDLYDVR 240  
DB 181 NELNWTSALEDFKKNREDPDLWQVFGSATGLARYYPASFPWDSNRPKNIDLYDVR 240  
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DB 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLTIRTSYSEMLETLSDDDFNVASFNSNAQD 300  
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DB 301 VSCFHLVQANVRNKKVLKDVANNITAKGITYKKGFSAFQQLNLYNVRANCNKIIML 360  
QY 361 FTDGGERAQEIFNKYKDKKVRVFRFSGQHNRYERGPQIOWMACENKGYIYEIPSGAIR 420

DB 361 FTDGGERAQEIFNKYKDKKVRVFRFSGQHNRYERGPQIOWMACENKGYIYEIPSGAIR 420  
QY 421 INTOEYLDVLRPMVLAGDKAKOVQWNTNVYLDALGLVITGTLPVNITQGFENKTNLK 480  
DB 421 INTOEYLDVLRPMVLAGDKAKOVQWNTNVYLDALGLVITGTLPVNITQGFENKTNLK 480  
QY 481 NOLILGVMGVDVSLIEDIKRLTPREFTLCPNGYFFAIDPNGYVLLHPNLPKPKQEPVTL 540  
DB 481 NOLILGVMGVDVSLIEDIKRLTPREFTLCPNGYFFAIDPNGYVLLHPNLPKPKQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNMKIDGESGKTFRLVKSQDRIYDKGNRTYTWTPVNGTDSL 600  
DB 541 DFLDAELENDIKVEIRNMKIDGESGKTFRLVKSQDRIYDKGNRTYTWTPVNGTDSL 600  
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DB 596 ALVLPYSFYIKAKLEETITQARKSKGKMDSETUKPDNFEESGYTFIAPRDYCNLDKI 655  
QY 661 SDNTEFLNFEIDRKTNNPSCNADLINRVLLDAGFTNELYVQYWSKQKNIKGVKAR 720  
DB 661 SDNTEFLNFEIDRKTNNPSCNADLINRVLLDAGFTNELYVQYWSKQKNIKGVKAR 720  
QY 721 FVTDGGITRVYPKEAGENWOENPETYEDSYKKSLDNDNTVFTAPYFNKSGPGAYESGI 780  
DB 721 FVTDGGITRVYPKEAGENWOENPETYEDSYKKSLDNDNTVFTAPYFNKSGPGAYESGI 780  
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DB 716 FVTDGGITRVYPKEAGENWOENPETYEDSYKKSLDNDNTVFTAPYFNKSGPGAYESGI 775  
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DB 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSNIENFTKTSIRDPCAGPVCCKRNSDVMDCVI 840  
QY 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSNIENFTKTSIRDPCAGPVCCKRNSDVMDCVI 835  
DB 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSNIENFTKTSIRDPCAGPVCCKRNSDVMDCVI 835  
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DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPDLMRHLNYSVYAFNKSVDYQSVCEPGAAPKQ 900  
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QY 896 GAGHRSAYVPSVADILQIGWATAAASILQOFLSLFPLLEAVEMEDDDFTASLSKQ 955  
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QY 961 SCITEOTOYFFDNDKSPSGVLDGNCNCRIFHGEKLMNTLIFIMVESKGTGCPDTRL 1018  
DB 961 SCITEOTOYFFDNDKSPSGVLDGNCNCRIFHGEKLMNTLIFIMVESKGTGCPDTRL 1018

RESULT 9  
US-08-455-543A-56  
; Sequence 56, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM-compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,543A  
; FILING DATE: May 31, 1995  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1084 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-455-543A-56

Query Match 98.9%; Score 5289.5; DB 1; Length 1084;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

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DDB 181 NELNWTLSALDEVEKKNREDDPSLLWQVFGSATGLARYYPASPVNDNSRPNKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLINTSVSEMLETSLDDDFVNVASFNSNAQ 300  
DDB 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLINTSVSEMLETSLDDDFVNVASFNSNAQ 300  
QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKITDYKKGFSFAFEOQLLYNVSRANCNIIML 360  
DDB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKITDYKKGFSFAFEOQLLYNVSRANCNIIML 360  
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DDB 361 FTDGGERAQEITFNKYNKDKKVVFRFVSQGHNYERGPQIOWACENKGYIYEIPSTIGAIR 420

QY 421 INTQEYLDVLGRPMVLAGDKAKQVQWNTNVYLDALGLVITGTLPVFNITQGFENKTNLK 480  
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QY 481 NQILGVMGVDVSLIEDIKRLTPRETLCPNGYIFADPNGYVLLHPNLPKPKSQEPVTL 540  
DDB 481 NQILGVMGVDVSLIEDIKRLTPRETLCPNGYIFADPNGYVLLHPNLPKPKSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
DDB 541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIIRAKLEETITQARSKKGKMDSETLPDNPFEESGYTFIAPRDYCNDLKI 660  
DDB 601 ALVLPYTFYIIRAKLEETITQARSKKGKMDSETLPDNPFEESGYTFIAPRDYCNDLKI 660  
QY 661 SDNTEFLNFEFIDRKTNNPSCNADLNRLVLLDAGFTNELVQWYWSKOKNIKGVKAR 720  
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DDB 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840  
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DDB 901 GAGHSAYVPSVADIIQIGWATAAASIIQOFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTQVFFDNDKSKFSFSGVLDCGNC SRIFHGEKLMNTNLI FIMVESKGTCPDTRL 1018  
DDB 961 SCITEQTQVFFDNDKSKFSFSGVLDCGNC SRIFHGEKLMNTNLI FIMVESKGTCPDTRL 1018  
RESULT 10  
US-08-223-305C-56  
; Sequence 56, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1084 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-56

Query Match 98.9%; Score 5289.5; DB 2; Length 1084;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1010; Conservative 0; Mismatches 1; Indels 7; Gaps 1;  
Qy 1 MAAGCLLALTTLFQSLGIPSSPEPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
Db 1 MAAGCLLALTTLFQSLGIPSSPEPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
Qy 61 YEKYQDLYTVEPNARQLVEAARDIEKLLNSRKALYSLSALEAEKVQAAHQWREDFASN 120  
Db 61 YEKYQDLYTVEPNARQLVEAARDIEKLLNSRKALYSLSALEAEKVQAAHQWREDFASN 120  
Qy 121 EVVYINAKDDLDPKNDSEPGSORIKPVFIEDANFGROI SYCHAAVHIPTDIYEGSTIVL 180  
Db 121 EVVYINAKDDLDPKNDSEPGSORIKPVFIEDANFGROI SYCHAAVHIPTDIYEGSTIVL 180  
Qy 181 NELNNTSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240  
Db 181 NELNNTSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240  
Qy 241 RPWYTOGAASPKDMLILYDVSGVSGLTFLKIRTSVSEMLETSLDDDFNVASFNSAQD 300  
Db 241 RPWYTOGAASPKDMLILYDVSGVSGLTFLKIRTSVSEMLETSLDDDFNVASFNSAQD 300  
Qy 301 VSCFOHLVQANVRNKKLVKDAVNNITAKGIDYKKGFSFAPEQLLNLYNVRANCNKIIML 360  
Db 301 VSCFOHLVQANVRNKKLVKDAVNNITAKGIDYKKGFSFAPEQLLNLYNVRANCNKIIML 360  
Qy 361 FTDGGEERAQEIFNKYNKDKKVRFRFVSQGHYERGPFIQMACENKGYVEIPSGAIR 420  
Db 361 FTDGGEERAQEIFNKYNKDKKVRFRFVSQGHYERGPFIQMACENKGYVEIPSGAIR 420  
Qy 421 INTQEYLDVGLRPMVLADKAKQVQWNTNYLDALGLVITGTLVPFNITGOFENKTNLK 480  
Db 421 INTQEYLDVGLRPMVLADKAKQVQWNTNYLDALGLVITGTLVPFNITGOFENKTNLK 480  
Qy 481 NQLILGVMGVDVSLSDIKRLTPRFTLCPNGYVFAIDPNGYVLLHPNLPKPKSQEPVTL 540

Db 481 NQLILGVMGVDVSLSDIKRLTPRFTLCPNGYVFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
Qy 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Qy 601 ALVLPYTSFYIIRAKLEETITQARSKKGMKDSFETLAKPDNFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTSFYIIRAKLEETITQARSKKGMKDSFETLAKPDNFEESGYTFIAPRDYCNLDKI 660  
Qy 661 SDNNTTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELYONYSWKOKNIKGVKAR 720  
Db 661 SDNNTTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELYONYSWKOKNIKGVKAR 720  
Qy 721 FVYTDGGITRVYPKEAGENWQENETVEDSEYKBSLNDNDNTVFTAPYFNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVYPKEAGENWQENETVEDSEYKBSLNDNDNTVFTAPYFNKSGPGAYESGI 780  
Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVANSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVANSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
Qy 841 LDGGLFLMANHDDYTNOIGRFFGEIDPDSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900  
Db 841 LDGGLFLMANHDDYTNOIGRFFGEIDPDSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ 900  
Qy 901 GAGHRSAYVPSVADILQIGWATAAANSILOOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960  
Db 901 GAGHRSAYVPSVADILQIGWATAAANSILOOFLLSLTPRLLAEVEMEDDDFTASLSKQ 960  
Qy 961 SCITEQTYQFFDNDKSPSGVLDGCGNCSRIFFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018  
Db 961 SCITEQTYQFFDNDKSPSGVLDGCGNCSRIFFHGEKLMNTNLIIFIMVESKGTCPDTRL 1018  
Qy 954 SCITEQTYQFFDNDKSPSGVLDGCGNCSRIFFHGEKLMNTNLIIFIMVESKGTCPDTRL 1011  
Db 954 SCITEQTYQFFDNDKSPSGVLDGCGNCSRIFFHGEKLMNTNLIIFIMVESKGTCPDTRL 1011

RESULT 11  
US-08-455-543A-53  
Sequence 53, Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206

;; FILING DATE: 15-AUG-1991  
;; PRIORITY APPLICATION DATA: US 07/620,250  
;; FILING DATE: 30-NOV-1990  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/482,384  
;; FILING DATE: 20-FEB-1990  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/603,751  
;; FILING DATE: 04-APR-1989  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/US89/01408  
;; FILING DATE: 04-APR-1989  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/176,899  
;; FILING DATE: 04-APR-1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seidman, Stephanie L.  
;; REGISTRATION NUMBER: 33,779  
;; REFERENCE/DOCKET NUMBER: 6362-52517  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619)238-0999  
;; TELEFAX: (619)238-0062  
;; INFORMATION FOR SEQ ID NO: 53:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1103 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FRAGMENT TYPE: internal  
US-08-455-543A-53

Query Match 98.6%; Score 5270; DB 1; Length 1103;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY	1	MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
DB	1	MAAGCLLALTTLFOSLLIGSPSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
QY	61	YEKYODLYTVEPNARQLVETAAARDIEKLLNSRKALVSLALEAEKVAQAHHQWREDFASN	120
DB	61	YEKYODLYTVEPNARQLVETAAARDIEKLLNSRKALVSLALEAEKVAQAHHQWREDFASN	120
QY	121	EVVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHTDIYEGSTIVL	180
DB	121	EVVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHTDIYEGSTIVL	180
QY	181	NELNWTSAIDVFKKNEEDPSLLWQVFGSATGLARYTPASFWVDNSRTPNKKIDLYDVR	240
DB	181	NELNWTSAIDVFKKNEEDPSLLWQVFGSATGLARYTPASFWVDNSRTPNKKIDLYDVR	240
QY	241	RPWYIQGAASPKDMLLVDSVSGVSLTKLIRTSVSEMLTSLDDDFVNVASNSNAQD	300
DB	241	RPWYIQGAASPKDMLLVDSVSGVSLTKLIRTSVSEMLTSLDDDFVNVASNSNAQD	300
QY	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVSRANCKIIML	360
DB	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVSRANCKIIML	360
QY	361	FTDGEERAQEIFNKYKDKKVRFRSVGOHNTERGPIOMACENKGYEYIPEISGAIR	420
DB	361	FTDGEERAQEIFNKYKDKKVRFRSVGOHNTERGPIOMACENKGYEYIPEISGAIR	420
QY	421	INTQEYLDVLRPNVLAGDKAKQVQWNTVYLDLGLVITGTLPVNTICQFENKLNK	480
DB	421	INTQEYLDVLRPNVLAGDKAKQVQWNTVYLDLGLVITGTLPVNTICQFENKLNK	480
QY	481	NQLILGVMGVDVSLDKRLTPRTLCPNGYFAIDPNGYVLLHPNLPQK-----	530
DB	481	NQLILGVMGVDVSLDKRLTPRTLCPNGYFAIDPNGYVLLHPNLPQKPIGVGPTIN	540

QY	531	-----NPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI	581
DB	541	LRKRRPNIQPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI	600
QY	582	DGNRTYTWTVPNGTDYSLALVLPYTSFYIKAKLEETITQARSKGKMKDSETLKPDNF	641
DB	601	DGNRTYTWTVPNGTDYSLALVLPYTSFYIKAKLEETITQARY-----SETLKPDNF	653
QY	642	EESGYTFIAPRDYCNLDKISDNNTFELNNEFIDRTKTPNPNPCNADLINRVLLDAGFTN	701
DB	654	EESGYTFIAPRDYCNLDKISDNNTFELNNEFIDRTKTPNPNPCNADLINRVLLDAGFTN	713
QY	702	ELVQNYWSKQKNIKGVKARFVTDGGITRVYPKEAGENMOENPETEYEDSYKKSLDNDNY	761
DB	714	ELVQNYWSKQKNIKGVKARFVTDGGITRVYPKEAGENMOENPETEYEDSYKKSLDNDNY	773
QY	762	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP	821
DB	774	VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP	833
QY	822	CAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPDLRHLVNIISVYA	881
DB	834	CAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPDLRHLVNIISVYA	893
QY	882	FNKSYDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPR	941
DB	894	FNKSYDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPR	953
QY	942	LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGCGNCSRIFPHGKLMNTNL	1001
DB	954	LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGCGNCSRIFPHGKLMNTNL	1013
QY	1002	IFIMVESKGTCPDTRL 1018	
DB	1014	IFIMVESKGTCPDTRL 1030	

RESULT 12  
US-08-223-305C-53  
; Sequence 53, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Hallier & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-53

Query Match 98.6%; Score 5270; DB 2; Length 1103;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1010; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLFOSLLIGPSSPEPPFSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60  
DB 1 MAAGCLLALTTLFOSLLIGPSSPEPPFSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60

QY 61 YEKYQDLTYVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120  
DB 61 YEKYQDLTYVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120

QY 121 EYVYNAKDDLPENKNDSPGSGQRKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
DB 121 EYVYNAKDDLPENKNDSPGSGQRKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180

QY 181 NELNWTSAIDVEFKKNREDDPSLLAQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
DB 181 NELNWTSAIDVEFKKNREDDPSLLAQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240

QY 241 RPWYIQAASPKDMLTLDVSGVSGLTLLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300  
DB 241 RPWYIQAASPKDMLTLDVSGVSGLTLLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300

QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITYKKGFSFAFQOLLNVNVRANCKNIIML 360  
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITYKKGFSFAFQOLLNVNVRANCKNIIML 360

QY 361 FTDGGEERAQELFNKYNKDKKVRVRFSGQHNRYERGPQWACENKGYIYIPISGAIR 420  
DB 361 FTDGGEERAQELFNKYNKDKKVRVRFSGQHNRYERGPQWACENKGYIYIPISGAIR 420

QY 421 INTQEYLDVGLGRPMVLGDKAQVQWNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480  
DB 421 INTQEYLDVGLGRPMVLGDKAQVQWNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480

QY 481 NQILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPK----- 530  
DB 481 NQILGVMGVDVSLDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKPIGVGPTIN 540

QY 531 -----NPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI 581  
DB 541 LKRRPNIQPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI 600

QY 582 DGNRTYTTPVNGTDYSLALVPTYSFYIYKAKLEETITQARSKKGMKDSKTLKPDNF 641  
DB 601 DGNRTYTTPVNGTDYSLALVPTYSFYIYKAKLEETITQARSKKGMKDSKTLKPDNF 653

QY 642 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN 701  
DB 654 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN 713

QY 702 ELVQYWSKQKNIKGVKARFVYVTDGTRVYPKEAGENWQENPETYEDSFYKRSLDNDNY 761  
DB 714 ELVQYWSKQKNIKGVKARFVYVTDGTRVYPKEAGENWQENPETYEDSFYKRSLDNDNY 773

QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLLKPAVVGKIDVNSWNIENFTKTSIRDP 821  
DB 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLLKPAVVGKIDVNSWNIENFTKTSIRDP 833

QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDVTNIGRFFGEIDPDSLMRHLVNI SYVA 881  
DB 834 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDVTNIGRFFGEIDPDSLMRHLVNI SYVA 893

QY 882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTTPR 941  
DB 894 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTTPR 953

QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCNCRIFHGEKLMNTNL 1001  
DB 954 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCNCRIFHGEKLMNTNL 1013

QY 1002 IFIMVESKGTCPCDTRL 1018  
DB 1014 IFIMVESKGTCPCDTRL 1030

RESULT 13  
US-08-455-543A-55  
; Sequence 55 Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,543A  
; FILING DATE: May 31, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/223,305  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seigman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
FRAGMENT TYPE: Internal  
US-08-455-543A-55

Query Match 98.2%; Score 5250; DB 1; Length 1079;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1005; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

Qy	1	MAAGCLLATLTFLQSLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI	60
Db	1	MAAGCLLATLTFLQSLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI	60
Qy	61	YEKQDLYTVENPNAQOLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN	120
Db	61	YEKQDLYTVENPNAQOLVETAAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN	120
Qy	121	EWYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQHAHVHPTDIYEGSTIVL	180
Db	121	EWYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQHAHVHPTDIYEGSTIVL	180
Qy	181	NELNWTSALEDFVKKNRDEPSLLQWFGSATGLARYYPASFWVDNSTPNKIDLYVRR	240
Db	181	NELNWTSALEDFVKKNRDEPSLLQWFGSATGLARYYPASFWVDNSTPNKIDLYVRR	240
Qy	241	RPWTIOGAASPKMDILVDSVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD	300
Db	241	RPWTIOGAASPKMDILVDSVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD	300
Qy	301	VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEQQLINYNVSRANCKIIML	360
Db	301	VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEQQLINYNVSRANCKIIML	360
Qy	361	FTDGEERAQEIFNKNKDKKVRFRFSVGOHNTYERGPIQWACENKGYEIPSIGAIR	420
Db	361	FTDGEERAQEIFNKNKDKKVRFRFSVGOHNTYERGPIQWACENKGYEIPSIGAIR	420
Qy	421	INTQYLDVLGRPMVLADGKAKQVQWTVNYLDALELGLVITGLTPVFNITQFENKTNLK	480
Db	421	INTQYLDVLGRPMVLADGKAKQVQWTVNYLDALELGLVITGLTPVFNITQFENKTNLK	480
Qy	481	NQLILGVNGVDVSLDKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPK	540

Db	481	NQLILGVNGVDVSLDKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPK	535
Qy	541	DFLDAELENDIKVEIRNKNMIDGESGEKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL	600
Db	536	DFLDAELENDIKVEIRNKNMIDGESGEKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL	595
Qy	601	ALVLTYSFYIYIKAKLEETITQARSKKGMKDSKSEILKPDNFESGYTFIAPRDYCNLDKI	660
Db	596	ALVLTYSFYIYIKAKLEETITQARSKKGMKDSKSEILKPDNFESGYTFIAPRDYCNLDKI	648
Qy	661	SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR	720
Db	649	SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR	708
Qy	721	FVVDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI	780
Db	709	FVVDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI	768
Qy	781	MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPGAGPVCDCKRNSDVMDCVI	840
Db	769	MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPGAGPVCDCKRNSDVMDCVI	828
Qy	841	LDDGGFLLMANHDDYTNOIGREFGEIDPSLMRHLVNIISVYAFNKSYDVOSVCEPGAAPKQ	900
Db	829	LDDGGFLLMANHDDYTNOIGREFGEIDPSLMRHLVNIISVYAFNKSYDVOSVCEPGAAPKQ	888
Qy	901	GAGHSAYVPSVADILQIGMWATAAAWSILOQLLSLTPRLEAVEEMEDDDFTASLSKQ	960
Db	889	GAGHSAYVPSVADILQIGMWATAAAWSILOQLLSLTPRLEAVEEMEDDDFTASLSKQ	948
Qy	961	SCITEQTOYFFDNDKSPSGVLDGCGNCSRIHFHGEKLMNTNLIFIMVESKGTCPDTRL	1018
Db	949	SCITEQTOYFFDNDKSPSGVLDGCGNCSRIHFHGEKLMNTNLIFIMVESKGTCPDTRL	1006

RESULT 14  
US-08-223-305C-55  
; Sequence 55, Application US/082233305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0099  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-223-305C-55

Query Match 98.2%; Score 5250; DB 2; Length 1079;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1005; Conservative 0; Mismatches 1; Indels 12; Gaps 2;  
QY 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTKSWDKQEDLVTLAKTAGSVNQLVDI 60  
Db 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTKSWDKQEDLVTLAKTAGSVNQLVDI 60  
QY 61 YEKYQDLTYVEPNNAAROLVEIARIEKLLSNRSLALSLAEKVAQAHOHREDFASN 120  
Db 61 YEKYQDLTYVEPNNAAROLVEIARIEKLLSNRSLALSLAEKVAQAHOHREDFASN 120  
QY 121 EYVYNAKDDLDPEKNDSEPGSQRKPFVIEDANGROISYOHAAVHIPTDIYEGSTIVL 180  
Db 121 EYVYNAKDDLDPEKNDSEPGSQRKPFVIEDANGROISYOHAAVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEVFKKNREEDPSLLQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
Db 181 NELNWTSSALDEVFKKNREEDPSLLQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
QY 241 RPWYTOGAASPKDMLILVDVSGSVGLTKLRTSYSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPWYTOGAASPKDMLILVDVSGSVGLTKLRTSYSEMLETSLDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLKADANNITAKGIDYKGFSPFAPOLLNLYNVRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLKADANNITAKGIDYKGFSPFAPOLLNLYNVRANCNKIIML 360  
QY 361 FTDGGEERAQEIFKNYKDKVRFVRSYGOHNYERGPQIOWMACENKGYEIPISGAIR 420  
Db 361 FTDGGEERAQEIFKNYKDKVRFVRSYGOHNYERGPQIOWMACENKGYEIPISGAIR 420  
QY 421 INTQEYLDVLRPMVLADKAKQOVNTNYLDALGLVITGTLVPFNITGOFENKTNLK 480  
Db 421 INTQEYLDVLRPMVLADKAKQOVNTNYLDALGLVITGTLVPFNITGOFENKTNLK 480  
QY 481 NQILGVMGVDVSLDIKRLTFRFTLCPNGYFAIDPNGYVLLHNPLOPKPKSOEPTVL 540  
Db 481 NQILGVMGVDVSLDIKRLTFRFTLCPNGYFAIDPNGYVLLHNPLOPKPKSOEPTVL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGSEKFTRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 536 DFLDAELENDIKVEIRNKMIDGSEKFTRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 595

RESULT 15  
US-08-435-675B-5  
; Sequence 5, Application US/08435675B  
; Patent No. 5710250  
; GENERAL INFORMATION:  
; APPLICANT: Ellis, Steven Bradley  
; APPLICANT: Williams, Mark E.  
; APPLICANT: Harpold, Michael Miller  
; APPLICANT: Schwartz, Arnold  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,675B  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/314,083  
; FILING DATE: 28-SEP-1994  
; APPLICATION NUMBER: US 07/914,231  
; FILING DATE: 13-JUL-1992  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 08-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-53193  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:



INFORMATION FOR SBO ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-435-675B-5

Query Match 96.1%; Score 5137.5; DB 1; Length 1106;  
Best Local Similarity 94.8%; Pred. No. 0;  
Matches 986; Conservative 13; Mismatches 12; Indels 29; Gaps 4;  
QY 1 MAAGCLLALTLTQFS--LLIGSSSEPPFSAVTKISWVKMOEDLVTLAKTAGVGNOLV 58  
Db 1 MAAGRPLAWTLTLQAWLILIGSSSEPPFSAVTKISWVKMOEDLVTLAKTAGVGNOLV 60  
QY 59 DIYEKYODLVTPNNARQLVEIARIEKLLNSRKALYSALAEKVAQAHHQWREDF 118  
Db 61 DIYEKYODLVTPNNARQLVEIARIEKLLNSRKALYRLALEAEKVAQAHHQWREDF 120  
QY 119 SNEVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHAVHIPTDIYEGSTI 178  
Db 121 SNEVYINAKDDLDPEKNDSEPGSQRIKPVFIEDANFRQVSYQHAHAVHIPTDIYEGSTI 180  
QY 179 VLNELNWTSSALDEVKKNREEDPSLWQVFGSATGLARYYPASPWDNSRTPNKKIDLYD 238  
Db 181 VLNELNWTSSALDEVKKNREEDPSLWQVFGSATGLARYYPASPWDNSRTPNKKIDLYD 240  
QY 239 RRPWTIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETLSDDDFVNVSFNSNA 298  
Db 241 RRPWTIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETLSDDDFVNVSFNSNA 300  
QY 299 QDYSCFOHLVQANVRNKKVLLKDAVNNTAKGIDYKKGFSFAFEQLINYNVSRANCKII 358  
Db 301 QDYSCFOHLVQANVRNKKVLLKDAVNNTAKGIDYKKGFSFAFEQLINYNVSRANCKII 360  
QY 359 MLFTDGEERAQEIFNKNKDKKRVRFVSGQHNTERGPIQWACENKGYEIPISGA 418  
Db 361 MLFTDGEERAQEIFAKYNKDKKRVFTSVGQHNDRGPQWACENKGYEIPISGA 420  
QY 419 IRLNTOEYLDVLRPNVLAGDKAKQVNTNVDLDAELGLVITGTLVPFNITGQFENKTN 478  
Db 421 IRLNTOEYLDVLRPNVLAGDKAKQVNTNVDLDAELGLVITGTLVPFNITGQFENKTN 480  
QY 479 LKNQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPK----- 530  
Db 481 LKNQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKIGVGIPT 540  
QY 531 -----NPKSQEPVTLDFDLAELENDIKVEIRNKNMIDGESGEKTFRTLVKSQDER 579  
Db 541 INLRKRPNVQNPKSEQEPVTLDFDLAELENDIKVEIRNKNMIDGESGEKTFRTLVKSQDER 600  
QY 580 YIDKGNRTYTWTPVNGTDY-SLALVLPYTSFYIKAKLETITQARSKKGMKMDSETLKP 638  
Db 601 YIDKGNRTYTWTPVNGTDYSSALVLPYTSFYIKAKIETITQARY-----SETLKP 653  
QY 639 DNPESGYTFIAPRDYCNLDKISDNNTEFLNENEFIDRKTNNPCSNADLINRVLLDAG 698  
Db 654 DNPESGYTFIAPRDYCSDLKPSDNNTEFLNENEFIDRKTNNPCSNADLINRVLLDAG 713  
QY 699 FTNELVQNTWSKQKNIKGVKAREVVTDDGTRVYPKEAGENWQENPETYEDSFYKRSLDN 758  
Db 714 FTNELVQNTWSKQKNIKGVKAREVVTDDGTRVYPKEAGENWQENPETYEDSFYKRSLDN 773  
QY 759 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI 818  
Db 774 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI 833  
QY 819 RDPGAGPVCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIS 878

Db 834 RDPGAGPVCCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIS 893  
QY 879 VYAFNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLT 938  
Db 894 VYAFNKSYDYQSVCEPGAAPKQAGHRSAYVPSIADILQIGWATAAAWSILOQFLLSLT 953  
QY 939 FPRLEAVEMEDDDFTASLSKQSCITEQTYFFONDSSKFSFVLDCCGNCSTRIFHGEKLMN 998  
Db 954 FPRLEAADMEDDDFTASMSKQSCITEQTYFFONDSSKFSFVLDCCGNCSTRIFHGEKLMN 1013  
QY 999 TNLIFIMVESKGTCPCDTRL 1018  
Db 1014 TNLIFIMVESKGTCPCDTRL 1033

Search completed: July 23, 2001, 07:38:46  
Job time: 513 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:37:40 ; Search time 84.28 seconds

(without alignments)  
920.096 Million cell updates/sec

Title: US-09-397-548-15

Perfect score: 5346

Sequence: 1 MAAGCLLALTTLFQSLIG.....TNLIFIMVSKTCPCDRL 1018

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	5346	100.0	1091 2 JH0565	calcium channel al
2	5145	96.2	1091 2 A44147	calcium channel pr
3	5132.5	96.0	1106 1 CHRBA2	calcium channel al
4	1085	20.3	1091 2 T30256	calcium channel al
5	607	11.4	734 2 S44617	C50C3.11 protein -
6	569.5	10.7	1148 2 T18770	probable calcium c
7	198	3.7	1450 2 C86880	hypothetical prote
8	194.5	3.6	886 2 S54355	inter-alpha-trypsi
9	185	3.5	886 2 S30350	inter-alpha-trypsi
10	164.5	3.1	889 2 JC5576	inter-alpha-trypsi
11	161	3.0	2706 2 T28155	variant-specific s
12	159	3.0	1984 2 A44396	p-type cation tran
13	157.5	2.9	575 2 D64998	hypothetical prote
14	155	2.9	1516 2 E71619	RAD2 endonuclease
15	155	2.9	2364 2 I40884	cytotoxin L - Clos
16	154.5	2.9	946 1 IYHU2	inter-alpha-trypsi
17	154.5	2.9	1315 2 T28679	fibrinogen-binding
18	153	2.9	932 2 JC5953	inter-alpha-inhibi
19	152	2.8	1291 2 S46431	botulinum neurotox
20	152	2.8	1291 2 A49777	botulinum neurotox
21	151.5	2.8	420 2 S76691	hypothetical prote
22	150.5	2.8	921 2 JC4625	inter-alpha-trypsi
23	150	2.8	654 2 A69656	methyl-accepting c
24	149	2.8	459 2 F64688	proteinase [EC 3.4
25	149	2.8	930 2 JX0368	inter-alpha-trypsi
26	148.5	2.8	2401 2 T28676	rhodopy protein -
27	148	2.8	964 2 S25855	DNA-directed DNA p
28	146.5	2.7	1285 2 B72430	hypothetical prote
29	146	2.7	4688 2 F82885	hypothetical prote

#### ALIGNMENTS

RESULT 1

JH0565

calcium channel alpha-2b chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999

C:Accession: JH0565

R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B. Neuron 8, 71-84, 1992

A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of A:Reference number: JH0564; MUID:92110010

A:Accession: JH0565

A:Molecule type: mRNA

A:Residues: 1-1091 <WIL>

A:Cross-references: GB:M76559; NID:g179761; PIDN:AAA51903.1; PID:g179762

A:Experimental source: basal ganglia

A:Note: several conflicts are found between GenBank submission, authors' translation and C:Comment: This protein is a subunit of the voltage dependent calcium channel.

C:Superfamily: calcium channel alpha-2 chain

C:Keywords: glycoprotein; phosphoprotein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-1067/Product: calcium channel alpha-2b chain status predicted <CAL>

F:32,268,326,339,535,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #

F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca F:501/Binding site: phosphate (Thr) (covalent) #status predicted

F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 100.0%; Score 5346; DB 2; Length 1091;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTTLFQSLIGPSSEPPFPFSAVTIKSWDKMQEDVLTAKTASGVNQLVDI 60

Db 1 MAAGCLLALTTLFQSLIGPSSEPPFPFSAVTIKSWDKMQEDVLTAKTASGVNQLVDI 60

Qy 61 YEKYQDLYTVPNNARQLVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

Db 61 YEKYQDLYTVPNNARQLVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

Qy 121 EYVYNNAKDDLDPEKNDSEPGSQRIKPVPFIEDANFGRLISYQHAHVHTPTDIYEGSTVL 180

Db 121 EYVYNNAKDDLDPEKNDSEPGSQRIKPVPFIEDANFGRLISYQHAHVHTPTDIYEGSTVL 180

Qy 181 NELNWTSALEDVFKKNRREDPSLLMQVFGSATGLARYYPASFPWVDSNRTPNKNIDLYDVR 240

Db 181 NELNWTSALEDVFKKNRREDPSLLMQVFGSATGLARYYPASFPWVDSNRTPNKNIDLYDVR 240

Qy 241 RPWYIQGAASPKDMLILDVDSGVSGLTKLIRTSVSEMLEFTLSDDDFVNVASFNSNAQD 300

Db 241 RPWYIQGAASPKDMLILDVDSGVSGLTKLIRTSVSEMLEFTLSDDDFVNVASFNSNAQD 300

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QY 301 VSCFOHLYQVANNKVKLVKDAVNNTAKGIDTYKKGFSAFEPQLLNINVSFRANCKNIIML 360
Db 301 VSCFOHLYQVANNKVKLVKDAVNNTAKGIDTYKKGFSAFEPQLLNINVSFRANCKNIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVQHNYERGPQIOWMACENKGYIYEIPSGAIR 420
Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVQHNYERGPQIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVGRPMVLADGKAKOVQWNTNYLDALGLVITGTLVPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVGRPMVLADGKAKOVQWNTNYLDALGLVITGTLVPVFNITGQFENKTNLK 480
QY 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKKSOEPTVL 540
Db 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKKSOEPTVL 540
QY 541 DFLDAELENDDIKVEIRNKMIDGESGKFTLTKVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDAELENDDIKVEIRNKMIDGESGKFTLTKVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPITYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPRDYCNLKI 660
Db 601 ALVLPITYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPRDYCNLKI 660
QY 661 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
Db 661 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
QY 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNYYFTAPYFNKSGPGAYESGI 780
Db 721 FVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNYYFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSHNIENFTKTSIRDPKAGVPCDCKRNSDVMDCV 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSHNIENFTKTSIRDPKAGVPCDCKRNSDVMDCV 840
QY 841 LDGGEFLMANHDDVTNQIGRFFGEIDPMSLRHLNINISYAFNKSVDYQVCEPGAAPK 900
Db 841 LDGGEFLMANHDDVTNQIGRFFGEIDPMSLRHLNINISYAFNKSVDYQVCEPGAAPK 900
QY 901 GAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTOYFFDNDSKFSFGLDGCNCSIFHGEKLMNTNLIFIMVESKGTCPDCTRL 1018
Db 961 SCITEQTOYFFDNDSKFSFGLDGCNCSIFHGEKLMNTNLIFIMVESKGTCPDCTRL 1018

RESULT 2
A44147
calcium channel protein alpha-2 chain precursor - rat
N:Alternate names: dihydropyridine-sensitive L-type
N:Contains: calcium channel alpha-2 chain
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
C:Accession: A44147
R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive
A:Reference number: A44147; MUID:92228762
A:Accession: A44147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1091 <KIM>
A:Cross-references: GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein
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Query Match 96.2%; Score 5145; DB 2; Length 1091;  
Best Local Similarity 95.8%; Pred. No. 2.6e-302;  
Matches 976; Conservative 22; Mismatches 19; Indels 2; Gaps 2;

RESULT 3  
CHBA2  
calcium channel protein alpha-2 chain precursor - rabbit

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QY 1 MAAGCLLALTTLTQSLILIGPSSPEPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLYDI 60
Db 1 MAAGCLLALTTLTQSLILIGPSSPEPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLADI 60
QY 61 YEKYQDLTYVTPNNARQIVEAARDIEKLLSNRSKALVSLALEAEKQVAAAHQWREDFASN 120
Db 61 YEKYQDLTYVTPNNARQIVEAARDIEKLLSNRSKALVSLALEAEKQVAAAHQWREDFASN 120
QY 121 EYVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGROIISQHAHVHIPTDIYESTIVL 180
Db 121 EYVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGROIISQHAHVHIPTDIYESTIVL 180
QY 181 NELNWTSALEDEVKKNREDDPSLWQVFGSATGLARYYPASVPVDNSRTPNKKIDLYDVR 240
Db 181 NELNWTSALEDEVKKNREDDPSLWQVFGSATGLARYYPASVPVDNSRTPNKKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLDSDDDFVNVASFNSNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLDSDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLYQVANNKVKLVKDAVNNTAKGIDTYKKGFSAFEPQLLNINVSFRANCKNIIML 360
Db 301 VSCFOHLYQVANNKVKLVKDAVNNTAKGIDTYKKGFSAFEPQLLNINVSFRANCKNIIML 360
QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVQHNYERGPQIOWMACENKGYIYEIPSGAIR 420
Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGVQHNYERGPQIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVGRPMVLADGKAKOVQWNTNYLDALGLVITGTLVPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVGRPMVLADGKAKOVQWNTNYLDALGLVITGTLVPVFNITGQFENKTNLK 480
QY 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKKSOEPTVL 540
Db 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPKKSOEPTVL 540
QY 541 DFLDAELENDDIKVEIRNKMIDGESGKFTLTKVKSQDERYIDKGNRTYTWTPVNGTDYS- 599
Db 541 DFLDAELENDDIKVEIRNKMIDGESGKFTLTKVKSQDERYIDKGNRTYTWTPVNGTDYS- 599
QY 600 LALVLPITYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPRDYCNL 659
Db 600 LALVLPITYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEESGYTFIAPRDYCNL 659
QY 660 ISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKA 719
Db 660 ISDNTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKA 719
QY 720 REVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNYYFTAPYFNKSGPGAYESG 779
Db 720 REVVTGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNYYFTAPYFNKSGPGAYESG 779
QY 780 IMVSKAVEIYIOGKLLKPAVVGKIDVNSHNIENFTKTSIRDPKAGVPCDCKRNSDVMDCV 839
Db 780 IMVSKAVEIYIOGKLLKPAVVGKIDVNSHNIENFTKTSIRDPKAGVPCDCKRNSDVMDCV 839
QY 840 ILDDGGFLMANHDDVTNQIGRFFGEIDPMSLRHLNINISYAFNKSVDYQVCEPGAAPK 899
Db 840 ILDDGGFLMANHDDVTNQIGRFFGEIDPMSLRHLNINISYAFNKSVDYQVCEPGAAPK 899
QY 900 QGAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAVEMEDDDFTASLSK 959
Db 900 QGAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAVEMEDDDFTASLSK 959
QY 960 QSCITEQTOYFFDNDSKFSFGLDGCNCSIFHGEKLMNTNLIFIMVESKGTCPDCTRL 1018
Db 960 QSCITEQTOYFFDNDSKFSFGLDGCNCSIFHGEKLMNTNLIFIMVESKGTCPDCTRL 1018
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N:Alternate names: dihydropyridine-binding protein, 140K  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 22-Jun-1999  
C:Accession: S10579; A39518; A33409  
R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell  
Science 241, 1661-1664, 1988  
A:Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of  
A:Reference number: S10579; MUID:88336904  
A:Accession: S10579  
A:Molecule type: mRNA  
A:Residues: 1-1106 <ELL>  
A:CROSS-references: EMBL:M21948; NID:9164762; PIDN:AA81562.1; PID:gl64763  
A:Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found  
R:Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, K.P.  
J. Biol. Chem. 266, 3287-3293, 1991  
A:Title: Structural characterization of the dihydropyridine-sensitive calcium channel al  
A:Reference number: A39518; MUID:91131638  
A:Accession: A39518  
A:Molecule type: protein  
A:Residues: 961-973 <JAY>  
A:Note: this sequence represents the amino end of a glycosylated peptide that appears at  
e at the amino end and identical molecular weights (17K) following deglycosylation  
R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.  
Biochemistry 28, 7820-7828, 1989  
A:Title: Subunit composition of the purified dihydropyridine binding protein from skelet  
A:Reference number: A33409; MUID:90122765  
A:Accession: A33409  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-44 'S', 46-47 <HAM>  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>  
F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:  
  
Query Match 96.0%; Score 5132.5; DB 1; Length 1106;  
Best Local Similarity 94.7%; Pred. NO. 1.5e-301;  
Matches 985; Conservative 14; Mismatches 12; Indels 29; Gaps 4;  
  
Qy 1 MAAGCLLALTILFQS--LLIGPSSEEPSPSNTIKSWDKMQEDLVILAKTASGVNQLV 58  
Db 1 MAAGPLAATLTQAWLILIGPSSEEPSPSNTIKSWDKMQEDLVILAKTASGVHQLV 60  
Qy 59 DIYEKQDLYTVEPNARQLVEIARDEKLLSNRSKALVSLALEAEKVQAAHQWREDF 118  
Db 61 DIYEKQDLYTVEPNARQLVEIARDEKLLSNRSKALVRLALEAEKVQAAHQWREDF 120  
Qy 119 SNEVYNAKDDLDPEKNDSEPGSORIKPVFTIEDANFGRQISYQAAHVHIPTDIYEGSTI 178  
Db 121 SNEVYNAKDDLDPEKNDSEPGSORIKPVFTIEDANFRRQVSQYQAAHVHIPTDIYEGSTI 180  
Qy 179 VLNELNWTSALEDEVKKREEDPSLLQVFGSATGLARYYPASWPVDSRPNKIDLDYDV 238  
Db 181 VLNELNWTSALEDDVFKKREEDPSLLQVFGSATGLARYYPASWPVDSRPNKIDLDYDV 240  
Qy 239 RRRPWYIOGAASPKDMLILVDVSGVSLGLTKLFTSYSEMLETSLDSDDFVNVASFNSNA 298  
Db 241 RRRPWYIOGAASPKDMLILVDVSGVSLGLTKLFTSYSEMLETSLDSDDFVNVASFNSNA 300  
Qy 299 QDVSCFQHLVQANRVNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNVNVRANCNKII 358  
Db 301 QDVSCFQHLVQANRVNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNVNVRANCNKII 360  
Qy 359 MLFTDGGERAQEIYKYNKKVFRFSPVQGHNYERGPTQWMAKNGYYEIPSGA 418  
Db 361 MLFTDGGERAQEIYKYNKKVFRFSPVQGHNYERGPTQWMAKNGYYEIPSGA 420  
Qy 419 TRINTQEVLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVNTIGQFENKTN 478  
Db 421 TRINTQEVLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVNTIGQFENKTN 480

Qy 479 LKNQLILGVMGVDSLEDIKRLTPRTTLCPCNGYFAIDPNGVYLLHPNLQPK----- 530  
Db 481 LKNQLILGVMGVDSLEDIKRLTPRTTLCPCNGYFAIDPNGVYLLHPNLQPKPIGVGPT 540  
Qy 531 -----NPKSQEPVTLDFDAELENLIKVEIRNMIDGESGEKTFRLVKSQDER 579  
Db 541 INLRRRRNQVQKSPQEPVTLDFDAELENLIKVEIRNMIDGESGEKTFRLVKSQDER 600  
Qy 580 YIDKGNRTYTPVNGTDY-SLALVLPYFYFYIKAKLEETITQARSKKGMKMDSETLKP 638  
Db 601 YIDKGNRTYTPVNGTDYSSALVLPYFYFYIKAKLEETITQARY-----SETLKP 653  
Qy 639 DNFEESGTYTAPRYCNDLKTSNDNTEFLNFEFIDRKTTPNPNNSCNADLNRLVLLDAG 698  
Db 654 DNFEESGTYTAPRYCNDLKPSDNTEFLNFEFIDRKTTPNPNNSCNADLNRLVLLDAG 713  
Qy 699 FTNELVQNWSKQKNIKGVKARFVYTDGITRVYKPEAGENQENPETYEDSFYKRSLDN 758  
Db 714 FTNELVQNWSKQKNIKGVKARFVYTDGITRVYKPEAGENQENPETYEDSFYKRSLDN 773  
Qy 759 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIQGKLLPAAVYGIKIDVNSWIENFTKTSI 818  
Db 774 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIQGKLLPAAVYGIKIDVNSWIENFTKTSI 833  
Qy 819 RDPGAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI 878  
Db 834 RDPGAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI 893  
Qy 879 VYAFNKSYDYQSVCEPAGAPKOGAGHRSAYVPSADIILQIGHWATAAAWSILQQFLLSLT 938  
Db 894 VYAFNKSYDYQSVCEPAGAPKOGAGHRSAYVPSADIILQIGHWATAAAWSILQQFLLSLT 953  
Qy 939 FPRLEAVEMEDDDFTASLSKSCITEQTYFFDNDKSFSGVLDGCGNCSRIFHGEKLMN 998  
Db 954 FPRLEAADMEDDDFTASMSKSCITEQTYFFDNDKSFSGVLDGCGNCSRIFHVEKLMN 1013  
Qy 999 TNLIFIMVESKGTCPDTRL 1018  
Db 1014 TNLIFIMVESKGTCPDTRL 1033  
  
RESULT 4  
T30256  
calcium channel alpha-2-delta-C chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T30256  
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.  
J. Neurosci. 19, 648-691, 1999  
A:Title: Molecular diversity of the calcium channel alpha2delta subunit.  
A:Reference number: 420794  
A:Accession: T30256  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1091 <KLJ>  
A:CROSS-references: EMBL:AJ010949; PIDN:CAA09423.1  
A:Experimental source: brain  
C:Superfamily: calcium channel alpha-2 chain  
  
Query Match 20.3%; Score 1085; DB 2; Length 1091;  
Best Local Similarity 28.7%; Pred. NO. 2.3e-57;  
Matches 309; Conservative 222; Mismatches 416; Indels 128; Gaps 40;  
  
Qy 3 ACCILALITLTLFQSLIGPSSEEPSPSNTIKSWDKMQEDLVILAKTASGVNQLVDIYE 62  
Db 14 ASALLA-TALLYAALGVVRSQQIPLSV-VKLWASAFGEIKRSTAAKYSSQLQKKTK 71  
Qy 63 KYODLYTVEPNARQLVEIARDEKLLSNRSKALVSLALEAEKVQAAHQWREDFASNEV 122  
Db 72 EYKDVATIEIDGLQVKKLAKIMEEMPHKKSEAVRRLVEAAEEAHLKEFDADL---QY 128  
Qy 123 VYINAK--DDLDPKNDSEPGSORIKPVFIEDANFGR-QISYQAAHVHIPTDIYEGSTIV 179

Db 129 EFYNAVLINERDGNFELGKEFI---LAPNDHENNLPVNLISLSDVQVPTNNYKNDPAI 185  
QY 180 LNELNWTSADEVFVKKNREEDPSLLQWFGSATGLARYYPASPWVDNDRTPNKKIDLYDVR 239  
Db 186 VNGVYSESLNKVFDNDRDPSLLQWFGSATGLARYYPASPWVDNDRTPNKKIDLYDVR 242  
QY 240 RRPWTIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVASNSNAQ 299  
Db 243 NRKWTIOAATSPKDVILVDVSGSMKGLRLTIAKOTVSSILDTGLDGDFFNIITYNEELH 302  
QY 300 DYS-CFO-HLVQANVRNKKVLADANNITAKGIDYKKGFSFAFOLLNLYNVSRA--CN 355  
Db 303 YYPECLNGTLVQDRTRNHEFHEDKKFKAGIGMDLTALNEAFNLLSDFNHTGGSTCS 362  
QY 356 KIIMFTDGEERAQEIFNKYN-KDKKRVFRVSQGHYNERGPIQWMAKNGYYEIP 414  
Db 363 QAIMLITDGAVDYDITPAKYNWPKRVIRFTYLGREAAPADNLKMAKNGFFTOIS 422  
QY 415 SIGAIRINTQEVLDVGRPMWLAGKAKOVQWNTVYL-----ALELGLVI--TGT 463  
Db 423 TLADVOENMYELHVLRSKPTV--DQEHVWVTEAYIDSTLPQAOKLADQGLVMTTVA 480  
QY 464 LPVENITGOFENKTNLKNOLILGVGVDSVLEDIKRLTPREFTLCPNGYFAIDPNGYVLL 523  
Db 481 MPVFS-----KQNETRSKG--ILGVGVGTDPVVKELKTIPIKGLGIGHYAFATNNGYIIL 535  
QY 524 HFNLOP---KNPKSQEP--VTLDLDAELNEDIKVEIRKMKIDGESGKTFRTLVKSQDE 578  
Db 536 HPELRPLYEKGKRRKPNYSYVDLSEVEDRDDV-LRNAMVNRKTGK--FPMVEYK---- 588  
QY 579 RYIDKGNRT-----YTWPVNGTDSLALVLPY--YSFYIYAKLEETITQARSKKGMK 631  
Db 589 KTVDKGRVYLVMTNDYYIDIRKTFPSGLVALSRHGKYFF-----RGNVT 634  
QY 632 DSETLKPDPNFEESGTYFIAPDYCN-DLKISONTEFLNENEFIDRKTNNPNSCNADLI 690  
Db 635 IEGEL--HLEHPDVSADENSYCWTDLHPEHRHLSQLEAIKLYLKGKEP-LLOCDKELI 691  
QY 691 NRVLDDAGFTNELVQNYWS-----KQKNIKGVKARFVVDGIGTRVYP----- 733  
Db 692 QEVLPDA-VVSPAIEAYWTSLALNKSNSDKGEVAFATRTGLSLINLFVGAEOQLTND 750  
QY 734 -KEAGENWQENPETEDSYKSLDN--DNYVETAPY-----FNKSGPGAYESGIMVSKAV 786  
Db 751 FLKAGKENIFNADHPFLWYRAAEOIAGSFYISIPFTSTGTNKS-----NVYTAESI 804  
QY 787 ETYIOGKLLKPAVVGKIDVNSWENFTKTSIRDCAGPVCCKRNSDVMDCVILDDGDF 846  
Db 805 QLLDERKSPVVAAGIOMKLEFPQKFWTASQCASLDCKCSISCDDETIVNCLYLDNNGF 864  
QY 847 LLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGAAPKQAGHRS 906  
Db 865 ILVS--EDYT-QTGDPDFGEVGAVMKLLTMTGSFKRITLYDQAMCR--ANKESDSAH 918  
QY 907 AYVPSVADILQGWATAAAILQFLSLFPPRLLEAVEMEDDDFTASLSEK-----QS 961  
Db 919 GLLDYPYKAF-----SAAKWINTLVFLVFEF---NLCSWMSHSDMTAKAKLQTLPE 968  
QY 962 CTEQOQYFEFDNDSKFSGLVDCGNSRIFHGEKLMNTNLIETVSKGTCPDCT 1016  
Db 969 CDEYPAFVSERTIKETTGNICEDCSKSFVIOQIPSSNLFVWVYDS--SCICES 1021

RESULT 5  
S44617  
C50C3.11 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: S44617  
R:Favella, A.D.  
submitted to the EMBL Data Library, May 1993  
A:Description: Sequence of the C. elegans cosmid C50C3.

A:Reference number: S44618  
A:Accession: S44617  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-734 <FAV>  
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650  
C:Genetics:  
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match 11.4%; Score 607; DB 2; Length 734;  
Best Local Similarity 26.6%; Pred. No. 8.7e-29;  
Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;

QY 47 LAKTASGVNQLVDIYEKYODLYTVEPNARQVVEAARDIEKLLNRS-----KALVSLAL 102  
Db 36 MKETSKSHETILKQNEKLEVEEQFQFRAELKSKKHRIEDYLVKRSFAYKAKIS--L 93  
QY 103 EAEKVOAAHONREDFASNEVVYVYNAKDDLDPEK--NDSEPGSORIKP-----VFIEDANF 155  
Db 94 EARSVRNDSTVNDPOSQSFIRFMSAKQGDGTIYESNHLGRLLKVNKNETKSNLTQANAF 153  
QY 156 -GRQISYQHAHVHPTDIYEGSTIVLNELNWTSADEVFVKKNREEDPSLLQWFGSATGL 214  
Db 154 YLPTSSVSSAVHPTPLYDRNEDLLRKIDW--SDDAVYRTNREETKDLAFQFCSEAGY 212  
QY 215 ARYYPASPMV--DNSTRPKNKIDLYVRRRPWYTOGAASPKDMLILVDVSGSVGLTLKLR 273  
Db 213 MRYYPAAASWFWNDQ--DEHLDLDFCRNTEWYINSATNSKNVILMLDMSGMLGQRYEVAK 270  
QY 274 TSVSEMLETLSDDDFVNVASFNSEA--QDVSCFOHLVQANVRNKKVLADANNITAKGI 330  
Db 271 QTEIALETLSHNDNFNMTFSKNTFLDGCNGTNGLLQATWNRKALKRRKDDTYQSEK 330  
QY 331 TDYKKGFSFAFOLLNLYN-----VSRANCKIIMLFTDGEERAQEIFNKYKDKKRVYF 385  
Db 331 AYEKALPLAFSVLLDINNNGGDNNGRACENVIMLITDGAAPNAKKIFDYNADKKRVYF 390  
QY 386 RFSVQHNVERGPIQWMAKNGYYEIPSGAIRINTQEYL-----DVLGRPMVLAGDKA 441  
Db 391 TELVGEAIDFNEVREMACNRRGYVHVANMADVDKEIHIIYRMSRVVGRYHYESGQLS 450  
QY 442 KQVQWNTVYLDALGLL--VITGTLVPFVNITGOFENKTN----- 478  
Db 451 ---WTVGVRELYLPPEIFAEPVPIITNQSFVAMNKAASRRKIRLOKSEARSMEVTVV 507  
QY 479 ----LKNQILGVGMVDVLSLEDIKRLTPREFTLCPNGYFFAIDPNGYVLLHPLNPKNP-- 532  
Db 508 SYPVIVNETFMGVAANVPLTEVAQKSHPANIGSKSYFFMLDQNGFVMTHPOLRPIDPFT 567  
QY 533 ---KQSEPVTLDPLD-----AELENDIKVEIRKMKID 561  
Db 568 KYHKQNNMMDLLELVGQNVRSQKSAQVSDLVCEGANYAECVDDLRKAVRKMID 627  
QY 562 GFSGEKTFRTLVKSODERY-----IDK---GNRTYTTPVNGTDSLALVLPYTFYFYIKA 614  
Db 628 CONSD-----VQQLDVLVATELLDRVYQTNVYVYAEINHANFVLGLAVAKGDDYRVK 681  
QY 615 KLEETITQARSKKGMK 631  
Db 682 K-----QKKYDFGRVK 692

RESULT 6  
T18770  
Probable calcium channel protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T18770; 125249  
R:Sulston, J.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z19019  
A:Accession: T18770

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1148 <N1>

A;Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6

A;Experimental source: clone B0491

R;Chui, C.

submitted to the EMBL Data Library, June 1995

A;Reference number: Z20004

A;Accession: T25249

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1148 <N1>

A;Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6

A;Experimental source: clone T24F1

C;Genetics:

A;Gene: CESP:T24F1.6

A;Map position: 2

A;Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.7%; Score 569.5; DB 2; Length 1148;  
Best Local Similarity 21.5%; Pred. No. 3.2e-26;  
Matches 234; Conservative 216; Mismatches 406; Indels 233; Gaps 42;

QY 37 VDKMOEDLVTLA-----KTASGVNQLVDYIEKYQDLYTVEPNNAOLVEIFAARDI 86

DB 99 VDTIEEAPASIAQSANTLRDFQTQSRFSLVQEEKLPDKIKSKKEDAAEKLVRATEHL 158

QY 87 EKLNSNRKALVSLALEAKVQAQAHQWEDFASNEVYVYNAKDDLDPEKNSEPSQR-- 144

DB 159 DRLVTNRVDAKLKASSAESA--DEYDDQAYAVPQADKRCE 201

QY 145 --IKPVTFEDANFGRIQYQH--AAVHIPDIYEGSTIVNELNWTSA--LDEYFKNR 197

DB 202 AYMKKNESDMHFVSNM--VENSRSIGIHTVESYQCDPRVMDFDWTGKLEKTMDSNK 260

QY 198 EEDPSLLMQVGSATGLARYPASPWVNSRTPKNIDYVRRRPWYIOGAASPKDMLIL 257

DB 261 EKAPEMGHQYIGTSGLRMPRRHW--KVEPTPIIDLFPRFRPFWNAESVVPKDIIVFL 319

QY 258 VDVSGSVSLTLKLRISVSEMLETSLDDDFVNVASFNAQD--VSCFOH--LVQANVRNK 315

DB 320 LDYSGSVGPTMHLKIKITLSTLSPNDYFGFYVNNHFNPIISCRANTPMPATTSNK 379

QY 316 KVLKAVANITAKGITDYKKGFSFAEOL--LNTNVS-----RANCKIIMLFTDGGEE 367

DB 380 KVFPEELGNLEEKDOAHATPLKFLSLDLVRLGNSQSLFADYRSEGHKLLIIFTGVDE 439

QY 368 RAQEIFN--KYNKDKVVRFRFSGQHYNERGPIQWACENKGYIYEIPSGAIRINTQ 424

DB 440 WPHQILDEEFOTRNSGLIRIFGSMGYTSLPLLOQYACKSHGGYSEIDSMVYKQSR 499

QY 425 EYLDVLRPMVLGDKAK-----OVQWTVNYLDALGLVITCTLPVNTGOFENKT 477

DB 500 TIQNVLSQ---VRGDELGTNAEKREPSWTQYMTQGTGPIVTLSPILT-----SEQR 551

QY 478 NLKNQILIGVMGVDSLEDIKRLTFRFLCPNGYIFAIDPNGYVLLHPLNQ--PKNPK--- 533

DB 552 IWRDQKLAGVAIDISIEFVKHLP--TSSEQMYGYIVDNGMLYVHQLQIPKTEVHCV 609

QY 534 -----SQEPV-----TLDFLDAELENDIKVETRN 557

DB 610 RRSACYDAQVQKQAGSLRVHYGFSDEVRVGLVGLIDSPTLDMYDLEGGDTAIRDLR 669

QY 558 KMDGESGEKFTLVKQODERYIDKGRNTYTWVNGFDYSIALV--LPTYSFYIKAK 615

DB 670 -----RIITKCYEARAKNSKHCYHCKSPFFTLVIVNNIQLKTVTIDSV 717

QY 616 LREETITQ-----ARSKKGMKMDSETLKPONFEESGYFTIAPRDYQ--NDLKISDNNT 665

DB 718 QELGLTDNKLVTFFPRDRVQCKWLDVAAHDFRV--WSDISEKEICAQDDMLRAPFT 775

QY 666 EFLNNEFIDRKTNNPNSCNADLRNLVLLDAGFTNELVQNVWSKOKNIKVKARFVVD 725

DB 776 KGLGSWTOSWPKSDIEHTTC-----LLAQYPENASVPHYVNS-----FVHTR 817

QY 726 GGITRVYKEAGENQWENPETEYDFYKSLDNDNYFTAFYFNKSGPGAYESGIMVSKA 785

DB 818 SKLTAFYPTCSSHDMKAVNKKFDEEI--KLTDNDFV---QFSMR-----SESLIYRT 866

QY 786 VEYIQGLKLPVAVGIIKIDVN---SWIENTFTKTSIRDPACAGPVCDCRNSD-----VMD 837

DB 867 IADYDNNEL--AVVGTQWKENFFDQYDFDFT-----RQNPDKWICKRQE 908

QY 838 CVILDDGGFLLMANHDDTYNIGREFGEIDPSLMRLHVNISVYAENKSVDYQSVCE--PGA 896

DB 909 CSIIITRNHGHVIASSAHRAPAHAKF---DPQLFESLVKVNLDVNSTWTEVQSECKAKRV 964

QY 897 APKQAGHRSA-----YVPSVADILQIGWATAAASLIQOFL-----SLTFP 940

DB 965 APWSAAPGSSSILRYFVTSIFKLAKTSFWR-----NLLESALTIVDAQPSMTGNTCTFO 1019

QY 941 RL--LEAVEMEDDDPTASLSKOSCTEOTQYFFDNDKSFSGVLDGNCRSRIFHGEKLMN 998

DB 1020 KIKPPERCFFMFFHYRMTLN---ITKQLQ-----LTGMSTCSRYSKLY---PVPH 1063

QY 999 TNLIFIMVE 1007

DB 1064 TTLSLIAD 1072

#### RESULT 7

C86880

hypothetical protein yvcC [imported] - Lactococcus lactis subsp. lactis (strain IL140

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001

C;Accession: C86880

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh

Genome Res. in press, 2001

A;Title: The complete genome sequence of the lactic acid bacterium.

A;Reference number: A86625

A;Accession: C86880

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1450 <SPO>

A;Cross-references: GB:AB005176; NID:gl2725093; PIDN:AAK06141.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: yvcC

Query Match 3.7%; Score 198; DB 2; Length 1450;

Best Local Similarity 21.0%; Pred. No. 0.0012;

Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56;

QY 37 VDKMOEDLVTLAKTAGVNVOLVDYIEKYQDLYTVEPNNAOLVEIFAARDIEK-----L 89

DB 69 INKTENDLKLKFFEGNQPIEBE--NESWTLKEKNT-----IISDFERENEGKIYL 120

QY 90 LSNRSKALVSLALEAKVQAQAHQW---EDFA-----SNEVYVNA 127

DB 121 RANNSISLNLLEIQDAKLIENDQEVISEDILAKKESTIFSLYIPENKADSKEDKNKT 180

QY 128 KDDLDPKNDSPFGSORIKP---VFIEDANFGRIQISYQHAHVH----- 167

DB 181 EEVLWNSSQEETVSQLKDSQLAFSPFNFGIKASFNDLAQNYENISPEYQDETGISP 240

QY 168 ----IPTDIYEGSTIVNELNWTSALEDFYKKNREDPSLLMQVGSATGLARYYPASPW 223

DB 241 NISWITP-----CNTTVVNHQGNF-----SSQWDGVNSNN--GEATNLSYIEYAG 287

QY 224 VDN-----SRTPNKIDLY--DVRRRPMYIOGAASPKDMLILYDVSGVSLTLK 270

DB 288 VNNPVDALRKVAKETETGLYDVVNLVRGN---VQNPIKPVLDIVLIDMSGSMQAKET 344

QY 271 LIRTSVSEMLETSLDD---DFNVN--ASFNSNAQDVSCFQHLVQANVRNKKVYLDK----A 321



Db 345 AVRCQVDFSLSTQNTAWADYVNVGIVCSFGNVVTGASCYITVPI--DKVSSSHVKS 402  
Qy 322 VNNITA---KGITDYKGFSAFAPOLLNYSRANKNIIMFLTDGGEERAEIFNKYNK 378  
Db 403 INOALAPOFGSGTFLGRKGTEML---EQDSSDNQKMMILMTDG---VPTESYKVN 455  
Qy 379 DKYR--VFRSVGHNYERG---PIQ---WACENKGYEYI-----PSIGAIRINTQE 425  
Db 456 ASKVDNVIYOGSFAESRDEPGNTSKIOSPYVKDINGGNSIEIRDTWAATIGEAIEISKQ 515  
Qy 426 YLDVLRGPMVLADG-----KAKQVQWTVNYLDALGLVITGTLVPFNITGOF 474  
Db 516 ISEIHTLQIOLGNDGSYLSQBEVKSRTSLIATGLYODANSAN-----DITDYLK 565  
Qy 475 NKTN-----LKNQLILGVGVDSVLEDKRLTPRTFLCPNGYFAIDPNGYVLLHPN 526  
Db 566 NOANVLSRFNTITNGLILDPLGAOFYKDKT-----FEITSVG-----604  
Qy 527 LOPKNPKSQEPVTLDFDAELENDIKVEIRKMGIDGESKTFRTLKVSQDERYDKGNR 586  
Db 605 -----EDSINLPTGKINKEGLEISLNI--GKNOEVOIHQVRLNTETDDFKTNY 653  
Qy 587 TY-----TWTPVNGT--DYSIALVLPYSFYIKAKLE-----ETITQARSKK 627  
Db 654 WQMGNETLTP--NGSNPDKNVFCPSAKSSGINLTLEKQWLANSENI PENVELLIGRR 712  
Qy 628 GKMDSE-----TLKPDNFBESGYTFIAPDYCNLDKISDNNTFELLNFNFBIDRKTNN 682  
Db 713 SAQISSDWTKTTLKEDDEWRSQLENPKYSILGBEFYIEKDEIVLN--SEIYDWITIGE 771  
Qy 683 PSCNADLNRVLDD---AGFTNELVQNVSKQKNIKGVKARFVVDGGRVYVPKEAGE 738  
Db 772 DKTITANIEKFLQLIKTSNHDNEPLSEVEFVLKNSQEEIDKAVTN-----EKGE 822  
Qy 739 --NQENPETEYDFSKRLSDNDYVFTAPYFNKSGPAGYSGIWSK-----AVEIYIQ 791  
Db 823 ILFDKTRNLNVEEYOLHEIKSPGHSLEGPWKIKT--EFENGQPIIKVDGEQIALDEHN 879  
Qy 792 GKLLPAPVGVKIDVNSWIEFTKISIRDCPAGVDCCKRNSDMVCILD-----DG-- 844  
Db 880 KFMIS--LNTINDIN--VEEF-----RNSVTIDKRAVDSEELDGAV 917  
Qy 845 -GFLMANHDDVTNOIGRFFGEIDPDLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQAG 903  
Db 918 FNLYQIESVDELTLQKPL--EITNMLPGL-----YALQESVSPNGYTRDDEV 964  
Qy 904 H--RSAYVPSVADILQIGWATAAAWSILOQFL-----IDPFLDENESKGNLNEENGDLHLTLIFY 1015  
Db 965 HFRVYKNGSIVAIGSEG-----IDPFLDENESKGNLNEENGDLHLTLIFY 1015  
Qy 940 ----PRLEAVEMEDDDTASLSKQSC--ITQOTQYFFNDS-----KFSGVLDGNCRSRI 990  
Db 1016 NOAVPPLQLEVDKIDDDFTSLAGVSEFELTRLGKSTDSVSKRINSFDRILKTFN--NE 1073  
Qy 991 FHGEKL--MNTNL 1001  
Db 1074 FTGETIALKNSL 1085

## RESULT 8

inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 04-Feb-2000  
C:Accession: S54355  
R:Chan, P.; Risler, J.L.; Raguenez, G.; Sallier, J.P.  
Biochem. J. 305: 505-512, 1995  
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse.  
A:Reference number: S54353; MUID:95194326  
A:Accession: S54355  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA

A:Residues: 1-886 <CHA>  
A:Cross-references: EMBL:X70393; NID:g695635; PIDN:CAA49843.1; PID:g695636  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match 3.6%; Score 194.5; DB 2; Length 886;  
Best Local Similarity 19.9%; Pred. No. 0.00091;  
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

Qy 27 FPSAVITKSWDKMOEDLVTLAKTAGSVQNVLDYIEKYQDLYTYEPNNARQLVEIAARDI 86  
Db 98 YPGNVKEVAQKQYKAVSOCKTAG---LVKASGRKLEKFTVSVNVAAGSKVTFELTY 153  
Qy 87 EKLLSNSKALVSLALEAEKQAAHQWREDFASNEVVYNAKDDLDPEKNDSEPSQRIK 146  
Db 154 EELL--KRNGKYEMLYKVPKQLVRHFEID-----AHIFEP-----Q 189  
Qy 147 PVFTEDANFRQISVQAAHVHIPTDIYEGSTIVLNMELNWTISALDEVFKKNEEDPSLLMQ 206  
Db 190 GISMLDAE-----ASFITNDL--LGSALTAKSF-----214  
Qy 207 VFGSATGLARYPASPWDNSRT--PNKID-----LYDVRRRP-----WYI-- 245  
Db 215 ---SGKKGVSPKPSLDQOOSCTCTDSLNGDFTIVDYNRESPGNVQIVNGFYVHF 269  
Qy 246 --OG--AASPKDMLILVDVSGVSGLTLLKLRISVSEMLETSLDDDDFVNVASFNSNAODV 301  
Db 270 FAPGLPVVPIVFIIDVSGMSGRIKQOTREALKILDDVKEDDYLNFILFST---DV 326  
Qy 302 SCFO--HLVQANVRNKKVLKDAVNNITAKGITDYKGFSAFAPQLLNNYVSRAN-----C 354  
Db 327 TTWKDHLVQATPANLKEAKTFVKNIHQDSMTNINDGLKGIEML---NKAREDHVTPERS 383  
Qy 355 NKIMLFTDG---GEERAQEIFNKYNK--DKKVVRFVSFGQHNRYERGPQWMAECENKG 408  
Db 384 TSIIIMLTGDDANTGESRPEKIQENVRNAIGGKFLYNLGFQ--NNLNTNFLETLAENHG 442  
Qy 409 YYEIPSGAIRINTQEVLDVLRGPMVLADGKAKQVQWTVNYLDALGL--VITGTLPV 466  
Db 443 LARRIYEDSDANLQOGFYEVANPLL-----TNVEVEYEPENAILDLTNSVPH 491  
Qy 467 FNITGQFENLKNQLILGVGVDSVLEDKRLTPRTFLCPNGYFAIDPNGYVLLHPN 526  
Db 492 F-----YDG-----SEIVVAGRLVDRNDN-----FKADVKGHGALN-- 523  
Qy 527 LOPKNPKSQEPVTLDFDAELENDIKVEIRKMGIDGESK--TFTLVKSQDERYIDKG 584  
Db 524 ---DLTFTEEVDMEENDALK-----EOGYIFSDYIERLWAYLTIEQLLEKRNKAG 572  
Qy 595 NRTYTWTPVNGTDYSLA--LVLPYTSFYIRAKLBETITQARSKGKMKDSE-----LK 637  
Db 573 DEKENIT--AEALDLSLKYHFTPLTSWVTPKPEDNEDQTSIADNAGEAFAETTTMSFLT 631  
Qy 638 PDNFEESYGTIAPRDYCNLDKISDNNTFELLNFNEFIDRKTNNPNSCNADLINRVLLDA 697  
Db 632 TQOSSQSPYIV-----DGDPHFIQI-----PGKNDSCIFNIDEKP 668  
Qy 698 GFTNELVQNVSKQKNIKGVKARFVVDGGRVYVPKEAGENWQENPETEYDFSKRLSD 757  
Db 669 GTVLRLIQD-----PVT--GIT-VTGQIIGD-----KRS-- 694  
Qy 758 NDNVVFTAPYFNKSGPAGYSGIWSKAVEIYIOCKLLKPAVVGIKIDVNSWIEFTKTS 817  
Db 695 NASSRTGTYTFGKLGITNWMDFRVEVTEKILG-----TGAEIITFSMLDVTVTQ 747  
Qy 818 IRDPCAGPVDCCKRNSDMVCILDG--GFLMAN-----HDDYTNQIGRFFGEIDP 868  
Db 748 ----TGLSVTINRKNV--VSFGDGSIFVILLHQVKKHPVHQDELG-----FYVVD 795  
Qy 869 SLMRHLVNI SVYAFNKSVDYQSV--CEPGAAP 898  
Db 796 HRMSAQTHGLLQGFQFPDFKVFGRPGSDP 826



Db	409	EYENLDKKGYSIN-TFLESLNHGKQCQ-----	-----DN 438
Qy	192	VFKKNEEDPSLLQVFGSATGLARYYPASP-----	-----WVDSNRPNKI 233
Db	439	IDKKNKTNFKNL-ETFGP-----SGYECACPIYGVKCSNEKCTPVTENWNSNRRLPTDT	493
Qy	234	DLYDVRRRFWYTGGAASPKMDLILVDVSGVSGLTGLKLRTSVSEMLETLSDDDFNVAS	293
Db	494	STKNLN-----ATNIDMLVDNGIGNAI-----	515
Qy	294	FNSNAODVSCFOHLVQANVRNKK-----VLKDAVNNTAKGITYDKKGFSPAFEQLL	345
Db	516	--DNELEKNTYGLIGLKKQKWOCYLNINIDOCKINNVSNSYFDNKAFLVFLQRLW	573
Qy	346	NYNVSBRANKNIIMLPTDGGEEARAQEIFNKYKDKKVRFRFSYGVQHNYERGPQIMWACE	405
Db	574	RYFVRDHRNLK-----EKIDVCIKKENINENICIKRCKTN-----CE	610
Qy	406	NKGYEYIEISGAIRI-----NQEYLDVLGRPWLVLGDKAKOVQWTVNYLDLLEGLVIT	461
Db	611	CVGKWLKEKAEWDKINOHYNKNHIMFILPYWITGYEK-ITFPDNDFKALE-----DV	665
Qy	462	GTLPVNITGQPEKNTLNKOLLGVMGVDVLSLEDIKRLTPRFLCPNGYVFAIDPNGYV	521
Db	666	DTINVLDTLKEOD-THCKIEKIRSI-DVDLKEIISWLQNKIEVCKS--HHDEDKREYC	721
Qy	522	LLHPNLQPNKPSQEPVTLDFDLAELENDIKVEIRNKMIDGESKGT-----FRT	571
Db	722	C---DILPKSVDDDEDD--EEDVEEKESSTQTKRN--ISQGTGKSAVCYKGCACIVKG	775
Qy	572	LKVSQERYID---KGNRTYTW-----TPVNGTD-----YSLALVLPYISF	609
Db	776	VLQOKNSGSDNCNAKNRKNKNEWQCDKNTFVDGNEGVCWPPRRKKSICIHNLTLLEOTKKN	835
Qy	610	Y-----YIRAKLEET-ITQARSKGKMKDSETLK---PDNFEE-SGVTFETAPRDYC--N	656
Db	836	YQLREAFICAAKETNLLWDKYNDKNEABELLKKGKIPEDFMRIMFTFGDFDFRCUEN	895
Qy	657	DL-----KISDNNTEFLNFNFIDRK-----TPNPPSC-NADLINRVLLDAGFTNEL	703
Db	896	DAGKQVDYKVKKNKYNFNSSKRGFKKIDPENWNWENGQIWNGLMICALIHADTKDSIKN	955
Qy	704	VQNY-----W-----SKOKNTKGVKARFVV	723
Db	956	KDNYKYEKVTILAKRDSGNMTLSEFAKPKPLRFVFEWYDDYCKEROKYLTVEASTCKS	1015
Qy	724	TGGITRV-----YPKAGENWQENPETYEDSYKKSLDN-----DNVV-762	
Db	1016	IDGQLKCDRGCKNKCDEYKKYMRKKKEPWNLODKYYKDKRENKIDGKPGTGIIVKDIVL	1075
Qy	763	-----FTAPYFNKSGPAYESGIMVSKAVEIYIQGLLPAVVYGIKIDVNSWI--	810
Db	1076	ANAKYLLKFTASCVTSSGKAONSATEEVKNIELLEEYQ-----YDAQYCGC	1126
Qy	811	-----ENFTKTSIRDPGAPVCDCK-----RNSDVMDCVIL	841
Db	1127	TKFHDDKYSKISGRSNCCLNSDAKKNKIKWRNSDEKDIAPL	1169
RESULT	12		
	A44396		
	P-type cation translocating ATPase - malaria parasite (Plasmodium falciparum)		
	C:Species: Plasmodium falciparum		
	C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000		
	C:Accession: A44396		
	R:Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; Robson, J. Cell Biol. 120, 385-398, 1993		
	A:Title: A family of cation ATPase-like molecules from Plasmodium falciparum		
	A:Reference number: A44396; MUID:93132070		
	A:Accession: A44396		
	A>Status: preliminary; not compared with conceptual translation		
	A:Molecule type: nucleic acid		
	A:Residues: 1-1984 <RR>		

0001 YI ---DCDKNTGANDERCHI.NN-----NLVSYNILKRF----- 912

QY 950 DDDFTASLSKQSCITEQTQYFFDNDKS 977  
 : : | : | : | : | :  
ph 913 --EFOSRLORMSVIVKST-YGNNNDDNN 937

RESULT 13  
D64998  
hypothetical protein b2270 - Escherichia coli (strain K-12)

C:Accession: D64998  
C:Author: Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of  
A:reference number: A64720: MUID:97426617

A:Accession: D64998  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

204.	score	157	5.	DB 2:	length	575:
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Query Match	2.9%	Score 137.15, 25.27	25
Best Local Similarity	21.6%	Pred. No. 0.078	25
Matches 111: Conservative	93	Mismatches 206	Indels 105; Gaps

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D6 22 QPENKESQQUPSTPTEQVLAAQQUAATK - EAEQSSAA  
AKAHEQQEVEEQZCEAQ... I S

QY 131 LDPEKND-----SEPGSQRIPVFIEDANFGRQISYQHAA---VHIPTDI 172

76 YOCPIQEAQTEFBAAKAKATHANPGTARYOOF--DDNPVKOVAONPLATESLDVDTGS 132

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QY	1/3 YEGSTIVLNE	-----	LNWISALDEVEFKNKREDD	SABWVZSCN
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Db 133 YANVRRFLNQGLPPFDVAVRVEEIVNYFSPDWDI--KDKQSIASKPIPFAMRYELA--- 18/

210 D A S C E T T N S E P T P N K T N I Y Q N V R P R P W V T O G A A S P K D M L I L V D V S G S - V S G L T L K L I R T S V S 277

[illegible]

DB 188 PA-PW-NEQRTLLKVDILANDRNSEELPAS - - NEVLEEDICCOONICDSEENALZANZGEEEN

QY 278 EMLETLSDDDFVNVA SFNSNAQDVSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGF 33/

243 r i t k e l p e o d n i a t i v t y a g d s p r i a - - - - l . p s t s g s h k a e i n a a i d s l d a e g s t n g g a g l 296

100

QY 338 SFAFEQLLNYSRANCNKILIMLFIDG-----GEENAQELTNKYNASAAVATKESVCE

Db 297 ELAYQQATK-GFIKGGINR-ILLATDGD FNVGIDDPKSIESMVKKQRESGVTLS TFFGVGN 354

303 \*\*\*\*\*CENVCVVVFIPSTGATPINTOEVI.DVI.GRPMVL.---AGDKAKOVO-----445

[illegible]

D6  
355 SNYNEAMVRIADVGNIGNYSI IDTLS ---EAKAVENSEMKNQMETTVANDVAHQZSEKARH

QY 446 WTNVYLDALGLVITGTLVPFNITGQFENKTNLKNQLILGVMGVD-VSLEDI---KRLT 501

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 104

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QY 502 PRFTLCPNGYFAIDPNGYVLLHPNLQFANPSQE 330

448 LFFELTLNGQKASIDKLRYA--PDNKLAKSDKTK 480

## RESULT 14

E71619 *Plasmodium falciparum*

C:Species: Plasmodium falciparum

C;Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Nov-1998

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R; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Perle, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998

A:Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.

A:Reference number: A71600; MUID: 99021743

A:Accession: E71619

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1516 <GAR>

A:Cross-references: GB:AE001383; GB:AE001362; NID:G3845135; PIDN:AC71842.1; PID:G3845135

A:Experimental source: clone 3D7

C:Genetics:

A:Gene: PF02465C

[illegible][illegible]

Query Match	2.9%;	Score 155;	DB 2;	Length 2364;
Best Local Similarity	18.7%;	Pred. No. 1;		
Matches 217;	Conservative 132;	Mismatches 342;	Indels 468;	Gaps
Qy	12	TLFOSLLIGSPSEPPFSAVTIKSWDKMQEOLVTLAKTAGVQNLVDIYEKYQDLTYVE	71	
Db	1137	TLDDKTI MPQDD-----LVLSEID-FNNNSITLGC-----EIWRAE	1173	
Qy	72	PNNARQLVETAAARDIEKLUNRS-----KALVS-----LALAEAKVQAAHQWREDFASNEVV	123	
Db	1174	GGSGHTLTDD---DIDHFFSSPSITYRKPELWSIYDLVNLIKKEKI-----DFSKDLMV	1221	
Qy	124	YYNAKD-----DLDPEKNDESPGSRKRP-----VFIEDANFGR-	157	
Db	1222	LPNAPNVFGYMGWTPGGRSLD---NODTKLLDRIDHYEQFTWRVFAFIADALITKL	1278	
Qy	158	QISYQHAHVHPIDIYEGSTIVLNEIWMTSALDEYFKNREEDPSLLMQVFGSATGLARY	217	
Db	1279	KPRYEDINVRILNDGNTRSFIV-----PVITTEQIRKN-----LSYSFYGS--GGSYS	1324	
Qy	218	YPASPWVDNSRTPNKIDLDVRRRPWYIOGAASPKDMLILVDVSGSVGGLIKLIRITSV	277	
Db	1325	LSLSPYNNM-----IDLALVENDTW-----VIDVMVKNKITESDEIQKG	1365	
Qy	278	EMLETSLDDDDFVNWASFNSNAQDVSCFHLVQANVRNKVKLKDVA NNITAK--GITYDK	334	
Db	1366	ELIENI-----LSKINATEDNKII--LNNHTINFYGDINESN	1399	
Qy	335	KGFSFAFEQLLNYN-----VSRA-----NCNKIIMLFTD-----GGEERAAQ	370	
Db	1400	RFISLTSILEDINIITIEDLVGSKYKILLGSCMKLIENSDDIOQKIDHIGFNGEHQKY	1459	
Qy	371	EIPN-----KYN-----KDKKYVRFPSVGOHNYERGPLOWMACENKYYEIEPSIGAIR	420	
Db	1460	IPYSYIDNETKYNGFIDYSKKEGLFTAEPFSNEIIRN--IYMPDSNNLFIYSSKDLKDIR	1517	
Qy	421	INTOEYLDVLGRPMVLADGAKQ-----VOMTNYVDLAEGLGVITGTLF	465	
Db	1518	IINK-----GDVKLLIGNVFYKDMKVSLSFTIEDNTIKLNGVYLDE-----NGVAQ	1564	
Qy	466	VFNITGQFENKTNKQOLLGVWGVVDVSLIEDIKRLTPRETLCPNGCYFAIDPNGYVLLHP	525	
Db	1565	ILKFMNNAKALATNSLNMFLNESINK-----NIFYANNLPDNIETFILOD	1609	

QY 526 NLOPKNPKSQEPVTLDFLDAELENDIKVEIRNMIDGESGEXTFTFLVKSQDERYIDKGN 585  
Db 1610 NF-----IISGNSIGQFE-LICDKDN-----1631  
QY 586 RYTWTPVNGDYSLALVPTYSFYIKAKLBETITQARSKKGMKDSLTLPDNEESG 645  
Db 1632 -----IQP-----YFINKIKET-----SYTLVYVGNQN--1655  
QY 646 YTFIAPRDYCNLIKSDNTEFLNENE---FIDR---KTPNPNPCNADLIN-----691  
Db 1656 -LIVESYHLDD---SGNLSVFINESQKLYLGIDRYVNVKIAPNLYTDEINITPVYKP 1711  
QY 692 -----RVLLDAGFTNE-----LVQNYW-----SKOKNIKGVKAREVVT 724  
Db 1712 NYICPEVITLDANYINEKINVININDLSIRVWMDNGSDLILIANSEEDNQPVKIRFV--1769  
QY 725 DGGITRVYPERAGE-----NQENPE-----TYEDSFYKR-----SLDNDNY 761  
Db 1770 -----NVFKSDTAADKLSFNFSKQDVSVSKIIISTFSLAAYSDFDYEFGLVSLDND--1822  
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVIYIOGKL--LKPAVVVGKIDVNSWIENFTKTSIR 819  
Db 1823 -----YFYINSGNMYVSGL-----IYINDSLYIEKP-----PKNNLITGFTTI---1860  
QY 820 DPCAGPVCDCKRNSVMDCVILDDGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNISV 879  
Db 1861 -----DGN-----KYFDPKSGAASIGBI-----TIDGKD 1886  
QY 880 YAFNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILOQFLLSLTF 939  
Db 1887 YFEN-----KQG-----ILQGVINTSDG---LKYFAPAGTL 1915  
QY 940 PRLEAVEME-----DDDFASLSKQSCITEOTOYFFDNDKSFSGVLDCG 985  
Db 1916 DENLEGESVNFICKLNDGKIYYFEDNYRAV-EWKLDDETYYFNPKEALKGLHQIG 1974  
QY 986 NCSRIFHGEKLMNTNLIFI 1004  
Db 1975 DNKYFDDNGIMOTGFITI 1993

Search completed: July 23, 2001, 07:37:58  
Job time: 495 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 07:47:59 ; Search time 66.28 Seconds  
(without alignments)  
526.133 Million cell updates/sec

Title: US-09-397-548-15

Perfect score: 5346

Sequence: 1 MAAGCLLALTLFOSLLIG.....TNLFIMVESKGTCPDTRL 1018

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5346	100.0	1091	1 CIC2_HUMAN	P54289 homo sapien
2	5145	96.2	1091	1 CIC2_RAT	P54290 rattus norv
3	5132.5	96.0	1106	1 CIC2_RABIT	P13806 oryctolagus
4	607	11.4	734	1 UN36_CAEEL	P34374 caenorhabdi
5	194.5	3.6	886	1 ITH3_MOUSE	Q61704 mus musculu
6	182	3.4	885	1 ITH3_HUMAN	Q06033 homo sapien
7	180.5	3.4	887	1 ITH3_RAT	Q63416 rattus norv
8	164.5	3.1	886	1 ITH3_MESAU	P97280 mesocricetu
9	161	3.0	1829	1 DPOL_THEST	O33845 thermococcu
10	159	3.0	1956	1 APX1_PLAPA	O38495 plasmodium
11	157.5	2.9	575	1 YPBK_ECOLI	P76481 escherichia
12	154.5	2.9	946	1 ITH2_HUMAN	P19823 homo sapien
13	152	2.8	1290	1 BXC1_CLOBO	P18640 clostridium
14	151.5	2.8	420	1 Y103_SYNY3	O55874 synecocyst
15	150.5	2.8	921	1 ITH4_PIG	P79263 sus scrofa
16	150	2.8	654	1 MCPB_BACSU	P54576 bacillus su
17	149	2.8	930	1 ITH4_HUMAN	Q14624 h inter-alp
18	148	2.8	964	1 DPOL_CBEPT	P30319 choristoneu
19	144	2.7	1087	1 XYNX_CLOTRM	P38535 clostridium
20	143	2.7	946	1 ITH2_MESAU	P97279 mesocricetu
21	142.5	2.7	382	1 YLJ0_CAEEL	P34373 caenorhabdi
22	141	2.6	1251	1 RBP2_PLAVB	Q00799 plasmodium
23	140.5	2.6	935	1 ITH2_PIG	O02668 sus scrofa
24	140	2.6	2710	1 TOXA_CLODI	P16154 clostridium
25	140	2.6	3305	1 APLP_MANSE	Q25490 manduca sex
26	139.5	2.6	764	1 PAG_BACRN	P13423 bacillus an
27	139	2.6	1513	1 STUL_YEAST	P38198 saccharomyc
28	138	2.6	1180	1 C4AA_BACTI	P16480 bacillus th
29	137	2.6	984	1 HYSA_STRAG	Q53591 streptococc
30	136.5	2.6	3063	1 CA1C_HUMAN	Q99715 homo sapien
31	135.5	2.5	946	1 ITH2_MOUSE	Q61703 mus musculu
32	134.5	2.5	2077	1 TEGU_HSV6U	P52340 human herpe
33	133	2.5	862	1 MUTS_BORBU	O51737 borrelia bu

## RESULT 1

## CIC2\_HUMAN

ID CIC2\_HUMAN STANDARD; PRT: 1091 AA.

AC P54289;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA

DE SUBUNITS PRECURSOR.

GN CACNA2D1 OR CACNL2A OR CCHL2A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92110010; PubMed=1309651;

RA Williams M.E., Feldman D.H., McCue A.F., Brenner R.,

RA Velicelebi G., Ellis S.B., Harpold M.M.;

RT "Structure and functional expression of alpha 1, alpha 2, and beta

subunits of a novel human neuronal calcium channel subtype.;"

RL Neuron 8:71-84(1992).

CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN

EXCITATION-CONTRACTION COUPLING.

CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:

ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS

HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND

AORTA TISSUES.

CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM

A PRECURSOR FORM (BY SIMILARITY).

CC -!- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

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EMBL; M76559; AAA51903.1; -;

MIM; 114204;

InterPro; IPR002035; -;

Pfam; PF00092; vwa; 1.

PROSITE; PS50234; VWFA\_DOMAIN; 1.

Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

Calcium channel; Glycoprotein; Phosphorylation; Signal.

SIGNAL 1 24

CHAIN 25 944

L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT

(BY SIMILARITY).

L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY

SIMILARITY).

POTENTIAL.

CHAIN 945 1091

TRANSMEM 446 469

TRANSMEM 906 930

## ALIGNMENTS

34 133 2.5 1323 1 ADRI\_YEAST P07248 saccharomyc  
35 132.5 2.5 547 1 SYA\_BUCAL P57210 buchera ap  
36 132.5 2.5 929 1 CAIC\_NOTVI Q91145 notopithalm  
37 132.5 2.5 1679 1 YIOG\_YEAST P40457 saccharomyc  
38 132 2.5 697 1 DE9C\_SCHPO O13773 schizosacch  
39 131 2.5 1634 1 DPOL\_METJA Q38295 methanococc  
40 130.5 2.4 987 1 YD94\_METJA Q58789 methanococc  
41 130.5 2.4 1018 1 YC14\_METJA Q58611 methanococc  
42 129.5 2.4 1658 1 YM67\_YEAST Q38661 saccharomyc  
43 129 2.4 1244 1 Y307\_MYCPN P75342 mycoplasma  
44 128.5 2.4 1254 1 UBPC\_YEAST P39538 saccharomyc  
45 128 2.4 1113 1 Y140\_MYCPN P75033 mycoplasma



TRANSMEM 1067 1086 POTENTIAL.  
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 769 769 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 883 883 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 973 973 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 986 986 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT MOD\_RES 501 501 PHOSPHORYLATION (BY CAPK)  
FT MOD\_RES 833 833 PHOSPHORYLATION (BY CAPK)  
FT MOD\_RES 833 833 PHOSPHORYLATION (BY CAPK)  
FT SEQUENCE 1091 AA; 123183 MW; 254E13EE29A47837 CRC64;  
FT SEQUENCE 1091 AA; 123183 MW; 254E13EE29A47837 CRC64;  
Query Match 100.0%; Score 5346; DB 1; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 2e-299;  
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAACLLALITLFSQSLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAACLLALITLFSQSLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKQDLYTVEPNARQLVEAARDIEKLSNRKALVSLALEAEKVQAAHOWREDPASN 120  
DB 61 YEKQDLYTVEPNARQLVEAARDIEKLSNRKALVSLALEAEKVQAAHOWREDPASN 120  
QY 121 EVVYNKADLLDPEKNDSEPGSQRIKPVFIEDANFRQISVQHAHVHPTDIYEGSTIVL 180  
DB 121 EVVYNKADLLDPEKNDSEPGSQRIKPVFIEDANFRQISVQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTALDVFVKKNEEDPSLLQVFGSATGLARYYPASPPWDNSRTNPKIDLYDVR 240  
DB 181 NELNWTALDVFVKKNEEDPSLLQVFGSATGLARYYPASPPWDNSRTNPKIDLYDVR 240  
QY 241 RPWTIOGAASPKMLILVDVSGVSGLTILRTSVSEMLETSDDDFVNVSFNSNAQD 300  
DB 241 RPWTIOGAASPKMLILVDVSGVSGLTILRTSVSEMLETSDDDFVNVSFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNVRANCNKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNVRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKNKDKVRVRESVGOHNYERGPQIWMACENKGYIYEIPSGAIR 420  
DB 361 FTDGGEERAQEIFNKNKDKVRVRESVGOHNYERGPQIWMACENKGYIYEIPSGAIR 420  
QY 421 INTOEYLDVLRPMVLADGAKAQVQWNTNVLDLGLVITGLTPVNTIGQFENKTNLK 480  
DB 421 INTOEYLDVLRPMVLADGAKAQVQWNTNVLDLGLVITGLTPVNTIGQFENKTNLK 480  
QY 481 NQLILGVAGVDVSLIEDIKRLTPRTCLPNGYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
DB 481 NQLILGVAGVDVSLIEDIKRLTPRTCLPNGYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
QY 541 DFLDAELNDIKVEIRNKMIDGESKERTFTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
DB 541 DFLDAELNDIKVEIRNKMIDGESKERTFTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
QY 601 ALVLPYTFYIYAKLETTTOARSKGKMDSETLPDPNFEESGYTFIAPRDYCNDLKI 660  
DB 601 ALVLPYTFYIYAKLETTTOARSKGKMDSETLPDPNFEESGYTFIAPRDYCNDLKI 660  
QY 661 SDNTEFLNFEIDRKTNNPNSCNADLNRVLLDAGFTNELVQVWSKQKNIKGVKAR 720  
DB 661 SDNTEFLNFEIDRKTNNPNSCNADLNRVLLDAGFTNELVQVWSKQKNIKGVKAR 720

DB 661 SDNTEFLNFEIDRKTNNPNSCNADLNRVLLDAGFTNELVQVWSKQKNIKGVKAR 720  
QY 721 FVYTDGGITRVYKPEAGENQENPETYEDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780  
DB 721 FVYTDGGITRVYKPEAGENQENPETYEDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIEFTKTSIRDPACAGPVCDCCKNSVMDCVI 840  
DB 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIEFTKTSIRDPACAGPVCDCCKNSVMDCVI 840  
QY 841 LDGSGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPKQ 900  
DB 841 LDGSGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPKQ 900  
QY 901 GAGHRSYVPSVADILQIGWATAAANSILQQFLLSLTPRLLAEAVEMEDDDFTASLSKQ 960  
DB 901 GAGHRSYVPSVADILQIGWATAAANSILQQFLLSLTPRLLAEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQYQYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIIFIMVESKGTCPDTRL 1018  
DB 961 SCITEQYQYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIIFIMVESKGTCPDTRL 1018  
RESULT 2  
CIC2\_RAT  
ID CIC2\_RAT STANDARD; PRT; 1091 AA.  
AC P54230;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DE 01-OCT-2000 (Rel. 40, Last annotation update)  
DE DTHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA  
DE SUBUNITS PRECURSOR  
DE CACNA2D1 OR CACNL2A OR CCHL2A.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92228762; PubMed=1314383;  
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;  
RT "Rat brain expresses an alternatively spliced form of the  
RT dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).  
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
CC EXCITATION-CONTRACTION COUPLING.  
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
CC A PRECURSOR FORM (BY SIMILARITY).  
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: M86621; AAA1088.1; -  
CC InterPro: IPR002035; -  
CC Pfam: PF00092; wavy 1.  
DR PROSITE: PS00234; VWF\_A DOMAIN; 1.  
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
KW Alternative splicing.  
FT SIGNAL 1 24 POTENTIAL  
FT CHAIN 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT

CHAIN	945	1091	(BY SIMILARITY) L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY SIMILARITY).
FT TRANSMEM	445	468	POTENTIAL.
FT TRANSMEM	906	930	POTENTIAL.
FT TRANSMEM	1067	1086	POTENTIAL.
FT CARBOHYD	92	92	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	184	184	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	323	323	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	347	347	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	474	474	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	584	584	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	593	593	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	663	663	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	769	769	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	812	812	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	876	876	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	883	883	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	973	973	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	986	986	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES	500	500	PHOSPHORYLATION (BY CAPK)
FT MOD_RES	833	833	PHOSPHORYLATION (BY CAPK)
FT SEQUENCE	1091 AA;	123822 MW;	(BY SIMILARITY).
SEQ			7054907D9D343B34 CRC64;

Query Match 96.2%; Score 5145; DB 1; Length 1091;  
Best Local Similarity 95.8%; Pred. No. 7, le-288;  
Matches 976; Conservative 22; Mismatches 19; Indels 2; Gaps 2;

Qy	1	MAAGCLLALTLFQSLIGPSSSEPPFSAVTKSWDKMQEDLVTLAKTASGVNQLVDI	60
Db	1	MAAGCLLALTLFQSLIGPSSSEPPFSPVTKSWDKMQEDLVTLAKTASGVNQLADI	60
Qy	61	YEKYQDLTVENNAQVLAARDIEKLLSNRSLVLALEAEKVAQAAHQRDFASN	120
Db	61	YEKYQDLTVENNAQVLAARDIEKLLSNRSLVLALEAEKVAQAAHQRDFASN	120
Qy	121	EVVYNAKDDLPENKSDPGSQRKPKVFIEDANFGRQISYQAAVHIPTDIVEGSTIVL	180
Db	121	EVVYNAKDDLPENKSDPGSQRKPKVFIEDANFGRQISYQAAVHIPTDIVEGSTIVL	180
Qy	181	NELNMTSALDEYFKKREDDPSLLMQVFGSATGLARYYPASPVDNRSRPNKIDLYDVR	240
Db	181	NELNMTSALDEYFKKREDDPSLLMQVFGSATGLARYYPASPVDNRSRPNKIDLYDVR	239
Qy	241	RPWYIGAAAPKMDLILVDVSGSVGLTKLRTSYSEMLETLSDDDFVNVASFNSNAOD	300
Db	240	RPWYIGAAAPKMDLILVDVSGSVGLTKLRTSYSEMLETLSDDDFVNVASFNSNAOD	299
Qy	301	VSCFQHLVQANVKNKVLKADAVNNITAKGTDYKKGFSFAFOLLNYSRANCNKIIML	360
Db	300	VSCFQHLVQANVKNKVLKADAVNNITAKGTDYKKGFTFAFOLLNYSRANCNKIIML	359
Qy	361	FTDGGEEAQEIPFNKDKKVRFRFSVQGHNYERGPQIWMACENKGYIYEPSICAIR	420
Db	360	FTDGGEEAQEIPFNKDKKVRFRFSVQGHNYERGPQIWMACENKGYIYEPSICAIR	419
Qy	421	INTQEYLDVLGRPMVLAKGAKQVQNTNVDLALGLVITGTPLVNITGQFENKTLK	480
Db	420	INTQEYLDVLGRPMVLAKGAKQVQNTNVDLALGLVITGTPLVNITGQFENKTLK	479
Qy	481	NQILGVMGVDVSLDIKRLTPFTLCPNGIYFAIDPQNGVLLHPNLPKNPKSQEPVTL	540
Db	480	NQILGVMGVDVSLDIKRLTPFTLCPNGIYFAIDPQNGVLLHPNLPKNPKSQEPVTL	539
Qy	541	DFLDAELNDIKVIRKMKIDGESGKFTFLVKSQDERYIDKGNRTYTPVNGTDYDYS-	599
Db	540	DFLDAELNDIKVIRKMKIDGESGKFTFLVKSQDERYIDKGNRTYTPVNGTDYDYS	599
Qy	600	LALVLPYSFYIKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFTIAPREYCNDLK	659

Db	600	LALVLPYSFYIKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFTIAPREYCNDLK	659
Qy	660	ISDNTTELLNFNEFIDRKTNNPSCNADLNRLVLLDAGFTNELVQNTWSOKNKGVKA	719
Db	660	PSDNTTELLNFNEFIDRKTNNPSCNADLNRLVLLDAGFTNELVQNTWSOKNKGVKA	719
Qy	720	RFVYTDGGITRVYPKEAGENQENPETYEDSFYKRSKLDNDNYVFTAPYFNKSGPAYESG	779
Db	720	RFVYTDGGITRVYPKEAGENQENPETYEDSFYKRSKLDNDNYVFTAPYFNKSGPAYESG	779
Qy	780	IMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPACGVPDCCKNSDVMDCV	839
Db	780	IMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPACGVPDCCKNSDVMDCV	839
Qy	840	ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNTSVYAFNKSVDYQSVCEPGAAPK	899
Db	840	ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNTSVYAFNKSVDYQSVCEPGAAPK	899
Qy	900	QGAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTFFPRLLEAVEMEDDDFTASLSK	959
Db	900	QGAGHRSAYVPSITDILQIGMWATAAASILQOFLLSLTFFPRLLEAVEMEDDDFTASLSK	959
Qy	960	QSCITEQTYFFPDNDKSFSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTCPDTRL	1018
Db	960	QSCITEQTYFFKNDTKFSGLLDGCNCSRIHFHGEKLMNTNLIIFIMVESKGTCPDTRL	1018

RESULT 3  
CIC2\_RABIT STANDARD; PRT; 1106 AA.  
AC P13806;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA  
DE SUBUNIT'S PRECURSOR.  
GN CACNA2D1 OR CACNL2A OR CCHL2A.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88336904; PubMed=2458626;  
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,  
RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A.,  
RA Schwartz A., Harpold M.M.;  
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2  
RT subunits of a DHP-sensitive calcium channel.";  
RL Science 241:1661-1664(1988).  
RN [2]  
RP SEQUENCE OF 961-973.  
RX MEDLINE=91131638; PubMed=1847144;  
RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,  
RA Campbell K.P.;  
RT "Structural characterization of the dihydropyridine-sensitive calcium  
RT channel alpha 2-subunit and the associated delta peptides.";  
RL J. Biol. Chem. 266:3287-3293(1991).  
RN [3]  
RP SEQUENCE OF 961-975; 992-1000 AND 1033-1050.  
RX MEDLINE=90368635; PubMed=2168391;  
RA de Jongh K.S., Warner C., Catterall W.A.;  
RT "Subunits of purified calcium channels. Alpha 2 and delta are encoded  
RT by the same gene.";  
RL J. Biol. Chem. 265:14738-14741(1990).  
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
CC EXCITATION-CONTRACTION COUPLING.  
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
CC HETERODIMERS THAT ARE DISULFIDE-LINKED.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE



RA	Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,	DB	451	---WMTGVYRRLVLPPEIFAEVPIITNQSFVAVNMKASRRKIRLQKSEARSFMTTV	507
RA	Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,	QY	479	---LNQLILGVGVDSVLEKILTRPTLCPNGYVEADPNGLVLLHPLNLPKPN--	532
RA	Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,	DB	508	SYPVIVNETMGVAANPIPLTEVAQKSHPANIGSKSYFFMLDQNGFVTHPQLPIDPFT	567
RA	Latrelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,	QY	533	--KSOEPTVTLDFLD-----AELNDIKVEIRNMID	561
RA	Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,	DB	568	KYHKQNNMDLLELVGQNVNRSQKQVSLVCSGANYAEVDLKRVRKMIID	627
RA	Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,	QY	562	GESGEKTRILVKSQDERY-----IDK---GNRTTVPNGTDSLALVLTFFYFIKA	614
RA	Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,	DB	628	CDNSD-----VOOLDVLYATELDRVYPTNTTYAECINHANFVLGLAVAKGDYRVVK	681
RA	Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,	QY	615	KLEETITQARSKKGMK	631
RA	Wohlman P.,	DB	682	K-----QKKYDFGRVK	692
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.				
RT	elegans."				
RL	Nature 368:32-38(1994).				
CC	-1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DB	EMBL: L14433; AAA27969.1; -				
DR	PIR: S44617; S44617.				
DR	WormPep; C50C3.11; CE00117.				
DR	InterPro; IPR002035; -				
DR	Pfam; PF00092; vwa; 1.				
DR	PROSITE; PS50234; VWFA_DOMAIN; 1.				
KW	Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;				
KW	Glycoprotein.				
FT	CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).				
FT	CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).				
SQ	SEQUENCE 734 AA; 85034 MW; CCFFB78CDBEA71F CRC64;				
QY	Query Match 11.48; Score 607; DB 1; Length 734;				
DB	Best Local Similarity 26.69; Pred. No. 1.4e-27;				
DB	Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;				
QY	47 LAKTAGVNLVDIYEKDYVTPNPNARQLVEIARDEIKLSNRS-----KALVSLAL 102				
DB	36 MKETFSKISHETILKQNYEKLVEEQFDPRAELKSKRRIEDYLKRSQFAYKAKIS--L 93				
QY	103 EAEKQVAAHOREDFASNEVVYNAKDDLPK-NDSEPGSORIKP-----VFTEDANF 155				
DB	94 EARSVRNSTVNDPQSKFIREFMSAKQNGDGTIYESNHLGRKLVNKTSEFNLTQANF 153				
QY	156 -GRQISYQAAVHIPTDIYEGSTIVNELNWTSSALDVEFKNREEDPSLLQVQFSATGL 214				
DB	154 YLPTSSVSSAVHIPTLYDRNEDLLRKIDW--SDIDAVRTNREETKDLAFLQFCSEAGY 212				
QY	215 ARYPASPWV--DNSTPNKIDLYVRRPWPVIQGAASPFMDLILVDVSGVSGLIKLIR 273				
DB	213 MRYTPAASWFWDNQ--DEHLDLDFCRNTEWYINSATNSKNVLMIDMSGLMGQRYEYAK 270				
QY	274 TSVSEMLETSLDDDFVNVASFNSSNA--QDVSCFQHLVQANVRNKKVLKDAVNTAKGI 330				
DB	271 QTTEAILTSLHNDVFNFTSKNTFLDGGCTNGTGLQATNRNKKALRKMDTQSEK 330				
QY	331 TDYKGFSAFEQLLYN-----VSRANCKIIMLFTDGEERAQEIFNKYKDKRVYF 385				
DB	331 REYKALPLASVLLDINNCGDNNRGACENVIMLITDGAPNAYKKIFDMYNADKKRVYF 390				
QY	386 RFSVGOHNYERGPIQWMAKNGEYIYIPSTGAIINTQEYL-----DVLGRPWVLADKA 441				
DB	391 TELVGEAIDFNEVREMACNNGRYGVHVANMADVDKIHYYIRMSRVVGRHYKESGQLS 450				
QY	442 KOVQNTNYLDALGL--VITGTLTPVFNITQCFENKTN----- 478				

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EMBL: X70393; CAA49843.1; -

MGI: 96620; Itih3.

InterPro; IPR002035; -

Pfam; PF00092; vwa; 1.

PROSITE; PS50234; VWFA\_DOMAIN; 1.

Serine protease inhibitor; Repeat; Signal; Multigene family;  
 Glycoprotein. 1 18 POTENTIAL.  
 FT SIGNAL 19 30 BY SIMILARITY.  
 FT PROPEP 31 646 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN  
 FT CHAIN 31 646 H3.  
 FT PROPEP 647 886 BY SIMILARITY.  
 FT DOMAIN 279 439 VMFA.  
 FT FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
 FT (BY SIMILARITY).  
 SQ SEQUENCE 886 AA; 98977 MW; 15955308C7F5030A CRC64;  
  
 Query Match 3.6%; Score 194.5; DB 1; Length 886;  
 Best Local Similarity 19.9%; Pred. No. 0.00089;  
 Matches 195; Conservative 138; Mismatches 347; Indels 261; Gaps 44;  
  
 QY 27 FPSAVTIKSWDKQEDLVLTAKTAGSNVQLVDYIKYQDLTYTPENNAQOLVEIAARDI 86  
 DB YGNVKEKEVAQYKAVSQGTAG---LVKASGRKLEKFTVSNVAAAGSKVTFELTY 153  
 QY 87 EKLISNRKALVSLAEAKVQAQHQWREFASNEVYVYNAKDDLDPEKNDSPGSGRIK 146  
 DB EELL-KRNGKGYEMLKVPQKLVRFHEID-----AHIFEP-----Q 189  
 QY 147 PVFTEDAFNGROISYQAHAHPTDIYEGSTIVILNELNWTSDALDEVFKKNREEDPSLLWQ 206  
 DB GISMIDAE-----ASFTNDL-LGSATKSF----- 214  
 QY 207 VFGSATGLARYPASPWWDSRT-PNKID-----LYDVRRRP-----WYI-- 245  
 DB ---SGKKGHSFKPSLDQOORSCPTCTDLSLLNGDFTIVYDVNRSPGNQOIVNGYEVHF 269  
 QY 246 ---QG-AASPKDMLILVDGSGVSGLTLLKIRTSVSEMLETSLDDDFVNVASFNQAQV 301  
 DB FAPQGLPVPKNIVFIVDVGSGMSGRKIQTREALLKILDVDEDDYDLNLFST---DV 326  
 QY 302 SCFO-HLVQAVNRNKKVLKDAVNNTAKGTIDYKKGFSFAFEOILLNVSANRAN-----C 354  
 DB TTWKDHLVQATPANLKEAKTFVNRNHDQSTNINDGLLKGIELM---NKAREDTVPERS 383  
 QY 355 NKIIIMFTDG---GEERAQEIFNKYK---DKKVRVFRFSVQGHYERGPQIWMACENKG 408  
 DB TSIIIMLTGDANTGESRPEKIQENVRNAIGKFPFLYNLGFQ-NLNYNLETALENHG 442  
 QY 409 YYEIPSGAIRINTQYLDVLGRPNVLADGKAKQVQWTVNYLDALBGL--VTGTPLV 466  
 DB LARRIYEDSANLQGFYEIVANPL-----TNVEVEYPENALDLTRNSYPH 491  
 QY 467 FNITGQENKTNLANQILGMVGVDVSELDIKRLTPFTLCPNGYYFAIDPBGVLLHPN 526  
 DB F-----YDG-----SEIVAGRLVDRNDN-----FKADVKHGHALN-- 523  
 QY 527 LQPNKPSQEPVTLDFDAELENDIKVEIRNKMIDGESGEK--TFRTLKVSQDRIYDKG 584  
 DB ---DLFTFEVDMEADAALK-----EGYIFGDIYERLWAYLIEQLLEKKNKAG 572  
 QY 585 NRTVTPVNGTDSL--LVLPYTSYYIKALEETITQARSKKKKQKQSET-----LK 637  
 DB DEKENIT-AEALDLSLVHFVPLTSMVTVPKPEDNQSTADNAGEAFAETTTMSFLT 631  
 QY 638 PDNFEESGYFIAPRDCYNDLKISDNTEFLNNEFDIKRTPNPNPCNADLNIRVLLDA 697  
 DB TQQSOSPPYVV-----DGDPHFIQI-----PGKNDISCFNIDEKP 668  
 QY 698 GFTNELQVYWSKQKNIKGVKARFVVDGTTTRYVPKEAGENWQENPETYEDSFYKRLSD 757  
 DB GTVLRLLQD-----PVI--GIT-VTQGLIGD-----KKS-- 694  
 QY 758 NDNTVFTAPYFNKSGPAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTS 817

[illegible]

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; X67055; CAA47439.1; -;  
DR EMBL; X14690; CAA32821.1; -;  
DR MIM; 146650; -;  
DR InterPro; IPR002035; -;  
DR Pfam; PF00092; vwa; 1;  
DR PROSITE; PS50234; VWFA\_DOMAIN; 1..1;  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 ? POTENTIAL.  
FT PROPEP 31 647  
FT CHAIN 31 647  
FT FT  
FT FT  
FT PROPEP 648 885  
FT DOMAIN 278 438  
FT CARBOHYD 87 87  
FT CARBOHYD 576 576  
FT BINDING 647 647  
FT BINDING 344 344  
FT CONFLICT 357 357  
FT CONFLICT 846 846  
FT CONFLICT 885 AA; 99121 MW; BC63836F8F5E4A1B CRC64;  
SQ SEQUENCE 885 AA; 99121 MW; BC63836F8F5E4A1B CRC64;

Query Match 3.4%; Score 182; DB 1; Length 885;  
Best Local Similarity 20.7%; Pred. No. 0.0046;  
Matches 136; Conservative 102; Mismatches 239; Indels 180; Gaps 34;

QY 27 FSAVTKSWDKQMDLTYTLAKTAGSVNQLVDIYEKYQDLYTVPNNARQLVEIARDI 86  
DB 97 YGKNVEKEVAKKQYKAVSQKTAG-----LVKASGRKL 131  
QY 87 EKLLNSRKAL---VSLAEAEKVAQAHQWREDFASNEVYVYNAKDDLPKNDSEPGSQ 143  
DB 132 EKFTSVNVAAGSKYTFELTYELLKRHGK-----YEMLYKVQPK-----Q 173  
QY 144 RIKPVEIDANFGRQISYQAAHVIPTDIYEGSTIVNLNWTSLDVEFKKNEEDPSL 203  
DB 174 LVKHFIE-----VDIFEPOGI-----SMLD-----AEASF 200  
QY 204 LKQVFGSA-----TGLARYYPASPWDNSRT-PNKID-----LYDVRRRP----- 242  
DB 201 TNDLGSALTGKSFSGKKGHVSKFSLDQQRSCPTCTDSLLNGDFTTYDVNRESPGNVQI 260  
QY 243 ---WYI-----QC-AASPKDMLILVDVSGVSLTKLIRTSVSEMLETSLDDDFNVAS 293  
DB 261 VNGYFVHFAPQGLPVVPRNVAFVDSISGMAGKLEQKLEALLRIEDKMEEDYLNFL 320  
QY 294 FNSNAQDVSCF-OHLVQAVNRNKKVLKAVNNITAGITDYDKGFGFAEQLLNYSVR- 351  
DB 321 FSG---DVSTWKEHLVQATPENLQEARTFVKSMDKGMTNINDGLLRGISML---NKARE 374  
QY 352 ----ANCKIIMLFDG---GEERAQEIFNKYNK--DKKVFVFRFSVQHNVERGPQ 400  
DB 375 EHRIPERSTIVMLDGDANVGSREPKIQENVRNAGKFFLYNLGFG-NLNINLFLE 433  
QY 401 WNAENKGYEYIEPSIGAIRINTEYLDVLRGPMVLGAKQVQWNTVYLDALD----- 455  
DB 434 NMALENGHARRIYEDSDADLQGYEEVAVNPL-LTGVEMEYPE--NALDLDTQNTYQH 490  
QY 456 ----LGLVITGLTPVNTIGQFNKNLK-----NOLILGVMGVDVSLDIKRLTRFTL 506  
DB 491 FYDGSIEIVVAGRL-VDEDMNSF--KADVKHGATNDL---TFTVEYDMKEMEK-----AL 539  
QY 507 CPNGYFAIDPN-----GYVLHPNLPK---NPKSQEPVTLDFDLAELENDIKVEIRN 557

DB 540 QERDYIFG---NYIERLWAYLTIEQLLEKRNKNAHGEEKENLTARALDLSLKHYHVTPLTS 596  
QY 558 KMDGESGKTRTLVKSDERYI-DKGNRTYTWTPVN-GTDSLALVLTFTSYFYL 512  
DB 597 MVTWKEP-----DNEDERAIDKPGDEAETVPSPAMSYLTSYQPPQNPYYV 644

## RESULT 7

ITH3\_RAT ITH3\_RAT STANDARD; PRT; 887 AA.  
AC Q63416;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY  
DE CHAIN H3).  
GN ITIH3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;  
RA Blom A.; Fries E.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
CC SIMILARITY).  
CC -!- SUBUNIT: 1-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY  
CC SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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DR EMBL; X83231; CAA58233.1; -;  
DR InterPro; IPR002035; -;  
DR Pfam; PF00092; vwa; 1;  
DR PROSITE; PS50234; VWFA\_DOMAIN; 1;  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 21 POTENTIAL.  
FT PROPEP 22 33 BY SIMILARITY.  
FT CHAIN 34 647 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
FT FT  
FT PROPEP 648 887 BY SIMILARITY.  
FT DOMAIN 282 442 VWFA.  
FT CARBOHYD 91 91 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 580 580 N-LINKED (GLCNAC...) (POTENTIAL).  
FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
FT (BY SIMILARITY)  
SQ SEQUENCE 887 AA; 99097 MW; 3B9F0FF96D514096 CRC64;

Query Match 3.4%; Score 180.5; DB 1; Length 887;  
Best Local Similarity 18.5%; Pred. No. 0.0057;  
Matches 173; Conservative 139; Mismatches 350; Indels 275; Gaps 39;



QY 27 FPSAVTIKSWDKWQEDLVYLAKTASGVNQLVDIYKQDLYTVTEPNAROLVEIAARDI 86  
Db 101 YPGSVKEVAQKQYKAVSQGTAG-----LVKASGRKLEKFTVSVNVAAGSKVIFELTY 156  
QY 87 EKLKNSRKALVSLALEKQVAAHQWRED--FASNEVVVYNNAKDDLDPEKNDSEPGSQ 143  
Db 157 BELL-KRNKGYEYLVKQVQLVHRFEIDAHIFEPOGISMLDA-----199  
QY 144 RIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVLNELNWTGALDEVFKKNEEDPSL 203  
Db 200 -----DASF-----ITNDL-LGSALTCSF-----217  
QY 204 LQWPGSATGLARYYPASPWNDSRT-PNKID-----LYDVRPP-----WY 244  
Db 218 -----SGKKGHVSFKPSLDQQRSCPTCTDSLLNGDFTIVDVNRESQNVQVINGYF 269  
QY 245 I-----QG-AASPDKMLTLDVSGSVSLTKLTKTSTVSEMLETSDDDFVNVASFNSNA 298  
Db 270 VHFPAQGLPVVPKNIATVIDVSGMSGRKIQOTREALKLLDDMKEDYLNFLFSTGV 329  
QY 299 QDVSCFOHLVQANVRNKKVLDAVNNTAKGIDYKKGFSFAFOLLNYSRAN-----353  
Db 330 -----TTWKHLVKATPANLEEARAFVKNIRDORSMTNINDGLLRGIELM---NKAREDHVPE 384  
QY 354 -CNKIMLFTDG-----GEARQETPNKYNKDKVRFVSYG-QHNYERGPIOWACENK 407  
Db 385 RSTSLVMLTDGDANTGESRPEKIQENYRNAIRKGFPYLNGLFGNNLNFLESIALENH 444  
QY 408 GYVYEIPSGAIRNTQBYLDVGLRPMVLADGKAKQVQWTVNYLDALDELGL--VITGTLF 465  
Db 445 GFARKIYEDSDASIQLOQGYFEVANPLL-----TVELEYENALIDLTRNSIP 493  
QY 466 VFNITQFENKTNLQILGVMDVDSLEDKLTPRTFLCPNGYYFAIDPNGYVLLHP 525  
Db 494 HF-----YDG-----SEIVAGRLVDRNVN-----FKADVKGHALN- 526  
QY 526 NLOPNKPSQEPVTLDFDALENDIKVEIRNKMIDGESGKTF-----RTLVKSQDER 579  
Db 527 -----DLTFTVEEDMKENDAALK-----EOGYIFGDYIERLWAYLIEOLLEKRNAR 574  
QY 580 YDKGNRYTTPVNGTDSL--LVLPYTFYIKAKLETITQARSKKGMKDSER--635  
Db 575 GDEKENIT-----AEALSLKYLHVFTPLTSMVYTKPDENOOTAIADKPGEEAISASTA 629  
QY 636 -LKPNDFESGYFTIAPRDYCNLDKISDNTEFLNF--NEFIDRKTTPNPNPSCNADLIN 691  
Db 630 YLTSSQSSHSPIYV-----DGDPHFIIQVQKNDTICFNIDEXPGTVLSLIQ 677  
QY 692 RVLLDAGFTNELVQVNSKQKNIKGVKARFVTDGITRVYPKEAGENWQENPETYEDSF 751  
Db 678 DPTVTGIATGQII-----GEGNNASSRTGKT-----704  
QY 752 YKRLSDNDNVPTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIE 811  
Db 705 -----YFGKLGITANWMPRIEVTTEKILGN-----GALSTFSWLD 742  
QY 812 NFKTSIRDPACPGVCDCKRNSDVNDVILDDG-GFLLMAN-----HDDYTNQIGRF 862  
Db 743 TVTVTQ-----TGLSVTINRKNMV--VSFEDGISFVIVLHVQVKKHPVHQDFLG-----790  
QY 863 FGEIDPSLRHLVNIISVAFNKSQYQSV-CEPGAAP 898  
Db 791 FYVVDSHRMSAQTGHLGLOFFQFPDFKVDVRPGSDP 827

RESULT 8  
ID ITH3\_MESAU STANDARD; PRT; 886 AA.  
AC P97280;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) (HC3).  
GN ITI H3.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.  
OC NCBI\_TaxID=10036;  
OX [1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RC MEDLINE=97420688; PubMed=9276673;  
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;  
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family.";  
RT J. Biochem. 122:71-82(1997).  
RL  
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).  
CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN. BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ITH FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
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CC EMBL; D89287; BAAL3940.1; -  
DR InterPro; IPR002035; -  
DR Pfam; PF00092; vwa; 1.  
DR PROSITE; PS50234; VWFA\_DOMAIN; 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 18 POTENTIAL.  
FT PROPEP 19 30 BY SIMILARITY.  
FT CHAIN 31 646 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3.  
FT PROPEP 647 886 BY SIMILARITY.  
FT DOMAIN 279 439 VWFA.  
FT CARBOHYD 88 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 577 577 N-LINKED (GLCNAC...) (POTENTIAL).  
FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE (BY SIMILARITY).  
SQ SEQUENCE 886 AA; 99018 MW; AC0594C685257688 CRC64;

Query Match 3.1%; Score 164.5; DB 1; Length 886;  
Best Local Similarity 23.2%; Pred. No. 0.047;  
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLQVFGSATGLARYYPASPWNDSRT-PNKID-----LYDVRPP-PWYIQGA--248  
Db 208 SALTAKSFSGKKGHVSFKPS---LDQQRSCPTCTDSLLNGDFTIVDVNRESQNVQVNG 264  
QY 249 -----ASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVASFNS 296  
Db 265 YVHFPAQGLPVVPKNIATVIDVSGMSGRKIQOTREALKLLDDMKEDYLNFLFST 324



Qy 297 NAQVSCFQHLVQAVNRNKKVYKLDVAVNNITAKGTDYKKGSFAFEQQLN-----YVNSRA 352  
Db 325 GV--TTWKDSLQVATPANLEARTFVRSISDQGTNINDGLLRIMTLDAREQHTVPER 382  
Qy 353 NCNKILMLFTDG----GEERAQEIFNKYKDKKVRVERFSVG-CHNYERGPIONMACENK 407  
Db 383 STSIILML-TDGDANTGESREPKTOENVKKAIEGRFPDLYNLFNGNNLNFLETMALENH 441  
Qy 408 GYYEIPISGAIRINTQBYLDVLRPMVLAGDKAKQVQWNTVYLD 452  
Db 442 GVARRIYDSANLQLOQFGYEEVANPLL-----TNVEVE 475

RESULT 9  
DPOL\_THEST STANDARD; PRT; 1829 AA.  
AC 03845;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE DNA POLYMERASE (EC 2.7.7.7).  
GN POL.  
OS Thermococcus sp. (strain TY).  
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.  
OX NCBI\_TaxID=86030;  
RN [1]  
RX MEDLINE=98094267; PubMed=9434178;  
RA Niehaus F., Frey B., Antranikian G.;  
RT "Cloning and characterisation of a thermostable alpha-DNA polymerase  
from the hyperthermophilic archaeon Thermococcus sp. TY";  
RL Gene 204:153-158(1997).  
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -  
N PYROPHOSPHATE + DNA(N).  
CC -1- PPM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES  
A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION  
(INTEINS) FOLLOWED BY PEPTIDE LIGATION.  
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; Y13030; CAA73475.1; -  
DR InterPro; IPR002064; -  
DR InterPro; IPR002203; -  
DR Pfam; PF00136; DNA\_pol\_B; 4.  
DR PRINTS; PR00379; INTEIN.  
DR PROSITE; PS00116; DNA\_POLYMERASE\_B; FALSE\_NEG.  
DR PROSITE; PS00881; PROTEIN\_SPLICING; 3.  
KW Transferase; DNA-directed DNA polymerase; DNA replication;  
KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;  
KW Protein splicing.  
FT CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).  
FT CHAIN 410 769 INTEIN I.  
FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).  
FT CHAIN 856 1392 INTEIN II.  
FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).  
FT CHAIN 1442 1598 INTEIN III.  
FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).  
SQ SEQUENCE 1829 AA; 211875 MW; A113A8BC57EB9CB3 CRC64;

Query Match 3.0%; Score 161; DB 1; Length 1829;  
Best Local Similarity 20.1%; Pred. No. 0.21;  
Matches 172; Conservative 101; Mismatches 301; Indels 282; Gaps 39;  
Qy 16 SLLIGSSEPPPS-----AVIKSV-----DKMQEDLVTLA 48

Db 229 TLLLGROKHEPEKTHRMGDSFAVEIKGRIHFDLPVVRRTINLPTTYLEAVIEAVLGT 288  
Qy 49 KTASGYNQVLDIYKYQDL-----YVPEPNARQVLETAARDIEKLLNSRKALVSLALE 103  
Db 289 KSKLGAEEIAAIWETEESMKLAQYSMB--DARATYEL-----GKEFPPEMAE 334  
Qy 104 AEKQAAHQWREDFAS--NEVVIY-----NAKDDLDPEKNDSEPGSQRIKPVFI----- 150  
Db 335 LAKLIGQSVWDVSRSSSTGNLWVILLRVAYERNELAPKNPDEEEYRRRLRTYILGGYKE 394  
Qy 151 EDANFGROISYQHAHAVHIPTD---IYEGSTIV---LNLNWTLSALDEVFKKNREEDPSL 203  
Db 395 PERGLWENIAYLDFRCH-PADTKVIVKKGIVNISDVKEGDIYLGIDG----- 441  
Qy 204 LMQVFGSATGLARYYPASPWDNSR---TPN-KIDLYVRRPWTYIQGAASPKDMLILVD 259  
Db 442 -WQ---RVKVKVYHVEGLKLNINGLKCTPNHKVPVVTENDRQTRI-----RDSLAKSF 491  
Qy 260 VSGSVGLTLKLRISVSEMLETSLDDDFVNVASPSN-----FETAEFEKNKPSEEEILKGLSGLI 537  
Db 492 LSGKVGK---KIITPKL-----FEKIAEFKNKPSEEEILKGLSGLI 537  
Qy 298 -AQVSCF-----OHLVQANV-RNKKVLKDAV-----NNITAKG----- 329  
Db 538 LRKDIEYFDSRGKKRISHQYRVEITIGENEKELLERILYFDKLGIRPSVKKKGDTNA 597  
Qy 330 --ITDYKKGFSFAFQOLLNYSRANCKIIMLFYDGGEEAQAQEIFNKYNDKKKVRVRF 387  
Db 598 LKITTAKAVVLIQIEELK-NIESLYAPAVLRG-----FERDATYNKIRS 642  
Qy 388 SV---GOHNTERGPIOWMACENKGY---YVEIPSIGAIRINTQYLDVLRPMVLAGDK 440  
Db 643 TIVTQGTNNKWKIDIVAKLLDSLSGIPYSRYEYKYEINGKELTKHILEITGRD----- 695  
Qy 441 AKQVQWTVYLDALDELGLVITGTPVFNITQFE-----NKTNLKNQLILGVMDV 491  
Db 696 -----GLILFQTLVGFISSEKNEALEKAEVRENNRLKNNSFYNLSTPE 739  
Qy 492 VSLIEDIKRLTPRTCPNGYFPAIDPNGVYLLHPNLQPNKPSQEPVTLDFDLDALENDI 551  
Db 740 VSSEYKGEVVDLTLEGNPYFA---NG-ILTHNSLYPSIIVTHN-VSPDTLRE----- 789  
Qy 552 KVEIRNKMIDSGSEKTFRTLVKSQDERYIDKGNRTYTTVPVNGTDYSLALVLPYSFY 611  
Db 790 -----GCKNYDVAPIVG--YKECKDFPG----F 811  
Qy 612 IKAKLEETITQARSKKGMKDSSETLKPONFESGY-----TFIAPRCYNDLKISD 662  
Db 812 IPSILGELITMFEQIKKMK--ATIDPIEKKMLDYRQRAVKLLANSILPNW---LPITE 866  
Qy 663 NNTFELLNFEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNTWSKOKNIKGVKARFV 722  
Db 867 NGEVAFVKIGEFIDRYMEQDKVFTVDNTEVLEVDNIFAFSLNKESKSEIKKVKAL--- 924  
Qy 723 VTDGGITRVYPKEAGE 738  
Db 925 -----IRHYKGEAYE 935

RESULT 10  
ATXL\_PLAFA STANDARD; PRT; 1956 AA.  
ID ATXL\_PLAFA  
AC Q04956;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE PROBABLE CATION-TRANSPORTING ATPASE 1 (EC 3.6.1.-).  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.



```
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9279503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -1- SIMILARITY: TO SYNCHOCYSTIS PCC 6803 SLL0103.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AE000317; AAC75330.1; ..
DR EcoGene; BG14095; yfBK.
DR InterPro; IPR002035; ..
DR Pfam; PF00092; vwa; 1.
DR PROSITE; PS0234; VWFA_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 575 AA; 63634 MW; 7BB6A1A77A2BE111 CRC64;

Query Match 2.9%; Score 157.5; DB 1; Length 575;
Best Local Similarity 21.6%; Pred. NO. 0.064;
Matches 111; Conservative 93; Mismatches 206; Indels 105; Gaps 25;

QY 71 EPNNARQLVEIARIDIELKLSNRKALVSLALEAEKVAQAAHQWREDFASNEVVYNAKDD 130
DB 22 QPENKESQQQPTPTQEQVLAQAQAATK---EAEQSA---AKALAQEQVQYSDKQA 75
QY 131 LDPEKND-----SEGSORIKVFETEDANFGISYQHA---VHIPIDI 172
DB 76 LOGRLQEAFTFAKAKAKATHANGTARYQOF---DNPYKQVAQNPLATSLDVGTS 132
QY 173 YEGSTIVNE-----LNWTSALDEVKKNREEDPSLLQWVFGSATGLARYY 218
DB 133 YANVRFLNGLPPDPAVRVEIYVPPSDWDI--KDKQSIKSPASKPIPFAMRYELA--- 187
QY 219 PASPWYDNRTPNKLIDYVRRPWHYIOGAAPKDMILVDVSGS-VSGLTILKLRYSVS 277
DB 188 PA-PW-NEQRTLLKYDILAKDRKSELPAS-----NLVFLIDTSGSMISDERLPLIQSLK 241
QY 278 EMLETLSDDDFVNVSFNSNAQDVSCFQHLVQAVRNKKVLKDAVNNITAKGITDYKGF 337
DB 242 LLVKELREQDNTAIVTYAGDSRIA-----LPSISGSHKAEINAAIDSLDREGSTGGAGL 296
QY 338 SFAFQLLNYSRANCKIIMLFTDG-----GEERAOEIFNKYKDKKRVFRFSVQ 391
DB 297 ELAYQQAATK-GFIKGGINR-ILLATDGFENVGIDDPKSTESNVKKQRESGVTLSTFGVN 354
QY 392 HNYERGIOMACENKGYIYTPSGAIRINTQEVLDVLRPMWL--AGDKAKQVQ---- 445
DB 355 SNYNEAMVRIADVGNYSYIDTLS-----EAQVLNSEMROMLITVAKDVRAQIEFNP 410
QY 446 WTNVYLDALGLGVITGTLPVNTIGQFENKTNLKNQLILGVMGVD-VSLEDI---KRLT 501
DB 411 WTEY---RQIG-----YE-----RQLRVEHFNNDVNDAGDVGAGKHIT 447
QY 502 PRFTLCPCGYIFAIDPNGVLLHPNLQPKNSOE 536
DB 448 LLFELTLNGKASIDKLRYA--PDNKLAKSDTK 480

RESULT 12
ID ITH2_HUMAN
AC P19823; Q15484; Q14659; STANDARD; PRT; 946 AA.
DT 01-FEB-1991 (Rel. 17, Created)
```

```
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY
DE CHAIN H2) (INTER-ALPHA-TRYPsin INHIBITOR COMPLEX COMPONENT II)
DE (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).
GN ITH2 OR IGHEP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE-88152237; PubMed-2450046;
RX Gebhard W., Schreitmuller T., Hochstrasser K., Wachter E.;
RT "Complementary DNA and derived amino acid sequence of the precursor
RT of one of the three protein components of the inter-alpha-trypsin
RT inhibitor complex.";
RL FEBS Lett. 229:63-67(1988).
RN [2]
RN SEQUENCE OF 384-865 FROM N.A.
RX MEDLINE-88068576; PubMed-2446322;
RX Sallier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
RX Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.P.;
RT "Isolation and characterization of cDNAs encoding the heavy chain of
RT human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous
RT evidence for multipolypeptide chain structure of I alpha TI.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
RN [3]
RN SEQUENCE OF 384-766 FROM N.A.
RX MEDLINE-89076497; PubMed-2462430;
RX Sallier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
RX Martin J.P.;
RT "Human inter-alpha-trypsin inhibitor. Isolation and characterization
RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence
RT of the H chain.";
RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).
RN [4]
RN PARTIAL SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE-88024442; PubMed-3663330;
RX Schreitmuller T., Hochstrasser K., Resinger P.W.M., Wachter E.,
RX Gebhard W.;
RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses three
RT different proteins.";
RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).
RN [5]
RN SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.
RX MEDLINE-89380192; PubMed-2476436;
RX Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
RT Polypeptide chain stoichiometry and assembly by glycan.";
RL J. Biol. Chem. 264:15975-15981(1989).
RN [6]
RN SEQUENCE OF 55-64.
RX TISSUE=Plasma;
RX MEDLINE-93039735; PubMed-1384548;
RX Malki N., Baiduyck M., Maes P., Capon C., Mizon C., Han K.K.,
RX Tartar A., Fournet B., Mizon J.;
RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor: their
RT isolation, their identification by electrophoresis and partial
RT sequencing. Differential reactivity with concanavalin A.";
RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
RN [7]
RN SEQUENCE OF 55-64 AND 681-702, AND CROSS-LINK STRUCTURE.
RX MEDLINE-93232026; PubMed-7682553;
RX Enghild J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,
RX Pizzo S.V., Hefta S.A.;
RT "Presence of the protein-glycosaminoglycan-protein covalent cross-link
RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain
RT 2/bikunin.";
RL J. Biol. Chem. 268:8711-8716(1993).
RN [8]
```

SEQUENCE OF 67-101, AND HYALURONAN BINDING.

TISSUE-Serum;

MEDLINE=94075371; PubMed=7504674;

Huang L., Yoneda M., Kimata K.;

"A serum-derived hyaluronan-associated protein (SHAP) is the heavy chain of the inter alpha-trypsin inhibitor.";

J. Biol. Chem. 268:26725-26730(1993).

[9]

SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.

TISSUE-Plasma;

MEDLINE=94229087; PubMed=7513643;

Morelle W., Capon C., Bauduyck M., Sautiere P., Kouach M., Michalski C., Fournet B., Mizon J.;

"Chondroitin sulphate covalently cross-links the three polypeptide chains of inter-alpha-trypsin inhibitor.";

Eur. J. Biochem. 221:981-988(1994).

-1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.

-1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.

-1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE.

-1- SIMILARITY: BELONGS TO THE ITIH FAMILY.

-1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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EMBL: X01773; CAA30160.1; ALT\_SEQ.

EMBL: M18193; AAA60558.1; -.

EMBL: M33033; AAA59195.1; -.

PIR: S00346; IYHU2.

PIR: B34245; B34245.

GlycoSuiteDB; P19823; -.

MIM: 146640; -.

InterPro; IPR002035; -.

Pfam; PF00092; vwa; 1.

PROSITE; PS02334; VWFA\_DOMAIN; 1.

Serine protease inhibitor; Repeat; Signal; Multigene family;

Glycoprotein. 1 18

SIGNAL 19 54

PROPEP 55 702

CHAIN

INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN

H2.

WVFA.

N-LINKED (GLCNAC. . .).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .).

CARBOXYLATION.

CARBOXYLATION.

CHONDROITIN 4-SULFATE, CROSS-LINK SITE.

P -> A (IN REF. 2 AND 3).

F -> S (IN REF. 2 AND 3).

N -> D (IN REF. 2 AND 3).

V -> A (IN REF. 2 AND 3).

K -> L (IN REF. 5).

SEQUENCE 946 AA; 106436 MW; 1478CF3E8F3BA776 CRC64;

Query Match 2.9%; Score 154.5; DB 1; Length 946;  
Best Local Similarity 19.9%; Pred. No. 0.19;

Matches 133; Conservative 106; Mismatches 259; Indels 171; Gaps 29;

QY 33 IKSWDKMQEDLVTLAKTAGSVNQLVDIYKYQDLYTVENPNARQLVEIARDEKLLSN 92

Db 26 LSEFVD--YEDLVEL---APKQQLVAENRRYORSLPGESEEMEEVDQVTLXSYKVOST 80

QY 93 RSKALVSLALEAEKYQAQHWRE-----DFASN-----EV 122

Db 81 ITSRMATTMTIOSKVVNNSPQNVVFDVQIPKGAIFSNFMTVDGKTRFSIRKKTGVR 140

QY 123 VYNAK-----DDLDPKNDSE---PGSRIKPVFIEDANFGRQISYOH----- 163

Db 141 LYAQAARAKGTAGLVRSALDMENFRTEVNVLPKAGVQFELHYQVWKRLGSEYHRIYL 200

QY 164 ----AAVHIPTDIYEGSTIVLNELNWTLSALD-----EVFKKREE-----DPSLLNQVVF 208

Db 201 QPGRLAHLEVDVWVIEPQGLRFLHVPDTEGHFDGVPYVISKGOQKARHVSFKPTVAQO-- 258

QY 209 GSATGLARYYPASPWDNSRTPNNKIDLYDVRRRP-----WYIOGAAS-----PK 252

Db 259 -----RICPSCR--ETAVDGEVLVLYDKREKAGELEVFNFYFVHFFAPDNLDPKP 309

QY 253 DMLILVDVSGSVGLTLKLTIRTSVSEMLETLSDDDFNVNVSFNSNAQDVSCFHLVQANV 312

Db 310 NLEFVIDVSGSMGVKKQVTEAMKTIILDDLRAEDHFSVIDFNQIR--TWRNDLISATK 367

QY 313 RNKKVLKDAVNNTAKGIDYKKGKGF---SFAFQOLLNVNVRANCNKIIMLFTDG----G 365

Db 368 TVADAKRYIEKIQPSGGTINIEALLRAIFLNEANNLGLDPPNSVSLIILVSDGDPVVG 427

QY 366 EERAQEFENKYNKKVVRFRFSVGO-----HNYERGPLOWM-----ACENK 407

Db 428 ELKLSKIQKNYKKNQIDNISLSLGMGFDVDYDFLKRUSNENHGIQRIYGNQDTSSQIK 487

QY 408 GYVEI--PSIGAIRIN--TQEYLDVL-----GRPMVLG--DKAKQVQWNTNYLD 452

Db 488 KFYQVSTPLRNQVFNPHYSVDVTQNNFHNHYEGSEIVVACKDFPAK-----LD 539

QY 453 ALEGLGVITGLTVFNITQFENKTNLKNQLILGVMGVDVDSLEDI-----KRLTPRTLC 508

Db 540 QIE--SVITA-----TSANTQLVLETLAQMDLQDLSKDKHADDPFTR-K 582

QY 509 NGYFAIDPNGVYLLHPNLQPNKPSQEPVLDLDALENDIKVEIKNMKIDGSGEKT 568

Db 583 LWAYLTIN---QLLAERSLAP--TAAKRRITRSILOSLDHHIVTPTLSLVINEAGDER 638

QY 569 FRTLKVSOD 577

Db 639 MLADAPPD 647

RESULT 13

EXCL\_CLOBO

ID BXCL\_CLOBO STANDARD; PRT; 1290 AA.

AC P18640;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE BOTULINUM NEUROTOXIN TYPE C1 PRECURSOR (EC 3.4.24.69) (BONT/C1)

DE (BONTOLIXISIN C1).

OS Clostridium botulinum.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;

OC Clostridium.

OX NCBI\_TaxID=1491;

RN [1]

RP SEQUENCE FROM N.A. PubMed=2204031;

RX MEDLINE=90370487; Kurazona H., Binz T., Niemann H., Gill D.M.,

RA Boquet P., Popoff M.R.;

RA "Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";

RL Nucleic Acids Res. 18:4924-4924(1990).

RN [2]

RP SEQUENCE FROM N.A.

FT	DISULFID	436	452	INTERCHAIN (PROBABLE).
FT	CONFLICT	84	84	P -> T (IN REF. 2).
SEQ	SEQUENCE	1290 AA;	148734 MW;	71FBE379F97129E8 CRC64;
Query Match		2.8%;	Score 152;	DB 1; Length 1290;
Best Local Similarity		20.3%;	Pred. No. 0.42;	
Matches	205; Conservative	125;	Mismatches 346;	Indels 334; Gaps 54;
QY	106	KVQAQAHQWRDEFPASVEVYVYNAKDDLDPEKNDSEFGSQRIK	---	PVIEDANFR----- 157
Db	138	KTROGNNWVTGTSINPSVIITG	-----	PRENIIDPSTFKLTNTTAAQEGFALSIIIS 192
QY	158	-----QISYQAAHVIPTDIYEGS	-----	TIVLNLNWTSLDADEVK---KNRE 198
Db	193	ISPRFMITYSNAT	-----	NDVGEGRFSKFCMDPILIMHELN---HAMHNLGYTAIPNDQ 246
QY	199	EDPSLLMQVFGSATGLARYYP	-----	ASPVWDSNRTPNKIDLYVRRRPWTYQGAASPKD 253
Db	247	TISSVTSNIFVSQYNVLEVAEIVAFGGPTID	---	LIPKSARKYPEERKALDYRSIAKRLN 304
QY	254	MLILVDVSG	-----	SVSGTGLTKLIR-----TSVSEMLETSLDDDDFVNVSFNSNAQDVSCF 304
Db	305	SITTANPSSFNKYIGEYKQKILIRKYRFVSESGEV	---	TVNKNKVEL---YNELQTIFTEF 360
QY	305	QHLVQANVRNKKV-LKDAVNNTAK	-----	GTTDYKKGFSPAFEOI-----LNVNYSR----- 351
Db	361	NYAKIYNQNRKTIYLSNVYTPVTANILDDNYDIQNGFNIPKSNLVLFPMQNLNRNAL	---	420
QY	352	---AMCNKIIMLFT	-----	DGGEERAQEIENK-----YNKD-----KKRVYFR 386
Db	421	RKVPENMLYLFTEFKHKAIDG	---	RSLYNKTLDCRELLVKNKTDLPFIGDISVKTDI 475
QY	387	FSVGQHNRYERGPIOWMACENKGYVEIPSIGAIRI	---	NTQEY---LDVL----- 430
Db	476	FLRKDINEETEVI	-----	YPDNVSDQVILSKNTSEHGQDLDLPSIDSESEILP 526
QY	431	GRPMVLADGKAKOVQWNT	---	VYLDALGLVITGTLPVENITGQFENKTN----- 478
Db	527	GENOVFYDNRTQNDYLSYYLSESQKL	---	SDNVEFTFTRSEEAALNSAKYTYYP 582
QY	479	-LKNQLILGVMG	-----	VDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLQPK 530
Db	583	TLANKVNAGVOGGLFLMWANDVVEFTTNILRKDTLDKISDVSAIIP	---	YIGPALNIS 638
QY	531	NPKSQEPTVLD	-----	LDALENDI-----KVEIRKNMIDGESGETFTL 572
Db	639	NSVRGRNGTEAFATVGTVILAEAPFTIPALGAFVIYSKQERNELI	---	-----KTIDNC 692
QY	573	VKSQDERYDKGNRTYTW	-----	TPVNGTDSLALVPTYSFYIRAKLSEITIQ 622
Db	693	LEQRTIKRKWD	---	SYEMWGTLSRIITOFNNISYQWDSL-NYQAGAIRAKID----- 742
QY	623	ARSKGKMKDSETLKP	---	DNFEESGYTFIAPRDYCNDLKISDNNTFEFLNFWNEFI----- 675
Db	743	LEYKYSQSDRENKISQVENLKN	-----	LDVKIS---EAMNINKFIRECSV 787
QY	676	-----	DRKTPNPNSCNADLINRVILDA	----- 697
Db	788	TYLFKNMLPKVIDELNEFDRT	---	KAKLIN-LIDSHNLIILVEYDKLIKAKVNSF 839
QY	698	-----GTN	---	ELVQNYW-----SKQNKIKGVKARFVVDGGITRVYKPEAGE 738
Db	840	QNTIPFNFTSYTNNSLLKDIINEXFNNINDSKILSLQNKNTLVDTSG	---	-----YNAEYSE 894
QY	739	---NWQENPETYDSFYKRSLODNDNVFATPYENKSGPGAYESGIMVSKAVEIYIOGKLLK	---	796
Db	895	EGDVOLNP	-----	IF--PFDFKLGSGEDGRGVITVQENINVIYNSMTE 935
QY	797	PAVVGIKIDVNSWIENFTKTSIRDPAGVPCCKNSDVMOCVILDDGGFLMANHD	---	853
Db	936	SFSISFWTRINKWNSNLPGYTIID	-----	SVKNSSWGSIQIISNLFVTLTKQNEQSDSEQ 988



KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 27  
FT CHAIN 28 921  
FT  
FT DOMAIN 270 428 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
FT CARBOHYD 80 80 H4.  
FT CARBOHYD 205 205 WFA.  
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 49 50 HT->SK (IN REF. 3).  
FT CONFLICT 703 703 D -> H (IN REF. 1; AA SEQUENCE).  
SQ SEQUENCE 921 AA; 102146 MW; E2BF95925DE8D07C CRC64;

Query Match 2.8%; Score 150.5; DB 1; Length 921;  
Best Local Similarity 19.9%; Pred. No. 0.32; Indels 265; Gaps 36;  
Matches 156; Conservative 100; Mismatches 264;

QY 4 GCLLALTLT-----FQSLLPSEEPFSPSAVTIKSWDK---MOED--- 43  
DB 10 GLLLVLPALLAVLQSTAHKNDINIYSLTVDKSVSRFAHTVVTSRVNVKSGSAVQEAETQ 69  
QY 44 -----LVTLAKTASGVNLVDIYK--YODLYT-VEPNARQLVEIAARDIEKL--- 89  
DB 70 MELPKKAFITNESMIIDGVTYGNIKERAAEQYSAVARGESAGLVRATGRKTEQFOVA 129  
QY 90 LSNRSKALVSLAEAKVQAAHQWREDPASNEWVYINAKDDLDPEKNDSEPGSORIKPVF 149  
DB 130 VSVAPAAKVTFLVTEELARH-----LGVTELLKIQOQ-----QLVKHLQ 171  
QY 150 IEDANFGRO-ISY-QHAAVHIPTDIYEGTIVLNE-----LNMTSALDEVFKKREEDPSL 203  
DB 172 MDIHIFEPQGISFLETSTFTNLAELATISONKTKAHIREKPTLSQO-QKSPEQOETV 230  
QY 204 L-----WQVFGSATG-----LARYSPSPWVDSRTPNPKIDLYDVRRRPWYIOG 247  
DB 231 LOGNETVRYDVNRTVTGSGIQIENGYSFVHYFAPEVW----- 266  
QY 248 RASPKDMLLVDVSGVSLGTLKLRITSYSEMLETSDDDFVNVASFNSNAODVSCFOHL 307  
DB 267 SAIPKNVIEVDITSGSMRGKIQOTREALIKILGDLGSRQDNLSVFSGEAPR-----RA 322  
QY 308 VOANVRNKKVLDAVNNTAKGITYKGFSAFEOGLNINYSRANCNKI-----IM 359  
DB 323 VAASAEVVEAKSYAAEIIHAQGTNINDAMLAVALQL-----ERANRELLPARSVTFII 377  
QY 360 LFTDG-----GEERAQIFNKNKDKVRV-----PFRSVGQHNRYERGPIQWMA 403  
DB 378 LLTDGDPVTGETNPSKI-----QKNVREAIQHSCLGFGFDVYAFLEK-----MA 426  
QY 404 CENKG-----YY-----YEIPSIGAIRINTQEYLDVL--GR 432  
DB 427 LENGGLARIYEDSDSALOEDFYQEVANPLRLVAFEYPS-NAVEEVTDQDNFRLEFKGS 485  
QY 433 PMVLAG---DKAKQVQWNTVYLDALDELGLVITGTLFVNITQGFENKTNLKNOLIIG--- 486  
DB 486 ELVAVAGKLRDQSPDV-----LSAKVRGQLHMENTVFMESRVAEQEAFLSPKY 534  
QY 487 -----VMGDVYSLEDI--KRLTPRTLCPCNGYYFAIDPNGVYLLHPNL 527  
DB 535 IPHSEMERLWAYLTIQALLAQTVSASDAEKKALEARALSLSLNSYFVTLTSMVITKPEG 594  
QY 528 QPNPKSQBPVTLDFDAELENDIKVEIRNKMIDGSEGETFTFLVKSQDERVIDKGNRT 587  
DB 595 QEQSQAERK-----YENGRNQGNTHSGHSSF-----QFHSVGDRT 630  
QY 588 YTWTPVNGTDYSLALVLPYTFYIIKAKLEETITQARSKKGMKMDSETLKPDPNFESGYT 647  
DB 631 SRLTGGSSVD-----PVFS-----HRRGWKGQAO-----GFEKMSY- 661  
QY 648 FIAPR 652

Db 662 -LPPR 665

Search completed: July 23, 2001, 07:48:12  
Job time: 573 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:46:48 ; Search time 125.88 Seconds

(without alignments)  
1069.960 Million cell updates/sec

Title: US-09-397-548-15

Perfect score: 5346

Sequence: 1 MAGCLLALTLFLFQSLIG.....TNLFIVNRSKGTCPDCTRL 1018

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_unclassified.\*
- 13: sp\_vertebrate.\*
- 14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5312.5	99.4	1110	4 Q9UIU0	Q9ui0 homo sapien
2	5288	98.9	1091	6 O77773	O77773 sus scrofa
3	5202	97.3	1091	11 Q9ERS3	Q9ers3 rattus norv
4	5134	96.0	1103	11 O08532	O08532 mus musculu
5	3570	66.8	745	4 Q9UDQ3	Q9udq3 homo sapien
6	2900	54.2	1150	4 Q9NY47	Q9ny47 homo sapien
7	2883.5	53.9	1156	11 Q9E0G2	Q9eqg2 mus musculu
8	2872.5	53.7	1143	4 Q9NY48	Q9ny48 homo sapien
9	2851.5	53.7	1145	4 Q9Y268	Q9y268 homo sapien
10	2851.5	53.3	1076	4 Q9UEW0	Q9uew0 homo sapien
11	2682	50.2	975	4 Q9NSA6	Q9nsa6 homo sapien
12	1085	20.3	1091	11 Q921L5	Q921l5 mus musculu
13	1015	19.0	997	4 Q9NY16	Q9ny16 homo sapien
14	925.5	17.4	2190	5 Q9NK64	Q9nk64 drosophila
15	912.5	17.1	2172	5 Q9VJMO	Q9vjmo drosophila
16	889	16.6	1191	5 Q9VJN7	Q9vjn7 drosophila
17	884	16.5	1255	5 Q9NK83	Q9nk83 drosophila
18	875	16.4	170	4 Q9UDL7	Q9udl7 homo sapien
19	832.5	15.6	1022	5 Q9V6T7	Q9v6t7 drosophila

20	738.5	13.8	519	4 Q9NY18	Q9ny18 homo sapien
21	589.5	10.7	1148	5 Q17517	Q17517 caenorhabdi
22	514.5	9.6	104	4 Q9UD81	Q9ud81 homo sapien
23	506	9.5	100	6 Q9GLH1	Q9gli1 bos taurus
24	498.5	9.3	121	4 Q9UD82	Q9ud82 homo sapien
25	482	9.0	98	4 Q9UDU5	Q9udu5 homo sapien
26	465	8.7	97	4 Q9UD80	Q9ud80 homo sapien
27	402	7.5	77	4 Q95026	Q95026 homo sapien
28	337.5	6.3	1185	4 Q9HCJ9	Q9hcj9 homo sapien
29	317.5	5.9	223	11 Q9RI42	Q9ri42 mus musculu
30	222	4.2	1449	5 Q9V917	Q9v917 drosophila
31	170.5	3.2	494	5 Q9U7P4	Q9u7p4 eufolliculi
32	167	3.1	796	1 Q9HJRO	Q9hjr0 thermoplasm
33	161	3.0	2706	5 O15870	O15870 plasmodium
34	156.5	2.9	903	6 Q9GLY5	Q9gly5 oryctolagus
35	155	2.9	1516	5 Q96154	Q96154 plasmodium
36	155	2.9	2364	2 Q46342	Q46342 clostridium
37	154.5	2.9	1315	2 O86488	O86488 staphylococ
38	153	2.9	932	11 Q35802	Q35802 rattus norv
39	152.5	2.9	789	2 Q45793	Q45793 bacillus th
40	152	2.8	1105	14 Q9EMZ8	Q9emz8 ansacta moo
41	151.5	2.8	2867	5 Q9N2M3	Q9n2m3 plasmodium
42	150.5	2.8	2771	5 Q26216	Q26216 plasmodium
43	150	2.8	946	6 Q9GLY6	Q9gly6 oryctolagus
44	149	2.8	459	2 Q25905	Q25905 helicobacte
45	149	2.8	930	4 Q9UQ54	Q9uq54 homo sapien

#### ALIGNMENTS

RESULT 1

Q9UIU0  
ID Q9UIU0 PRELIMINARY; PRT; 1110 AA.  
AC Q9UIU0;  
DT 01-MAY-2000 (TREMREL. 13, Created)  
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE DIHYDROXYRIDINE RECEPTOR ALPHA 2 SUBUNIT.  
GN CACNA2D1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_taxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20005942; PubMed=10534405;  
RA Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;  
RT "Genomic structure and functional expression of a human alpha(2)/delta  
RL calcium channel subunit gene (CACNA2).";  
RL Genomics 61:201-209(1999).  
DR EMBL; AF083854; AAF03259.1; JOINED.  
DR EMBL; AF083817; AAF03259.1; JOINED.  
DR EMBL; AF083818; AAF03259.1; JOINED.  
DR EMBL; AF083819; AAF03259.1; JOINED.  
DR EMBL; AF083820; AAF03259.1; JOINED.  
DR EMBL; AF083821; AAF03259.1; JOINED.  
DR EMBL; AF083822; AAF03259.1; JOINED.  
DR EMBL; AF083823; AAF03259.1; JOINED.  
DR EMBL; AF083824; AAF03259.1; JOINED.  
DR EMBL; AF083825; AAF03259.1; JOINED.  
DR EMBL; AF083826; AAF03259.1; JOINED.  
DR EMBL; AF083827; AAF03259.1; JOINED.  
DR EMBL; AF083828; AAF03259.1; JOINED.  
DR EMBL; AF083829; AAF03259.1; JOINED.  
DR EMBL; AF083830; AAF03259.1; JOINED.  
DR EMBL; AF083831; AAF03259.1; JOINED.  
DR EMBL; AF083832; AAF03259.1; JOINED.  
DR EMBL; AF083833; AAF03259.1; JOINED.  
DR EMBL; AF083834; AAF03259.1; JOINED.  
DR EMBL; AF083835; AAF03259.1; JOINED.  
DR EMBL; AF083836; AAF03259.1; JOINED.  
DR EMBL; AF083837; AAF03259.1; JOINED.

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DR EMBL; AF083838; AAF03259.1; JOINED.
DR EMBL; AF083839; AAF03259.1; JOINED.
DR EMBL; AF083840; AAF03259.1; JOINED.
DR EMBL; AF083841; AAF03259.1; JOINED.
DR EMBL; AF083842; AAF03259.1; JOINED.
DR EMBL; AF083843; AAF03259.1; JOINED.
DR EMBL; AF083844; AAF03259.1; JOINED.
DR EMBL; AF083845; AAF03259.1; JOINED.
DR EMBL; AF083846; AAF03259.1; JOINED.
DR EMBL; AF083847; AAF03259.1; JOINED.
DR EMBL; AF083848; AAF03259.1; JOINED.
DR EMBL; AF083849; AAF03259.1; JOINED.
DR EMBL; AF083850; AAF03259.1; JOINED.
DR EMBL; AF083851; AAF03259.1; JOINED.
DR EMBL; AF083852; AAF03259.1; JOINED.
DR EMBL; AF083853; AAF03259.1; JOINED.
DR InterPro; IPR000885; -.
DR Pfam; PF002035; -.
DR ProDom; PD002078; -.
DR KW Receptor.
SQ SEQUENCE 1110 AA; 125307 MW; 8358DC6AD489C074 CRC64;

Query Match 99.4%; Score 5312.5; DB 4; Length 1110;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1015; Conservative 1; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGCLLALTTLFQSLLLIGPSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTTLFQSLLLIGPSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNNAQLVEIAARDEIKLLSNRSLVSLALEAEKVQAAHQRWEDFASN 120
DB 61 YEKYQDLYTVEPNNAQLVEIAARDEIKLLSNRSLVSLALEAEKVQAAHQRWEDFASN 120
QY 121 EYVYNAKDDLPENKNDSPGSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPENKNDSPGSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
QY 181 NELNWTLSALDEYFKKNREDDPSLLQWVGSGATGLARYYPASPDWNSRTPNKIDLYDVR 240
DB 181 NELNWTLSALDEYFKKNREDDPSLLQWVGSGATGLARYYPASPDWNSRTPNKIDLYDVR 240
QY 241 RPWYIQAASPRDMLILVDVSGVSLTLKLRISYSEMLETSLDDDFNVASFNSAQD 300
DB 241 RPWYIQAASPRDMLILVDVSGVSLTLKLRISYSEMLETSLDDDFNVASFNSAQD 300
QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFQQLLNYNVSRANCKNIIML 360
DB 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFQQLLNYNVSRANCKNIIML 360
QY 361 FTDGGEERAQAEIFNKYNDKKVRFVFSVQGHNYERGPQWACENKGYIYIPISGAIR 420
DB 361 FTDGGEERAQAEIFNKYNDKKVRFVFSVQGHNYERGPQWACENKGYIYIPISGAIR 420
QY 421 INTQYLDVLGRPMVLGADKAKQVQWNTVYLDALDELGLVITGLPVENTIGOFENKTLK 480
DB 421 INTQYLDVLGRPMVLGADKAKQVQWNTVYLDALDELGLVITGLPVENTIGOFENKTLK 480
QY 481 NOLILGVMGVDVSLDEIKRLTPRFTLCPNGYFPAIDPNGYLLHPNLQPK----- 530
DB 481 NOLILGVMGVDVSLDEIKRLTPRFTLCPNGYFPAIDPNGYLLHPNLQPK----- 530
QY 531 -----NPKSQEPVILDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSODERYI 581
DB 541 LKRRNPNTQNPQSQEPVILDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSODERYI 600
QY 582 DKGNTYTWTPVNGDYSLALVLPYTFYVYIKAKLEETITQARSKKGMKQSEITLKPDPF 641
DB 601 DKGNTYTWTPVNGDYSLALVLPYTFYVYIKAKLEETITQARSKKGMKQSEITLKPDPF 660
QY 642 EESGYTFIAPRDYCNLDKISDNTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTN 701

661 EESGYTFIAPRDYCNLDKISDNTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTN 720
702 ELVQNYWSKQKNIKVKARFVVTDDGGITRVYPKAENQENPETYEDSFYKRSNDNY 761
721 ELVQNYWSKQKNIKVKARFVVTDDGGITRVYPKAENQENPETYEDSFYKRSNDNY 780
762 VETAPYFNKSGGAYESGIMVSKAVEIYIQGLLKPAVVGKIDVNSWIENFTKTSIRDP 821
781 VETAPYFNKSGGAYESGIMVSKAVEIYIQGLLKPAVVGKIDVNSWIENFTKTSIRDP 840
822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQWIGRFFGEIDPSLMRHLVNI SVYA 881
841 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQWIGRFFGEIDPSLMRHLVNI SVYA 900
882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAASWIIQQOFLSLTFPR 941
901 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAASWIIQQOFLSLTFPR 960
942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGCGNCSRIFFHGKLMNTNL 1001
961 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGCGNCSRIFFHGKLMNTNL 1020
1002 IFIMVESKGTCPCDTRL 1018
1021 IFIMVESKGTCPCDTRL 1037

RESULT 2
ID 077773 PRELIMINARY; PRT; 1091 AA.
AC 077773;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2 DELTA SUBUNIT PRECURSOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel
RT subunit from porcine cerebral cortex. Expression of a soluble form of
RL the protein that retains [3H]gabapentin binding activity.";
RL J. Biol. Chem. 273:25458-25465(1998).
DR EMBL; AF077665; AAC36289.1; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
DR KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 1091 VOLTAGE-DEPENDENT CALCIUM CHANNEL
FT SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9EE60E CRC64;

Query Match 98.9%; Score 5288; DB 6; Length 1091;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFQSLLLIGPSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTTLFQSLLLIGPSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKYQDLYTVEPNNAQLVEIAARDEIKLLSNRSLVSLALEAEKVQAAHQRWEDFASN 120
DB 61 YEKYQDLYTVEPNNAQLVEIAARDEIKLLSNRSLVSLALEAEKVQAAHQRWEDFASN 120
QY 121 EYVYNAKDDLPENKNDSPGSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPENKNDSPGSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180
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Db	121	EWYVNAKDDLDPEKNDSEPGSQRIKPVFIDANFGROISYQHAHVHPTDIYEGSTIVL	180
Qy	161	NELNWTSSALDEVEFKNREDESLWQVGSATGLARYYPASPWDNSRTPNKNIDLYDVR	240
Db	181	NELNWTSSALDEVEFKNREDESLWQVGSATGLARYYPASPWDNSRTPNKNIDLYDVR	240
Qy	241	RWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD	300
Db	241	RWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD	300
Qy	301	VSCFQHLVQVNRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML	360
Db	301	VSCFQHLVQVNRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML	360
Qy	361	FTDGGERAQEIFNKNKDKKVRFRFSYQHNRYERGPQIOWMACENKGYIPEISGAIR	420
Db	361	FTDGGERAQEIFNKNKDKKVRFRFSYQHNRYERGPQIOWMACENKGYIPEISGAIR	420
Qy	421	INTQEYLDVLGRPMVLGDKAKQVQWNTNYLDALGLVITGTPVFNITGQFENKTNLK	480
Db	421	INTQEYLDVLGRPMVLGDKAKQVQWNTNYLDALGLVITGTPVFNITGQFENKTNLK	480
Qy	481	NQILGVMGVDSLEDIKRLTPRFTLCPNGYYPADPNQVYLLHPNLQPNKPSQEPVIL	540
Db	481	NQILGVMGVDSLEDIKRLTPRFTLCPNGYYPADPNQVYLLHPNLQPNKPSQEPVIL	540
Qy	541	DFLDALENDIKVEIRNKMIDGESGKFTPLVKSQDERYIDKGNRTYTWTPVNGTDYSL	600
Db	541	DFLDALENDIKVEIRNKMIDGESGKFTPLVKSQDERYIDKGNRTYTWTPVNGTDYSL	600
Qy	601	ALVLPYTFYIYKAKLEETITQARSKGKMDSETLKPDPNFESGYTFIAPROYCNDLKI	660
Db	601	ALVLPYTFYIYKAKLEETITQARSKGKMDSETLKPDPNFESGYTFIAPROYCNDLKI	660
Qy	661	SDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELQVYWSKQNKIGVKAR	720
Db	661	SDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELQVYWSKQNKIGVKAR	720
Qy	721	FVYTDGGITRVYKPEAGENQWENPETEYDSFYKRSNDNDNYVFTAPYFNKSGPGAYESGI	780
Db	721	FVYTDGGITRVYKPEAGENQWENPETEYDSFYKRSNDNDNYVFTAPYFNKSGPGAYESGI	780
Qy	781	MYSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDPCAGPVCDCKRNSDMDCVI	840
Db	781	MYSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDPCAGPVCDCKRNSDMDCVI	840
Qy	841	LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLNYSVAFNKSVDYQSVCEPGAAPQ	900
Db	841	LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLNYSVAFNKSVDYQSVCEPGAAPQ	900
Qy	901	GAGHSAYVPSVADILQIGWATAAASILQOFLSLFPRLLEAEMEDDDFTASLSQ	960
Db	901	GAGHSAYVPSVADILQIGWATAAASILQOFLSLFPRLLEAEMEDDDFTASLSQ	960
Qy	961	SCITEQTOYFFDNDSKPSGVLDGNCGRIFPHVEKLMNTNLFIMVESKGTCPDCTRL	1018
Db	961	SCITEQTOYFFDNDSKPSGVLDGNCGRIFPHVEKLMNTNLFIMVESKGTCPDCTRL	1018

RESULT 3  
 QERS3 QERS3 PRELIMINARY; PRT: 1091 AA.  
 ID QERS3  
 AC QERS3;  
 DT 01-MAR-2001 (TREMREL. 16, Created)  
 DT 01-MAR-2001 (TREMREL. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
 DE VOLTAGE-GATED CALCIUM CHANNEL ALPHA2/DELTA-1 SUBUNIT.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;		
RA	Lin Y., Lipscombe D.;		
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF286488; AAG28164.1; -		
FT	VARIANT 209 212	GSAT -> AADR.	
FT	VARIANT 338 338	S -> T.	
FT	VARIANT 599 600	SL -> RY.	
FT	VARIANT 869 869	S -> R.	
SQ	SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;		
Query Match 97.3%; Score 5202; DB 11; Length 1091;			
Best Local Similarity 96.6%; Pred. No. 0;			
Matches 983; Conservative 20; Mismatches 15; Indels 0; Gaps 0;			
QY	1 MAAGCLLATLTTLFQSLILGSPSEEPFSAVITKSWDKMQEDLVTLAKTASGVNQLVDI	60	
DB	1 MAAGCLLATLTTLFQSLILGSPSEEPFSAVITKSWDKMQEDLVTLAKTASGVQLADI	60	
QY	61 YEKYQDLYVPEPNARQLVEIAARDIEKLSNRKALVSLALAEAKVQAAHQWREFASN	120	
DB	61 YEKYQDLYVPEPNARQLVEIAARDIEKLSNRKALVSLALAEAKVQAAHQWREFASN	120	
QY	121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL	180	
DB	121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL	180	
QY	181 NELNWTSSALDEVEFKNREDESLWQVGSATGLARYYPASPWDNSRTPNKNIDLYDVR	240	
DB	181 NELNWTSSALDEVEFKNREDESLWQVGSATGLARYYPASPWDNSRTPNKNIDLYDVR	240	
QY	241 RPWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD	300	
DB	241 RPWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD	300	
QY	301 VSCFQHLVQVNRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML	360	
DB	301 VSCFQHLVQVNRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML	360	
QY	361 FTDGGERAQEIFNKNKDKKVRFRFSYQHNRYERGPQIOWMACENKGYIPEISGAIR	420	
DB	361 FTDGGERAQEIFNKNKDKKVRFRFSYQHNRYERGPQIOWMACENKGYIPEISGAIR	420	
QY	421 INTQEYLDVLGRPMVLGDKAKQVQWNTNYLDALGLVITGTPVFNITGQFENKTNLK	480	
DB	421 INTQEYLDVLGRPMVLGDKAKQVQWNTNYLDALGLVITGTPVFNITGQFENKTNLK	480	
QY	481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYYPADPNQVYLLHPNLQPNKPSQEPVTL	540	
DB	481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYYPADPNQVYLLHPNLQPNKPSQEPVTL	540	
QY	541 DFLDALENDIKVEIRNKMIDGESGKFTPLVKSQDERYIDKGNRTYTWTPVNGTDYSL	600	
DB	541 DFLDALENDIKVEIRNKMIDGESGKFTPLVKSQDERYIDKGNRTYTWTPVNGTDYSL	600	
QY	601 ALVLPYTFYIYKAKLEETITQARSKGKMDSETLKPDPNFESGYTFIAPRYCNDLKI	660	
DB	601 ALVLPYTFYIYKAKLEETITQARSKGKMDSETLKPDPNFESGYTFIAPRYCNDLKP	660	
QY	661 SDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNKIGVKAR	720	
DB	661 SDNTEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNKIGVKAR	720	
QY	721 FVYTDGGITRVYKPEAGENQWENPETEYDSFYKRSNDNDNYVFTAPYFNKSGPGAYESGI	780	
DB	721 FVYTDGGITRVYKPEAGENQWENPETEYDSFYKRSNDNDNYVFTAPYFNKSGPGAYESGI	780	
QY	781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDMDCVI	840	
DB	781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDMDCVI	840	
QY	841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLNYSVAFNKSVDYQSVCEPGAAPQ	900	
DB	841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLNYSVAFNKSVDYQSVCEPGAAPQ	900	



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QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENTFTKTSIRDP 821
DB 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENTFTKTSIRDP 833
QY 822 CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYA 881
DB 834 CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYA 893
QY 882 FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQOFLLSLTPR 941
DB 894 FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQOFLLSLTPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQFFNDKSFSGVLDGCGNCSRFHGEKLMNTNL 1001
DB 954 LLEAVEMEDDDFTASLSKQSCITEQTQFFNDKSFSGVLDGCGNCSRFHGEKLMNTNL 1013
QY 1002 IFIMVESKTCPCDTRL 1018
DB 1014 VFIMVESKTCPCDTRL 1030

RESULT 5
ID Q9UDQ3 PRELIMINARY; PRT; 745 AA.
AC Q9UDQ3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE WUGSC: HJD056004.1 PROTEIN (FRAGMENT).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Mead K., Bauer C.;
RT "The sequence of Homo sapiens PAC clone RP4-560014.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006145; A020938.1;
FT InterPro; IPR002035;
FT NON_TER
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;

Query Match 66.88; Score 3570; DB 4; Length 745;
Best Local Similarity 99.78; Pred. No. 7.1e-220;
Matches 670; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 347 YNVRANCKIIMLFTDGEERAQEIFNKYNKDKKRVFRFSVGOHNYRGPPIOMACEN 406
DB 1 YNVRANCKIIMLFTDGEERAQEIFNKYNKDKKRVFRFSVGOHNYRGPPIOMACEN 60
QY 407 KGYEYIPEISGAIRINTQYLDVLRPMLAGDKAKQVQWNTNVDLDELGLVITGLPV 466
DB 61 KGYEYIPEISGAIRINTQYLDVLRPMLAGDKAKQVQWNTNVDLDELGLVITGLPV 120
QY 467 FNITQFENKTNKQLILGVNGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPN 526
DB 121 FNITQFENKTNKQLILGVNGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPN 180
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QY 527 LQPNKPSQEPVTLDFDALENDIKVEIRNKMIDGSEKFTFTLVKSQDRIYDKGNR 586
DB 181 LQPNKPSQEPVTLDFDALENDIKVEIRNKMIDGSEKFTFTLVKSQDRIYDKGNR 240
QY 587 TYTWPVNGTDSYSLALVPTYSFYIKAKLETITQAKSKGKMDSETLKPDNFEESY 646
DB 241 TYTWPVNGTDSYSLALVPTYSFYIKAKLETITQAKSKGKMDSETLKPDNFEESY 300
QY 647 TPIAPRDYCNLDKISDNNTFEFLNNEFDRTKTPNPNPCNADLINRVLLDAGFTNELVN 706
DB 301 TPIAPRDYCNLDKISDNNTFEFLNNEFDRTKTPNPNPCNADLINRVLLDAGFTNELVN 360
QY 707 YWSKOKNIKGVKARFVVTGGITRVYPKEAGENQWNPETEDSFYKRSILDNDNYVFTAP 766
DB 361 YWSKOKNIKGVKARFVVTGGITRVYPKEAGENQWNPETEDSFYKRSILDNDNYVFTAP 420
QY 767 YFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENTFTKTSIRDP 826
DB 421 YFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENTFTKTSIRDP 480
QY 827 CDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSY 886
DB 481 CDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSY 540
QY 887 DYQSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQOFLLSLTPRLEAV 946
DB 541 DYQSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQOFLLSLTPRLEAV 600
QY 947 EMEDDFTASLSKQSCITEQTQFFNDKSFSGVLDGCGNCSRFHGEKLMNTNLIFIMV 1006
DB 601 EMEDDFTASLSKQSCITEQTQFFNDKSFSGVLDGCGNCSRFHGEKLMNTNLIFIMV 660
QY 1007 ESKGTCPCDTRL 1018
DB 661 ESKGTCPCDTRL 672

RESULT 6
ID Q9NY47 PRELIMINARY; PRT; 1150 AA.
AC Q9NY47;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GN CACNA2D2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Klugbauer N.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Hobom M., Dai S., Marats E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251368; CAB86193.1;
DR InterPro; IPR002035;
SQ SEQUENCE 1150 AA; 129875 MW; 37B75F687AFE573C CRC64;

Query Match 54.28; Score 2900; DB 4; Length 1150;
Best Local Similarity 54.78; Pred. No. 9.6e-177;
Matches 564; Conservative 164; Mismatches 273; Indels 30; Gaps 13;

QY 7 LALTTLFQSLIGPSEEPFSAVTIKSWDKMOEDLVTLAKTAGVNLVIEKYQD 66
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Db 44 LWLLPPLPAAAPGASAYSPQQHMQHARRLEQVDGVMRIFGGVQQLREIYKDRN 103
Qy 67 LTVFENARQIUEAARDIEKLLSNRSKALVSLALEAEKQVAAHQWREDFASNEVYIN 126
Db 104 LFEVQENEPQKLEKRVAGDIESLLDRKQVALKRLADAAENFKAHQWQDNKEEDIVYD 163
Qy 127 AKDDL---DPEKNDSPEGSQ--RIKPVIEDANFGRQISYQAAHVHPTDIYEGSTIVLN 181
Db 164 AKADAELODPESEDVERGSKASTLRDIEDPNFNKNYNSYAAVQIPTDIYKGSTVLN 223
Qy 182 ELNWTLSALDEYFKKREDDPSLLWQVFGSATGLARYYPASPWVDSRTPNPKIDLYDVRRR 241
Db 224 ELNWTLEALFNEMENRRDPDILLWQVFGSATGLARYYPASPWVDSRTPNPKIDLYDVRRR 279
Qy 242 PWYIOGASPKDMLILVDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNSAQDV 301
Db 280 PWYIOGASPKDMLILVDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNSAQDV 339
Qy 302 SCFOHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNRYNVRANCNKIIMLF 361
Db 340 SCFTHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNRYNVRANCNKIIMLF 399
Qy 362 TDGGEERAQEIFNKNY--KDKKRVFRFVSQGHNYERGPIONMACENKGYIYFIPSGAIR 420
Db 400 TDGGEEDRVQDVFYKYNPNRTVRVFTFVSQGHNYERGPIONMACENKGYIYFIPSGAIR 459
Qy 421 INTQEYLDVGRPMVLGADKAKQVQWNTNVLDALEGLVITGTLFVFNITQGFENKTLK 480
Db 460 INTQEYLDVGRPMVLGADKAKQVQWNTNVLDALEGLVITGTLFVFNITQGFENKTLK 517
Qy 481 NOLLGVGMVDVSLDKRLTPRTLCFNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540
Db 518 NOLLGVGMVDVSLDKRLTPRTLCFNGYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 577
Qy 541 DFLDAELENDIKVIRNKMIDGEGEFTFTLVKSODERYIDKGNRTYTPVNGTIDYSL 600
Db 578 DFLDAELENDIKVIRNKMIDGEGEFTFTLVKSODERYIDKGNRTYTPVNGTIDYSL 637
Qy 601 ALVLPYTSFYIYKAKLEETITQARKKGMKDSITLKPDPNFESGYTFIAPRDYCNLKI 660
Db 638 GLVLPYTSFYIYKAKLEETITQARKKGMKDSITLKPDPNFESGYTFIAPRDYCNLKI 697
Qy 661 SDNTEFLANFEIDRKTNNPSCNADLNRLVLLDAGTNELVQNTWSKQK--NIKGVKA 719
Db 698 SDNTEFLANFEIDRKTNNPSCNADLNRLVLLDAGTNELVQNTWSKQK--NIKGVKA 757
Qy 720 RFVYTDGGITRVYPKEAGNWOENPTYEDSFYKRSLDNDNYVFTAPYFNK--SGPGAYES 778
Db 758 RFVYTDGGITRVYPKEAGNWOENPTYEDSFYKRSLDNDNYVFTAPYFNK--SGPGAYES 817
Qy 779 ---GIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIEF-----TKTSIRDP--CAGP--- 825
Db 818 DTGVLVSTAVELSLGRRTLRPAVGVKLDLEAWAEKFKVLASNRTHQDPQKC--GPNSH 876
Qy 826 -VDCRNSDVMDCVLDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI-SVAFNK 884
Db 877 CEMDCYNNEDLLCVLDDGGFLVLSNQNHQWQVGRFFSEVDANLMLALYNSFYTRKE 936
Qy 885 SYDQSVCEPGAAPKOGAGHRSAYSVADILQIGWATAAASIIQQFLLSITFFRLLLE 944
Db 937 SYDQSVCEPGAAPKOGAGHRSAYSVADILQIGWATAAASIIQQFLLSITFFRLLLE 996
Qy 945 AVEMEDDDFTASLSKOSCIQTEQYFFDNDKSKFSGLVDCGNCGRIFPHGKLMNTNLI 1004
Db 997 ADPAEAG--SPETRESSCVMKQYFYFGSVNYSNAILDCGNCGRIFPHGKLMNTNLI 1055
Qy 1005 MVESKCTCPD 1015
Db 1056 VAEKPLCSQCE 1066
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RESULT 7

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Q9EQG2
ID Q9EQG2 PRELIMINARY; PRT; 1156 AA.
AC Q9EQG2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2-DELTA-2 SUBUNIT.
GN CACNA2D2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TKDU;
RX MEDLINE=21015416; PubMed=11130987;
RA Barclay J., Rees M.;
RT "Genomic organization of the mouse and human alpha2delta2 voltage-
RT dependent calcium channel subunit genes.";
RL Mamm. Genome 11:1142-1144(2000).
DR EMBL; AF247139; AAC47846.1;
SQ SEQUENCE 1156 AA; 130611 MW; A732545A2B302A52 CRC64;

Query Match 53.9%; Score 2883.5; DB 11; Length 1156;
Best Local Similarity 54.2%; Pred. No. 1.1e-175;
Matches 560; Conservative 168; Mismatches 274; Indels 31; Gaps 14;

Qy 6 LLATLTLFOSLLIGP--SSEPPFSAVTIKSWDKMEDLVLTAKTAGVGNQLVDIYEKY 64
Db 45 LLLPPLPPLPAAAPGASAYSPQQHMQHARRLEQVDGVMRIFGGVQQLREIYKDRN 104
Qy 65 QDLVTVENPNNARQLVETAAARDIEKLLSNRSKALVSLALEAEKQVAAHQWREDFASNEVY 124
Db 105 RNFEVQENEPQKLEKRVAGDIESLLDRKQVALKRLADAAENFKAHQWQDNKEEDIMY 164
Qy 125 YNAKDDL---DPEKNDSPEGSQ--RIKPVIEDANFGRQISYQAAHVHPTDIYEGSTIV 179
Db 165 YDAKADAELODPESEDVERGSKASTLRDIEDPNFNKNYNSYAAVQIPTDIYKGSTVI 224
Qy 180 LNELNWTLSALDEYFKKREDDPSLLWQVFGSATGLARYYPASPWVDSRTPNPKIDLYDVR 239
Db 225 LNELNWTLEALFNEMENRRDPDILLWQVFGSATGLARYYPASPWVDSRTPNPKIDLYDVR 280
Qy 240 RRPWYIOGASPKDMLILVDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNSAQ 299
Db 281 RRPWYIOGASPKDMLILVDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNSAQ 340
Qy 300 DVSCFOHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNRYNVRANCNKIIM 359
Db 341 PVSCFTHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNRYNVRANCNKIIM 400
Qy 360 LFTDGGEEERAQEIFNKNY--KDKKRVFRFVSQGHNYERGPIONMACENKGYIYFIPSGA 418
Db 401 MFTDGGEDRVQDVFYKYNPNRTVRVFTFVSQGHNYERGPIONMACENKGYIYFIPSGA 460
Qy 419 IRTNTOEYLDVGRPMVLGADKAKQVQWNTNVLDALEGLVITGTLFVFNITQGFENKTN 478
Db 461 IRTNTOEYLDVGRPMVLGADKAKQVQWNTNVLDALEGLVITGTLFVFNITQGFENKTN 518
Qy 479 LKNOLLGVGMVDVSLDKRLTPRTLCFNGYFAIDPNGYVLLHPNLOPKNPKSQEPV 538
Db 519 KKNOLLGVGMVDVSLDKRLTPRTLCFNGYFAIDPNGYVLLHPNLOPKNPKSQEPV 578
Qy 539 TLDLDAELENDIKVIRNKMIDGEGEFTFTLVKSODERYIDKGNRTYTPVNGTIDY 598
Db 579 TLDLDAELENDIKVIRNKMIDGEGEFTFTLVKSODERYIDKGNRTYTPVNGTIDY 638
Qy 599 SLALVLPYTSFYIYKAKLEETITQARKKGMKDSITLKPDPNFESGYTFIAPRDYCNL 658
Db 639 SLGLVLPYTSFYIYKAKLEETITQARKKGMKDSITLKPDPNFESGYTFIAPRDYCNL 698
Qy 659 KISDNNTPELLNFNEFIDRKTNNPSCNADLNRLVLLDAGTNELVQNTWSKQK--NIKGV 717
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61 KYQALKLADAAENFQKAHRWQNIKEEDIVYDAKADAELDPESEDVERGSKASTLRL 120  
QY 148 VFTEDANFGROISQOHAHPIPTDIYEGSTIVLNELNWTISALDEVPKKNREEDPSLLQV 207  
DB 121 DFEDPKNKKNVSYAAVQIPTDIYKGSIVLNELNWTISALENVFENRRQDPTLLQV 180  
QY 208 FGSATGLARYYPASPVDNSTRPNKIDLYVRRRPWTIOGAASPKOMLILVDVSGSGL 267  
DB 181 FGSATGTRYYPATP-----RAPKKIDLYVRRRPWTIOGASPKDMVIVDVSGSGL 236  
QY 268 TLKLRISVSEMLETLDSDDFVNVASFNASNAQVSCFOHLVQANVRNKVYLKDAVNITA 327  
DB 237 TLKLMKTSVCEMLDTSDDDFVNVASFNASNAQVSCFOHLVQANVRNKVYKFAVQKVA 296  
QY 328 KGITDYKGFSAFAPOLLNVRANCKIIMLTDFGGEERAQIFNKNY-KDKKRVFR 386  
DB 297 KGITGYKAGFEYAFDQLNSNITRANCKIMMTDFGGEERQVDFEYKYNWPNTRVFT 356  
QY 387 FSVGQHNYRGPIONMACENKGYEYIPSGAINTQEVLDVLRPMVLGAKQVOW 446  
DB 357 FSVGQHNVDVTPLOWMACANKGYEYIPSGAINTQEVLDVLRPMVLGAKQVOW 416  
QY 447 TNYVLDALGLVGTGTPVFNITQFENKTNLKNOLILGVMGVDSLEDKRLTPFTL 506  
DB 417 TNYVEDALGLGVGTGTPVFNLTQ--DGPCKKNQLLGVMGIDVANDIRLTPNYTL 474  
QY 507 CPNGYFAIDPNGVYLLHPNLQPNKPSQEPVTLDFDAELENDIKVEIRKNMIDGESSE 566  
DB 475 GANGYVFAIDNGVYLLHPNLKPTNFRPVPVTLDFDAELENDKEIRSMIDGNKGH 534  
QY 567 KTFRLVKSODERYIDKGNRTYTPVNGTDYSLALVLPYTSFYIYKAKLEETQOARSK 626  
DB 535 KQIRTLVKSODERYIDVTRNYTPVIRSTNYSGLVLPYTSFYIYKAKLEETQOARSK 590  
QY 627 KGMKDSLETPDNFESGYFIAPRDYCNDLKISDNNTFELLNFEIDRKTNPNSCN 686  
DB 591 ---VKYFEFLPSSFESGHHVFIAPREYCKOLNASDNNTFELLNFEIDRKTNPNSCN 647  
QY 687 ADLNRVLDAAGFVNLQYVWSKQ-NIKGVKARFVVTGGITRVYKPEAGENQENPE 745  
DB 648 NELLNLIDTGTQOLVERWRQDLNYSILAVFAATDGTIRVFPNKAEDWTENPE 707  
QY 746 TYEDSFYKRSLDNDNYFTAFYFNK-SGPAYES---GIMVSKAVEIYQKLLKPAVVG 801  
DB 708 PFNASFYRRSLDNHGYVFKPPHQDALLRPLENDTVGILYSTAVELSLGRTRLPVVG 767  
QY 802 IKIDVNSWENF-----TKTSIRDP--CAGP-----VCDCKRNSVMDCVILDDGGFLMA 850  
DB 768 VKLDLEAWAEKFKVLAASRTHQDQPKC-GPNSHCMDCEVNNEDLLCVLIDDDGGFLVLS 826  
QY 851 NHDDYTNOIGRFFGIDPDLMLHNLVNSIYAFNKSIDYQVCEPAAPKQAGHRSAYVP 910  
DB 827 KQNHQWDQVGRFFSVSDANLMLALNNFYRKESYDYQAACAPPPGNLGAAPRGVFP 886  
QY 911 SVADTLOIGMWATAAASILQOFLSLTFPRLEAVEMEDDDFTASLKQSCITQOTYF 970  
DB 887 TVADFLNLAWTSAASWSLFOQLLYGLVHWSFQADPAEAG-SPEPRESSCVMTQOTY 945  
QY 971 FDNDSKFSVGLDCNCSRIFHGEKMLNTLFIWVESKGTCPCD 1015  
DB 946 FGSVNASYNAIIDCGNCSRLFAORLTNTNLLFVVAEKPLCSQCE 990

RESULT 11  
QNSA6 PRELIMINARY: PRT: 975 AA.  
ID QNSA6  
AC QNSA6;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE LUAC11.1 (CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 2D SUBUNIT  
DE (KIAA0558)). (FRAGMENT).  
GN LUAC11.1.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barlow K.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Z84492; CAB41767.2; -.  
DR InterPro: IPR02035; -.  
FT NON\_TER 1  
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;

Query Match 50.2%; Score 2682; DB 4; Length 975;  
Best Local Similarity 57.4%; Pred. No. 6.3e-163;  
Matches 518; Conservative 134; Mismatches 217; Indels 34; Gaps 13;

QY 132 DPEKNDSEPGSO--RIKPVFTEDANFGROISQOHAHPIPTDIYEGSTIVLNELNWTISAL 189  
DB 2 DPESEDVERGSKASTLRLDFIEDPKNKKNVSYAAVQIPTDIYKGSIVLNELNWTISAL 61  
QY 190 DEVFKKREEDPSLLQVFGSATGLARYYPASPVDNSTRPNKIDLYVRRRPWTIOGAA 249  
DB 62 ENVMENRRQDPTLLQVFGSATGTRYYPATP-----RAPKKIDLYVRRRPWTIOGAS 117  
QY 250 SPKOMLILVDVSGSGLTLKLRISVSEMLETLDSDDFVNVASFNASNAQVSCFOHLVQ 309  
DB 118 SPKDMVIVDVSGSGLTLKLMKTSVCEMLDTSDDDFVNVASFNASNAQVSCFOHLVQ 177  
QY 310 ANVRNKVYKDAVNITAKGITDYKGFSAFAPOLLNVRANCKIIMLTDFGGEERA 369  
DB 178 ANVRNKVYKDAVNITAKGITDYKGFSAFAPOLLNVRANCKIIMLTDFGGEERA 237  
QY 370 QEIFNKYN-KDKKRVFRFSGQHNYRGPIONMACENKGYEYIPSGAINTQOARSK 428  
DB 238 QDVEKYNWPNTRVFTSVGQHNVDVTPLOWMACANKGYEYIPSGAINTQOARSK 297  
QY 429 VLGRPMVLGAKQVOWTNYVLDALGLVGTGTPVFNITQFENKTNLKNOLILGV 488  
DB 238 VLGRPMVLGAKQVOWTNYVLDALGLVGTGTPVFNITQFENKTNLKNOLILGV 355  
QY 489 GVDVSLDILKRLTPFTLCPNGYFAIDPNGVYLLHPNLQPNKPSQEPVTLDFDAELE 548  
DB 356 GIDVANDILKRLTPFTLCPNGYFAIDPNGVYLLHPNLKPTNFRPVPVTLDFDAELE 415  
QY 549 NDIKVEIRKNMIDGESSEKTFRLVKSODERYIDKGNRTYTPVNGTDYSLALVLPYS 608  
DB 416 DENKEIRSMIDGNKGHKGHKGHKGHKGHKGHKGHKGHKGHKGHKGHKGHKGHKGH 475  
QY 609 FYYIKAKLEETITQARSKKGMKDSLETPDNFESGYFIAPRDYCNDLKISDNNTFELL 668  
DB 476 TFYQLANLSDQILQ-----VKYFEFLPSSFESGHHVFIAPREYCKOLNASDNNTFELL 528  
QY 669 LNFNEFIDRKTNPNSCNADLNLNRLVLDAGFTNELVQYVWSKQ-NIKGVKARFVVTGG 727  
DB 529 KNFIELMEKVTDPDSKOCNNFLHNLILDTGTITQOLVERWRQDLNYSILAVFAATDGG 588  
QY 728 ITRVYKPEAGENQENPEYEDSFYKRSLDNDNYFTAFYFNK-SGPAYES---GIMVYS 783  
DB 589 ITRVYKPEAGENQENPEYEDSFYKRSLDNDNYFTAFYFNK-SGPAYES---GIMVYS 648  
QY 784 KAVEIYQKLLKPAVVGKIDVNSWENF-----TKTSIRDP--CAGP-----VCDCKR 832  
DB 649 TAVELSLGRTRLPVVGKIDVNSWENF-----TKTSIRDP--CAGP-----VCDCKR 707  
QY 833 SDVMDCVILDDGGFLMLANHHDDYTNOIGRFFGIDPDLMLHNLVNSIYAFNKSIDYQV 892  
DB 708 NEDLLCVLIDDDGGFLVLSQNHQWDQVGRFFSVSDANLMLALNNFYRKESYDYQAAC 767  
QY 893 EFGAAPKQAGHRSAYVPSVADITQIGMWATAAASILQOFLSLTFPRLEAVEMEDDD 952  
DB 768 AFQPPGNLGAAPRGVFPVTVADFLNLAWTSAASWSLFOQLLYGLVHWSFQADPAEAG 827



58 FI---LAPNDHFNLPVNIISLSDVQVPTNNYNDPAIVNGVYWSSESLNKYFVDFNFRDPS 114  
 203 LLWQVGSATGLARYPASPWPVNSRTPNPKIDLYDVRPRWYIQAASPRKMLILVDVSG 262  
 115 LIWQVGSAGTFQRPYGIKWEDE---NGVIAFCRNKKYIQAATSPKDVILVDVSG 171  
 263 SVSGLTLKLTARTSVSEMLETSDDDDFNVASFNNAQDVS-CFQ-HLVQANVRNKKVLKD 320  
 172 SMKGLRLTIKQVSSILDTLGGDDFFNIAYNEELHYVEPCLNGTLVQADRNKHEFRE 231  
 321 AVNITAKGIDYKKGSPFAFQELLNVNVRAN--CNKIIMLFTDGGEEAQAELFNKN- 377  
 232 HLDKLFAGKMLDIALNEAFNLSDFNHTGQGSICQAIIMLITDGAVDYDTIFAKINW 291  
 378 KDKVRVFRSVGHNRYERGIOWMACENGYVEISGAIRINTQYILDVLRPMVLA 437  
 292 PDKVRIFTLIGREAAFAFNKMACANKGFFQIOTSLADVQENVMEYLHLVSRPKVI- 350  
 438 GDKAKQVQWNTNVLIDLAL-----ELG--LVITGTLPVNTITGQFNKTNLKNQILG 486  
 351 -DQEHVWTEAYIDSLPQAQKLTDDGQVLMTTVAMPVS-----KONETRSKG-ILLG 404  
 487 VMGVDSLEDKRTPFTLCPNGYYPFAIDPNGVYLHPNLQ---PKNPKSQEP--VTLG 541  
 405 VVGTDVPVKELLTPKYKLGIGHYAFATNNGYILTHPELRLLYEEGKKRKNYSVD 464  
 542 FLDAELNDIKVETRNKIDGSEKFTLVKSQDERYIDKGNRT-----YTWTPVNG 595  
 465 LSEVWEEDRDVV-URNANVRNKTGK--FSMEVK-----KTVDKGRVLVMTNDYITDIKG 517  
 596 TDYSLALVLPY-YSFYIKAKLEETITQARSKKGKMDSETLPKDPNFEEGYTFIAPRY 654  
 518 TFFSLGVALSRGHGKYF-----RGNVTIEEGL--HDLHPDVSGLADEWSY 561  
 655 CN-DLKISDNTEFLLNFEIDRTPNPNPCNADLNRVLIDAGFTNELVQNTWS----- 709  
 562 CNTDLHPHRLHSOLEAIKLYLKGEP-LLOCDKELIQEVLFD-AVSAPEAYWTSIAL 619  
 710 --KQNIKGKARFVTDGGTTRVYP-----KEAGENWQENPEYEDSFYKRS 755  
 620 NKSENSDKGVEAFVIGTGTLSRNLNFGAQLTNQDLFLKADKENIENADHFLPWYRA 679  
 756 LDN--DNTVFTAPYFNKSGPAGYESGIMVSKAVEYIYQGLKLPVAVGKIDVNSWIENF 813  
 680 AEQIPGSFVYSIPF--STGPNKSNVVTASTSIQLLDERKSPVVAAGIQMKLEFFQRF 737  
 814 TKTSIRDPACGVCCKNSVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRH 873  
 738 WTASRQCASLDGKCSISCDDETVCYLIDNNGFILVS--EDYT-OTGDFGIEGAVMKN 794  
 874 LVNISVYAFNKSVDYQVCEPAAPKQGA-GHRSVAVPSVADILQIGWATAAASILQQ 932  
 795 LTMGSFKRITLDYQAMCRANKESSDGAHGLDPI-----NAFLSAVKIMIMEL 844  
 933 FLTLSTFPRLLEAVEMEDDFTASLSK-----QSCITEQTOFFDNDKSKFSGLVDCGN 987  
 845 VLFLVEF-----NLCSSWHSDMTAKAQLKQTLPECDTEYPAVSERTIKETGTNIACEDC 900  
 988 SRIFFGEKIMNTNLIFIMVESKGTCPDCT 1016  
 901 SKSFVQIQIPSSNLFMVVYDS--SCLCES 927

RESULT 14  
 Q9NK64 ID Q9NK64 PRELIMINARY; PRT; 2190 AA.  
 AC Q9NK64;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE HYPOTHETICAL 249.8 KDA PROTEIN.  
 GN BG:DS07473.1 OR CG12455.

OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Y, CN BW SP;  
 RX MEDLINE=99403001; PubMed=10471707;  
 RA Ashburner M., Misra S., Rotee J., Lewis S.E., Blazej R., Davis T.,  
 Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,  
 Hong L., Houston K., Hoskins G., Johnson G., Martin C., Moshrefi A.,  
 Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,  
 Cealiker S., Rubin G.M.;  
 RA "An exploration of the sequence of a 2.9-Mb region of the genome of  
 RT Drosophila melanogaster: the Adh region.";  
 RL Genetics 153:179-219(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Y, CN BW SP;  
 RA Cealiker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,  
 Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,  
 Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,  
 Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,  
 Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,  
 Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequelira A.,  
 Sethi H., Snir E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,  
 Zieran L.L., Rubin G.M.;  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AE003415; AAF4988.1;  
 DR FlyBase: FBgn0028859; BG:DS07473.1.  
 DR InterPro: IPR002035;  
 KW Hypothetical protein.  
 SQ SEQUENCE 2190 AA; 249754 MW; B8C657A2F80F226E CRC64;

Query Match 17.4%; Score 929.5; DB 5; Length 2190;  
 Best Local Similarity 25.1%; Pred. No. 2.4e-50;  
 Matches 276; Conservative 213; Mismatches 387; Indels 225; Gaps 42;

QY 29 SAVTIKSWVDKQEDLVTLAKTAGVNLVDIYKQDYLYVEPNARQLVIEIARDIEK 88  
 DB 13 SKATVQKWATQGDLEFALQKITKQBEIKYKYN--ARVELKNGTELKSIKTNVGR 70  
 QY 89 LLSNRKALVSLALEAEKVAQAHQWRDFASNEVVY-----NAKDDLDPKNDSE 139  
 DB 71 MLARKMDAVRCIOERAAYNVNENFNLTYALQNFYFSKYSTFNNGNSELEP--NEAE 128  
 QY 140 PG---SQRKIPVFTEDANF-GROIYQAAVHIPTDIYEGSTIVLNLNMTSALDEVFK 194  
 DB 129 FAWMYRNRELNP---DTHFYNTPYDTEHSSVHVFSNIWDRSERVLKTIWSEHLDEVR 184  
 QY 195 KNREEDPSILLWQVFGSATGLARYPASPWPVNSRTPNPKIDLYDVRPRWYIQAASPRKM 254  
 DB 185 QNYQSDPALSMQYFCGDTGLRHYPAAQWTPRPNRDDADTYDCRKRWSYIETATCSKI 244  
 QY 255 LILVDVSGVSGLTLLKLTSTVSEMLETSDDDDFNVASFNNAQD-VSCFQ-HLVQANV 312  
 DB 245 VILLDHSGMTGFRHHVAKFTIRSIDTFSNDDFTILYRISSEVNDIIPCFNGALVQATP 304  
 QY 313 RNKKVYLKDAVNNI-TAKGITDYKKGSPFAFQELLNVNVRAN-----ANCKIIMLFTDGE 366  
 DB 305 ENIEFVNOQIEQLDDPEGYANLTLAYETAFQLLRKYDSRHCVTSTCQAIMLYTDGVA 364  
 QY 367 ERAQEIFKNYN-----KDKKRVYFRFSVGQHNRYERGIOWMACENGYVEISGA 418  
 DB 365 GNTVEFYQYNNNGENGSTQMDTRVFTLLGKEVTKVREIQMACNLNRYISHVOTLDE 424  
 QY 419 IRIQTQYLDVLRPMVLAGDKAKQVQWNTNVLIDLAL-----ELGLVITGTLPVFNI 469  
 DB 425 VHEEVLKYVDVIATPLVQLNEQHPPT-WTHAFTDKTYDPKTSNEKRPRLMISVGVPAFOR 483  
 QY 470 TQGFENKTNLKNQILGVMGVDVSLDEIKRLIPRFTLCPNGYYPFAIDPNGVYLHPNLQ 529

484 FYRHANSTNPRARL-LGVAGTDPVEDIDKLTPLPKLGVNGSYFVVSNNGYVLLHPLRLP 542  
QY 530 -----KNPKSQEPTVLPDLAE-LENDIK-----VEIRNKMIDGSGE-KTFRTLV 573  
Db 543 ICTGNKMNPNYN---SIDPTEVHLFDQSPREPGEISILHIRNMAVRHEANEFKSISVKF 599  
QY 574 KSDERYIDKGNRTWTVPVNGTDSALVLP-TYSFYIKAKLEETITQARSKKGKKD 632  
Db 600 HYDKMRVSEKQDIFAPLPNPTFTGLVMPSEYKWKVIRKVEEDV-----KNKHKINI 655  
QY 633 SETLKPDPNFE-----SGYTFIAP-----RDYC-----NDLKISDNNTPELLNFN 672  
Db 656 SDFEIGENKWKVHPDVYKYHLEGEHEKTPPEALREFLAKQNDKWKSEQVAEDSDWD 715  
QY 673 EFID-----AKTNPNPS--CNADLINRVLDAGFTNELVONYH-----SKQKNIKGVKA-- 719  
Db 716 DKDDLNCGRKTLGDDDAYCYCNKELVNLIFDAKVTNS-SYGVWRFESDEERQOLIERFRADL 774  
QY 720 RFVVTDDGGITRYVPKEAGENWO-----ENPETYEDSFYKRSI-----D 757  
Db 775 RFVATMSGUTR-----WQIFGEVEVDTRFGDYHTTAIDETWYSAILQHHEDR 825  
QY 758 NDNYFTAPYFNKSPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKS 817  
Db 826 AESFYVSKYD-----DPMEDSE 844  
QY 818 IRDPCAGPVCDCRNSDVMDVILDDGFLMANHDDYTNQIGRFEIGEDPSLMRLHLYNI 877  
Db 845 VRCNHLCPIC-----TDDDDVDCVVIDNNAYIVIGON---INTTGFKEFGHGVMTAMVER 897  
QY 878 SYVAFNKSVDYQSVG--EPGAAPKQAGHRSAYVPSVAD-ILQIGWATAAAWSILQOFL 934  
Db 898 GFLSTEVDYEOQKEEPAKVN-----YTDEIDEYVAVGGGKSSA----- 941  
QY 935 LSLTFRLLEAVEMEDDDPTASLSK-----QSCITEQTOYFFDNDKSFSGVLDC--G 985  
Db 942 -----SKPKDSDSDENAMFDEPEPPDIYKACDKRSTLAL--QPSALVGINDFVEA 990  
QY 986 NCSRIFPHGKLMNTNLIFTMV 1006  
Db 991 PSTRPFLVKIPNSNLVLVV 1011  
RESULT 15  
Q9VJMO PRELIMINARY; PRT; 2172 AA.  
AC Q9VJMO;  
DT 01-MAY-2000 (TREMELrel. 13, Created)  
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
DE CG12455 PROTEIN.  
GN BG:DS07473.1 OR CG12455.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
RN NCBI\_Taxid=7227;  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RX MEDLINE=20196006; PubMed=107311132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankkoch C., Baldwin D.,  
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).  
DR EMBL; AE003650; AAF53505.1.  
DR Flybase; FBgn0028859; BG:DS07473.1.  
DR InterPro; IPR002035;  
SQ SEQUENCE 2172 AA; 247574 MW; 39AA7BCB470DIA39 CRC64;  
Query Match 17.1%; Score 912.5; DB 5; Length 2172;  
Best Local Similarity 25.1%; Pred. No. 2.9e-49;  
Matches 275; Conservative 207; Mismatches 383; Indels 229; Gaps 42;  
QY 29 SAVTTSKVVDMQEDLVTLAKTAGVNLQVLDIYKQDLYTVEPNNAOLVIAARDIEK 88  
Db 13 SKATVCKWATQFGDELPAQAQITKSOEIKYKEYN--ARVELANGTELIIKINVR 70  
QY 89 LLSNRSKALVSLAEAEKQVAAHWRDEFA--SNEVYVYNKDDLDPEKNDSEPG----S 142  
Db 71 ML-----ARKMDAVRCIQEHFTYFSKYSTFNNGSSELEPEAEFAWMYRN 117  
QY 143 QRIKPVFTEDANF-QRQISYQHAHVHPTDIYEGSTIVLNLNWTLSALDEVEFKKREEDP 201  
Db 118 MELNP---DTHFYNTPTDTESSVHVPSNIWDRSERVLKTIWSEHLDEVERQYQSDP 173  
QY 202 SLLQVFGSAGLARYPASPWVDSNRPKNKIDLYDVRPWPYIOGAASPKDMLILVDVS 261  
Db 174 ALSWQYFGSDTGILRHYPAAQWTDTRPNKDDADTDCKRARSWIETATCSKDIVILLDS 233  
QY 262 GSVSGILTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD-VSCFO-HLVQANVRNKKVLK 319  
Db 234 GSMTGRHHVAKFTIRSLIDTFSNDDFFILAYSSEVNDIIPCFNGALVQATPENIEVEN 293  
QY 320 DAVNNI-TAKGITDYKKGFSFAFQQLNNVNSR-----ANCNKIIMLTDDGGEERAQEIF 373  
Db 294 QOIEQLDDPEGYANLTLAYETAFLQLLRKYDYSRHCVTNSTCQAINLVTDVAGNTEYF 353  
QY 374 NKNY-----KDKKVRVRESVGHNVNVERGPIONMACENKGYIYFISGAIRINTOE 425  
Db 354 QKYNWNGENGTSQMDTRVFTVLLGKVTKEVREIOMACLNKRGYTSHTVLDDEVIEVUK 413  
QY 426 YLDVLGRPVLAKAKAQVQWNTNVLDAI-----ELGLVITGTLPVFNITQGFENK 476  
Db 414 YVDVATPLVLQNEQHPPT-WTHATDKTYDTPKTSNEKRPRLMISVGVPAFDFRYHANS 472  
QY 477 TNLKNQILGVNGVDSLEDKRLRPRFTPLCPNGYFYAIDPNGYVLLHPNLOP-----K 530  
Db 473 TNPRARL-LGVAGTDPVEDIDKLTPLPKLGVNGSYFVVSNNGYVLLHPLRLP 531

QY	531	NPKSOBPVTLDFDAE--LENDIK-----VEIRKNKIDGEGE-KVFRTLVSQQDERY	580
Db	532	NNPN----SIDTEHELFQDSPREGESILHIRNAMVRHEANEFKSISVKFYHDKMRR	588
QY	581	IDKGRTYTWTVPNGTDYSIALVLPT-YSFYYIRAKLEETITOARSKKGKMDSETLKP	639
Db	589	VSEEKODYFPALPNTFTGLGVMPSEYKGWIKWVGEEVD---KNRHKMINISDFFIGE	644
QY	640	NPEE-----SGYTFIAP---RDYC-----NDLKISDNNTPELLNFNFD---	676
Db	645	NKVHPDVTYKYHYLEGHEFYPAEELREFLAKMONDKWKSEQYAEDSDWDKDDLNC	704
QY	677	-RTPNPNS--CNADLINRVLLDAGFTNELVQNYW-----SKQKNIGVKVA--RFVVYDG	726
Db	705	GKRTLGD DAYCENKELVNLLIFDAKVTVNS-SYGWRFESDEERQLIERFRADLRFAV	763
QY	727	GITRVYPKEAGENWQ-----ENPTYEDSYKKSL-----DNDNYVFT	764
Db	764	GLTR-----WOFIFGEVDTDRFGDYHTTAIDETWYKSAILQHEDRAESFVYS	814
QY	765	APYFNKSGPGAYESGIWMSKAVEIVIQGLKLPAVVGIKDWNSTIENTFTSTRDP	824
Db	815	VKIYD-----DPMDEUSEVKCHCL	833
QY	825	PVDCCKRNSDVMDCVILDGGFLLMANHDYDTNQIGRFFGEIPDSLMRHNVINSYAF	884
Db	834	PIC-----TDDDVDVCVIDNNAYIVIGN---INTTKGFGEFHGDVMTAMVERGIFLS	886
QY	885	SDYQSVCC-EFGAAPKQAGHRSAIVVSADV-IHQHWATAAANWSILOQFLSLTFR	941
Db	887	VDYQOQCKEEKEPKAVME-----YTBIEDEYVAVGDGKSSA-----	923
QY	942	LLEAVEMEDDDDTASLSK-----QSCITEOTQYFFONDKSFSGVLDC--GNCSRI	992
Db	924	--SKPRDSDDENAMEDEFEPDIYKACDKRSTLVAL-QPSALVGINDFEAPSTRE	979
QY	993	GEKLMNTNLI FIMV	1006
Db	980	VKKIPNSNLV VV	993

Search completed: July 23, 2001, 07:47:07  
Job time: 593 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:36:25 ; Search time 92.97 Seconds

(without alignments)  
675.556 Million cell updates/sec

Title: US-09-397-548-16

Perfect score: 5443

Sequence: 1 MAGCLLALFLFQSLIG.....RLIQARQTSQGNPCDMVK 1036

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

- 1: /cgnl\_9/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /cgnl\_9/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /cgnl\_9/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /cgnl\_9/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /cgnl\_9/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /cgnl\_9/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /cgnl\_9/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 8: /cgnl\_9/gcgdata/geneseq/geneseq/AA1987.DAT.\*
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- 22: /cgnl\_9/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5443	100.0	1091	16	AA1980
2	5443	100.0	1091	19	AA1981
3	5443	100.0	1091	21	AA1982
4	5439	99.9	1091	19	AA1983
5	5437	99.9	1091	14	AA1984
6	5423.5	99.6	1110	19	AA1985
7	5403.5	99.3	1086	16	AA1986
8	5403.5	99.3	1086	19	AA1987
9	5403.5	99.3	1086	21	AA1988
10	5386.5	99.0	1084	16	AA1989
11	5386.5	99.0	1084	19	AA1990

12	5386.5	99.0	1084	21	AA1991
13	5367	98.6	1103	16	AA1992
14	5367	98.6	1103	19	AA1993
15	5367	98.6	1103	21	AA1994
16	5347	98.2	1079	19	AA1995
17	5347	98.2	1079	21	AA1996
18	5341	98.1	1079	16	AA1997
19	5229.5	96.1	1106	18	AA1998
20	5229.5	96.1	1106	21	AA1999
21	5229.5	96.1	1106	21	AA1999
22	5208.5	95.7	1106	16	AA1999
23	5101.5	93.7	1100	10	AA1999
24	2907.5	53.4	1145	21	AA1999
25	2581.5	47.4	508	19	AA1999
26	2581.5	47.4	508	19	AA1999
27	1087	20.0	1085	21	AA1999
28	1067	19.6	1120	21	AA1999
29	1037	19.1	1096	21	AA1999
30	992.5	18.2	1096	21	AA1999
31	733.5	13.5	519	21	AA1999
32	161	3.0	1829	18	AA1999
33	158.5	2.9	894	20	AA1999
34	158.5	2.9	962	20	AA1999
35	158.5	2.9	962	20	AA1999
36	158.5	2.9	962	20	AA1999
37	158.5	2.9	962	20	AA1999
38	158.5	2.9	962	20	AA1999
39	158.5	2.9	962	20	AA1999
40	155	2.8	1516	21	AA1999
41	154.5	2.8	946	21	AA1999
42	154.5	2.8	1315	20	AA1999
43	154	2.8	903	15	AA1999
44	152.5	2.8	789	17	AA1999
45	152.5	2.8	789	18	AA1999

# ALIGNMENTS

## RESULT 1

AA1999

ID AA1999 standard; Protein; 1091 AA.

XX AA1999

AC AA1999

DT 01-DEC-1995 (first entry)

XX Human neuronal calcium channel subunit alpha 2b.

DE Human neuronal calcium channel subunit alpha 2b.

XX Calcium channel subunit; antagonist; agonist; diagnosis;

KW Lambert Eaton Syndrome.

XX Homo sapiens.

XX WO9504822-A.

XX 16-FEB-1995.

XX 11-AUG-1994; 94WO-US09230.

XX 11-AUG-1993; 93US-0105536.

PR 05-NOV-1993; 93US-0149097.

(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;

WPI; 1995-090900/12.

N-PSDB; AAQ84664.

DNA encoding human calcium channel sub-unit(s) - used for developing prods. for studying calcium channels, e.g. for obtaining agonists and antagonists

XX Disclosure; Page 166-171; 285pp; English.

XX Human neuronal alpha 2 coding sequence (AA084664) transcript is

CC differentially processed in skeletal muscle, aorta, and CNS in

CC the region corresp. to nt 1595-1942 of AA084664 in each of the

CC tissues. Five alternatively spliced variant transcripts that differ

CC in the presence or absence of one to three different portions of

CC this region. There are three sequences involved (see AA084664 FT

CC and AA084665 FT), sequence 1, sequence 2 and sequence 3. The five

CC alpha 2 encoding transcripts from the different tissues include

CC different combinations of the three sequences, except for one of

CC the alpha 2 transcripts expressed in aorta which lacks all three

CC sequences. The five alpha 2 forms identified are (1) a form that

CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle

CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS

CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in

CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,

CC expressed in aorta and (5) one that lacks sequences 1 and 3

CC called alpha 2e.

XX SQ Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 16; Length 1091;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 maagcillaltltlqslilgspseepfpeavtikswdkmqedlvtlaktasvngldvi 60

QY 61 YEKYQDLYTVEPNARQVLEIARDIEKLSNRKSKALVSLALEAEKVQAHOHREDFASN 120

DB 61 yekyqdytvepnarqlveiaardieklisnrskalsvslaleaekvqaahqwredfasn 120

QY 121 EVVYNAKDLDPKNDSEPSGRIKPVFTEDANFGROISYQHAHVHPDIEVSGSTIVL 180

DB 121 evvynakddlpeknndsepgsgrikpvftedanfgrqisyqhaahvhpdiyegstivl 180

QY 181 NEIWNLSALDEVFKKNEEDPSLLQWVFGSATGLARYYPASPVWDSRTPNKIDLYDVR 240

DB 181 neiwnlsaldevfkneedpsllwvfgsatglaryypasvpwdsrtpnkdilydvrr 240

QY 241 RPWYIOGAASPKDMLILVDVSGVSGITLKITRVSSEMLETISDDDFVNVASFNSNAQD 300

DB 241 rpywiggaaspkdmililvdvsgvsgitlkitrsvsemlletisdddfvnvasfnsnaqd 300

QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKGFSAFEQLLNYSRANCNKIIML 360

DB 301 vscfqlhvganvrnkkvldavnnitakgtdykgfSAFEQLLNYSRANCNKIIML 360

QY 361 FTDGGEERAQEIFNKYKDKVRFRFSVQGHYERGPQIOWMACENKGYEYIPIPSIGAIR 420

DB 361 ftdggeeraqeifnkynkdkvrfrfsvqghyergrpiowmacenkgyeypisigair 420

QY 421 INTOQYLDVZGRPMVLAGDKAKQVQMTNVYLDALGLVITGTLPVFNITQFENKTNLK 480

DB 421 intqeyldvzgrpmvlagdkakqvqmntvnyldalglvltgtlpvfnitqfentknlk 480

QY 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYEYFAIDPANGYVLLHPNLQPNKSPQEPVIL 540

DB 481 nqlilgvmgvdvsliekrltpftlcpngyeyfaidpangyvlhpnlpknpsqepvtl 540

QY 541 DFLDAELNDIKVEIRNMKIDGSGEFTFTLVKSOBERYIDKGNRTYTTPVNGTDYSL 600

DB 541 dfldaelndikveirnmkidgsegeftftlvksqberyidkgnrtytvtpvngtdysl 600

QY 601 ALVLPTYSYFYIAKLEETITQARSKGKMKDSETLKPDNFEEESGYTFIAPRDYCNLDKI 660

DB 601 alvlptysfyiyakleetitqarskgkkmkdsethylkpdnfeesgytfiaprdycndlki 660

QY 661 SDNTEFLNENFIDRKRTNNPNSCNADLNRVLLDAGFTNELVQVNSQKNIKGVKAR 720

DB 661 sdnnteflnfnfdrkrtnnpnsnclnrvllldagftnelvqywsqknkngvkar 720

QY 721 FYVTGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYFTTAPYFNKSGPGAYESGI 780

DB 721 fvtvtdggitrvyypkeagenwqenpetyedsfkyrslndndnyvftapyfnkspggavesgi 780

QY 781 MYSKAVEIYIQGLKLPKPAVVGKIDVNSHIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840

DB 781 mvskaiveiyiqgllkpkpavvgkldvnswnienftksirtpcagpvcdckrnsdvmdcvi 840

QY 841 LDGGFLLMANHDDYTNIQIRFEFGEIDPSLMRHLNIVSYAFNKNKSYDYQSVCEPGAAPKQ 900

DB 841 ldggfllmanhddytngirffgeidpslmrhlvsnisyafnksydyqsvcepgaapkq 900

QY 901 GAGHRSAYVPSVADILQIGWATAAASLQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960

DB 901 gaghrsayvpsvadilqigwataaawslqgllsltpfllleavemedddftaslskq 960

QY 961 SCITQTQYFFDNDKSPSGVLDGNCNCRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020

DB 961 scitqtqyffndksksfsgvldcncsrifhgeklmntnlifimveskgtcpdtrlll 1020

QY 1021 QAEQTSDDGNPCDMVK 1036

DB 1021 qaeqtsdgnpcdmvk 1036

RESULT 2

AAW63145

ID AAW63145 standard; Protein; 1091 AA.

XX AAW63145;

AC AAW63145;

DT 12-OCT-1998 (first entry)

XX Human calcium channel alpha-2 subunit.

DE Alpha-2 subunit; human; calcium channel; assay; detection;

XX characterisation; Lambert Eaton Syndrome; LES; diagnosis.

OS Homo sapiens.

XX US5792846-A.

PN 11-AUG-1998.

XX 31-MAY-1995; 95US-0455543.

XX 04-APR-1994; 94US-0223305.

PR 04-APR-1988; 88US-0176899.

PR 04-APR-1989; 89US-0603751.

PR 04-APR-1989; 89WO-US01408.

PR 20-FEB-1990; 90US-0482384.

PR 30-NOV-1990; 90US-0620250.

PR 15-AUG-1991; 91US-0745206.

PR 31-MAY-1995; 95US-0455543.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;

PI Williams ME;

XX WPI; 1998-456192/39.

DR N-PSDB; AAV42689.

XX DNA encoding human calcium channel alpha 1B sub-unit protein -

PT useful for recombinant production of the channel for screening of

PT its modulators, and diagnosis of Lambert Eaton Syndrome

XX Claim 4; Columns 283-288; 166pp; English.

XX The present sequence represents the alpha-2 subunit of a human calcium

CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
CC that allow controlled entry of calcium ions into cells. This leads  
CC to depolarisation events required for muscle contraction. The recombinant  
CC subunit, when expressed with nucleic acids encoding the complete calcium  
CC channel, can be used in assays for the detection and characterisation of  
CC compounds that modulate the channel. The DNA encoding the subunits can  
CC be alternatively spliced when transcribed, giving more than one form of  
CC the protein from the same transcript, each having slightly different  
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
CC molecules from the serum of an individual with Lambert Eaton Syndrome  
CC (LES) can be used as a diagnostic for the disease.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 19; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALRLTLFQSLILIGPSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 maagcillaltitlifsilgspseepfapsavtikswvdkmqedlvtlaktasgvnqlvdi 60

QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLNSRSKALVSLALEAEKVQAAHQHREDPASN 120  
DB 61 yekyqdytvepnarqlveiaardieklinsrskalvslaleaekvqaahqwhredfasn 120

QY 121 EVVYNAKDDLDPEKNDSEPSGRIRKPVFIEDANFRQISYQHAHVHPIPDIEGSIIVL 180  
DB 121 evvyynakddldpekndsepsgrirkpvfiedanfrqisyqhaavhpidiegstivl 180

QY 181 NELNWSALDEVKKNREEDPSLLMQVFGSATGLARYYPASPWWDSNRTPNKIDLYDVR 240  
DB 181 nelnwsaldevkknreepdpsllmqvfgsatglaryypaspwwdsnrtpnkidlydvr 240

QY 241 RPVYIOGAASPKMLIVDVGSGVGLTLKIRTSYSEMLETSLDDDFNVASFNSNAQD 300  
DB 241 rpvyiogaaspkmlivdvgsgvgtlklrtsysemlletlstddfnvafnsnaqd 300

QY 301 VSCFQHLVQANRKNKVLKDAVNNTAKGITDYKKGFSFAFEOLLNYSRANCNKIIML 360  
DB 301 vscfqlhvanrnkvkdaavnntakgitdykkgfsfafelnllynsrancnkiiml 360

QY 361 FTGGEERAQEIFKNYKDKKRVFRFSGOHNYERGIQWACENKGYIYEIPSIGAIR 420  
DB 361 ftggeeeraqeifknykdkkrrvfrfsgvghnyerqiwacenkgyiyeipsigair 420

QY 421 INTQEYLDVLRPMVLADGAKQVQWNTNVYLDALGLVITGILPVFNITGQFENKTNLK 480  
DB 421 intqeyldvlgpmvladgakqvqwnvnyldalglvitgilpvfnitgqfenktnlk 480

QY 481 NQILGVMGVDVSLIEDIKRLTFRFTLCPNGYYFAIDPNGVYLLHPNLQPNKSOEPTVL 540  
DB 481 nqilgvmgvdvsliedikrltfrftlcpngyyfaidpngvylhpnlpknksqepvtl 540

QY 541 DFLDAELENDIKVEIRNMKTGDSGEKFTFLVKSDERYIDKGNRTYTPVNGTDYSL 600  
DB 541 dfldaeendikveirnmktgdsgektftlvksqderidkgnrtytvpvngtdysl 600

QY 601 ALVLPYFYFYIAKLEETIQARSKKGMKDSITLKPDPNFESGYTFIAPRDCNDLKI 660  
DB 601 alvlpfyfyfyiakleetiqarskkgmkdsetlkdpdfesgytfiaprdcndlki 660

QY 661 SDNNTFLLNFEDIRKTPNPNPSCNADLNRYLLDAGFTNELVQYWSKOKIKGVKAR 720  
DB 661 sdntefllnfnedirktpnnpncnadlnrylldagftnelvqywsqknikgvkar 720

QY 721 FVYTDGIGTRVYKPEAGENQENPEYEDSFYKRSRLDNDNYFTAFYFNKSGPAYESGI 780  
DB 721 fvytdgigtrvykpeagenqenpeyedsfykrslndndnyftafyfnksppayesgi 780

QY 781 MVSKAVEIYIQGLLPVAVGIIKIDVNSWJENTTKTSIRDPACGVCDCRNSDVMDCVI 840  
DB 781 mvskaveiyyiqglpavvgiikidvnswjenttktsirdpacgvcdcrnsdvmdcvi 840

DB 781 mvskaveiyyiqgllkbpavvgikidvnswjenttktsirdpacgvcdcrnsdvmdcvi 840

QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPCLMRHLVNTSVYAFNKSXYQSVCEPAAPKQ 900  
DB 841 ldgggflmanhdtytnqigrffgeidpclrhlvntsvyafnksydyqsvcepgaapkq 900

QY 901 GAGHRSAYVPSVADILQIGHWATAAANSILQOFLLSLTFFPRLLEAVEMEDDFTASLSKQ 960  
DB 901 gaghrsayvpsvadilqigwataaawsilqqflsltfprlleavemeddftaslskq 960

QY 961 SCTEQOYQYFDDNDSKFSFGLDCGNCGRIFPHGKLMNTNLFIMVESKGTCPDTRLLI 1020  
DB 961 sciteqoyqyffddndskfsfvgldcgcncsrifphgkmlntnlifimveskgtcpdtrlli 1020

QY 1021 QAEQTSQGNPCDMVK 1036  
DB 1021 qaeqtsdggnpcdmvk 1036

RESULT 3  
AAB10576  
ID AAB10576 standard; Protein; 1091 AA.  
XX  
AC AAB10576;  
XX  
DT 22-DEC-2000 (first entry)  
XX  
DE Human calcium channel alpha-2 subunit protein.  
XX  
KW Human; calcium channel; calcium channel subunit; diagnosis;  
KW Lambert Eaton Syndrome; calcium channel subunit alpha-2.  
XX  
OS Homo sapiens.  
XX  
PN US6096514-A.  
XX  
PD 01-AUG-2000.  
XX  
PF 25-MAY-1995; 95US-0450562.  
XX  
PR 04-APR-1988; 88US-0176899.  
PR 02-FEB-1990; 90US-0482384.  
PR 08-NOV-1990; 90US-0603751.  
PR 30-NOV-1990; 90US-0620250.  
PR 15-AUG-1991; 91US-0745206.  
PR 10-APR-1992; 92US-0868354.  
PR 13-JUL-1992; 92US-0914231.  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
PR 07-FEB-1994; 94US-0193078.  
PR 04-APR-1994; 94US-0223305.  
PR 11-AUG-1994; 94US-0290012.  
PR 23-SEP-1994; 94US-0311363.  
PR 28-SEP-1994; 94US-0314083.  
PR 07-NOV-1994; 94US-0336257.  
PR 13-MAR-1995; 95US-0404950.  
XX  
XX (SIBI-) SIBIA NEUROSCIENCES INC.  
XX  
XX Ellis SB, Williams ME, McCue AF, Harpold MW;  
XX WPI; 2000-548230/50.  
XX N-PSDB; AAA71707.  
XX  
XX Human calcium channel beta subunit polynucleotides, useful for  
XX producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
XX Syndrome  
XX  
XX Example IV; Column 135-144; 153pp; English.  
XX  
XX This invention describes a novel isolated DNA molecule (I) comprising a  
XX sequence encoding a beta3-1 subunit of a human calcium channel.  
XX Nucleic acid probes comprising 14-30 contiguous nucleotides of

CC beta\_3 subunit encoding DNA are useful for isolation and cloning of  
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
CC express heterologous calcium channel are useful for identifying compounds  
CC that modulate calcium channel activity and in assays for identifying  
CC agonists and antagonists of calcium channel activity in humans. Human  
CC calcium channel subunit or eukaryotic cells expressing the channel are  
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
CC sequence represents the human calcium channel alpha-2 subunit which is  
CC described in the method of the invention.  
XX  
SQ Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 21; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTLFOSLLIGPSEPPFSAVTIKSWDKMQEDLYTLAKTAGSVNQLVDI 60  
DB 1 MAAGCLLALTLFOSLLIGPSEPPFSAVTIKSWDKMQEDLYTLAKTAGSVNQLVDI 60  
QY 61 YEKYQDLYTEPNARQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOWREDFASN 120  
DB 61 YEKYQDLYTEPNARQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOWREDFASN 120  
QY 121 EYVYNAKDDLPKNDSPGQRIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180  
DB 121 EYVYNAKDDLPKNDSPGQRIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSADEVFKKNEEDPSLLQVFGSATGLARYYPASVPWDSNRTPNKIDLYDVR 240  
DB 181 NELNWTSADEVFKKNEEDPSLLQVFGSATGLARYYPASVPWDSNRTPNKIDLYDVR 240  
QY 241 RPWYIGASPRKMLILVDVSGVSLIKLRTVSSEMLETLSDDDFVNVSFNSAQD 300  
DB 241 RPWYIGASPRKMLILVDVSGVSLIKLRTVSSEMLETLSDDDFVNVSFNSAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKITDYKKGFSFAFQQLNLYNVSRANCKNIML 360  
DB 301 VSCFQHLVQANVRNKKVLDVANNITAKITDYKKGFSFAFQQLNLYNVSRANCKNIML 360  
QY 361 FTDGGEERAQEIFNKNYKDKVYRFVSQHNRYGPIQWMACENKGYIYIPSGAIR 420  
DB 361 FTDGGEERAQEIFNKNYKDKVYRFVSQHNRYGPIQWMACENKGYIYIPSGAIR 420  
QY 421 INTQEVLDVLPWLAGKAKQVQNTVYLDALGLVITGTLVPFNITGOFENKTNLK 480  
DB 421 INTQEVLDVLPWLAGKAKQVQNTVYLDALGLVITGTLVPFNITGOFENKTNLK 480  
QY 481 NOLILGVMGVDVSLIEDIKRLTPRFLCPNGYFAIDPNGYVLLHNPLOPKPKSOEPVTL 540  
DB 481 NOLILGVMGVDVSLIEDIKRLTPRFLCPNGYFAIDPNGYVLLHNPLOPKPKSOEPVTL 540  
QY 541 DFLDAELENDIKVEINRNMIDGESSEKFTPLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
DB 541 DFLDAELENDIKVEINRNMIDGESSEKFTPLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYSPYIKAKLEETITQARSKGKMKSEFLKPNPFESGYTFTAPRDYCNDLKI 660  
DB 601 ALVLPYSPYIKAKLEETITQARSKGKMKSEFLKPNPFESGYTFTAPRDYCNDLKI 660  
QY 661 SDNNTFELNFEIDRKPNNPSCNADLINRVLLDAGFTNELVQNSKQNKIGVKAR 720  
DB 661 SDNNTFELNFEIDRKPNNPSCNADLINRVLLDAGFTNELVQNSKQNKIGVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
DB 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSHENTFTKTSIRDPGAGPVCDCKRNSDMDCVI 840  
DB 781 MYSKAVEIYIQGLKLPVAVGKIDVNSHENTFTKTSIRDPGAGPVCDCKRNSDMDCVI 840

QY 841 LDDGFLILMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
DB 841 LDDGFLILMANHDDYTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSATVSPVADILQIGWATATAAASILQOFLLSLTFPRLEAVEVDDDDFTASLSKQ 960  
DB 901 GAGHSATVSPVADILQIGWATATAAASILQOFLLSLTFPRLEAVEVDDDDFTASLSKQ 960  
QY 961 SCITPOTQYFFDNDKSPSGVLDGCGNSRIFPHGEKLMNTNLIIFIMVESKGTCPDTRLII 1020  
DB 961 SCITPOTQYFFDNDKSPSGVLDGCGNSRIFPHGEKLMNTNLIIFIMVESKGTCPDTRLII 1020  
QY 1021 QAEQTSDDGPNPCDMVK 1036  
DB 1021 QAEQTSDDGPNPCDMVK 1036  
RESULT 4  
AAW37879  
ID AAW37879 standard; Protein; 1091 AA.  
XX AAW37879;  
XX 28-AUG-1998 (first entry)  
XX Human calcium channel a2d subunit.  
XX Calcium channel; human; central nervous system disorder;  
XX Lambert-Eaton syndrome; diagnosis; therapy.  
XX Homo sapiens.  
XX W09811131-A2.  
XX 19-MAR-1998.  
XX 11-SEP-1997; 97WO-US16146.  
XX 16-SEP-1996; 96US-0713118.  
XX (AMHP ) AMERICAN HOME PROD CORP.  
XX Chen ARS, Franco R, Shuey DJ;  
XX WPI: 1998-207325/18.  
XX N-PSDB; AAV29060.  
XX DNA encoding human neuronal calcium channel subunit(s) - useful for  
XX diagnosis of and treatment of central nervous system disorders, e.g.  
XX Lambert-Eaton syndrome  
XX Disclosure; Fig 2; 89pp; English.  
XX This polypeptide comprises the a2d subunit of the human neuronal  
XX calcium channel. cDNA clones (see AAV29059-61) encoding the a1b  
XX subunit (see AAW37878), the a2d subunit and a b3 subunit (see AAW37880)  
XX have been isolated. These have been inserted into expression  
XX vectors and are stably expressed in transformed cell lines. The  
XX transformed cells show omega-conotoxin GVIA binding activity,  
XX and omega-conotoxin GVIA toxin sensitive potassium-stimulated  
XX calcium uptake, indicating that the proteins expressed by the  
XX clones are capable of forming a functioning calcium channel.  
XX Nucleic acids encoding the 3 subunits, as well as vectors, host  
XX cells and methods of isolating nucleic acids encoding related  
XX calcium channels are disclosed. Fusion proteins incorporating the  
XX subunit proteins, antibodies, and assays for identifying agents  
XX that modulate calcium channel activity are also provided. Such  
XX agents can be used to treat certain central nervous system  
XX disorders by altering calcium channel activity. Methods of  
XX diagnosing diseases associated with particular calcium channels,  
XX such as Lambert-Eaton syndrome, are disclosed.  
XX Sequence 1091 AA;

Query Match 99.9%; Score 5439; DB 19; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSYGNQLVDI 60  
DB 1 maagcllaltltlqsligpsseepfppsavtikswdkmqedlvtlaktasgynqlvdi 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVOAAHQRDFASN 120  
DB 61 yekyqdltyvepnarqlveiaardieklslsnrskalvslaleaeekvqaahqrdfasn 120

QY 121 EVVYNKDDLDPEKNDSEPGSRQIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTVL 180  
DB 121 evvynakddldpekndsepgsrqikpvfiedanfgqisqyhaavhiptdiyegstvl 180

QY 181 NELNWTSALEVPKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTNPKIDLYDVR 240  
DB 181 nelnwtasaldevfkknreedsllwqvfgsatglaryypaspwvdsrtpkidlydvr 240

QY 241 RPWTIOGAAPKDWLIIYVSGVSGITLKLIRTSVSEMLETISDDDFVNVASFNSNAOD 300  
DB 241 rpwyiggaaspkdwlliyvsgvsgitlklirtsvsemlletisdddfvnavsfnsnaod 300

QY 301 VSCFOHLVQANVRNKKVYLKDAVNNTAKGITYDKKGFSAFQQLNLYNVRANCNKIIML 360  
DB 301 vscfghlvqanvrnkylkdavnntakgitdykkgfafeqllnlynvrancnkliiml 360

QY 361 FTDGGERRAQEIEFNKYNKDKVRFRPSVQCHNYERPIQWACENKGYIYEIPSGAIR 420  
DB 361 ftdggeeraqeiefnkynkdkvrfrpsvqchnyerpiqwmacenkgyyiyeipsigair 420

QY 421 INTQEYLDVLRPMVLADGAKOVQWNTVYLDALGLVITGLPVFNITQGFENKYNLK 480  
DB 421 intqeyldvlrpmvladgakovqwnvtyldalglvitglpvnfnitqgfenkynlk 480

QY 481 NQILGVMGVDVSLDKRITRPTLCPNGYIFAIDPNGYVLLHNPLOPNKPSQEPVTL 540  
DB 481 nqilgvmgvdsledikritrptlcpngyifaidpnygvalhpnlpknpsqepvltl 540

QY 541 DELDAELENDIKVIRNKMIDGESGKFTFLYKSDQERYIDKGNRTYTPVNGTDYSL 600  
DB 541 deldaelendikveirnkmidgesgkftflvksdqeryidkgnrtytpvngtdysl 600

QY 601 ALVLPYSFYIYIAKLETTIQAQSKGKMDSETLKPDPNFEESGYTFIAPRDYCNLDKI 660  
DB 601 alvlpysfyiyiakleetitqarskkgkmdsetlkdndfeesgytfiaprdycondki 660

QY 661 SDNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNTWSKOKNKGVKAR 720  
DB 661 sdntefllnfnedrkttpnpnpscnadlinrvlldagftnelvqnywskgnkgvkar 720

QY 721 FVYTDGTRIVYKAEAGENQENPETVEDSFYKRSLDNDNVTAPTFNKSQGPAYESGI 780  
DB 721 fvtytdgtrivypkaegenqenpetyedsfykrsldndnvyftapfynksqgpayesgi 780

QY 781 MYSKAVEIYIQGLKLPVAVGIIKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840  
DB 781 mvskaaveiyiqgllkpvavvgikidvnswienfktksirdpacgpcvdcnrnsdvmdcvi 840

QY 841 LDGSGFLMANHDDYTHQIGRFGEEIDPFLMRHLVNTSVAFNKSXYDSQVCEPGAAPKQ 900  
DB 841 ldgsgflmanhddytqigrfgelgdpflmrhlvntsvafnksydsqvscepgaapqk 900

QY 901 GAGHSAYYSVADILQIGWATAAANSILQQFLLSTLTFPRLLEAVEMEDDDFTASLSKQ 960  
DB 901 gaghsayysvadilqigwataaansilqqfllstltpfrrlleavemedddftaslskq 960

QY 961 SCITEQYQYFFDNDKSFSGVLDGNCGRIFPHGSKLMTNLIFIMVSKGTCPCDTRILLI 1020  
DB 961 sciteqyqyffndksfsgvldcncgrifphgsklmtnlifimveskgtcpcdtrilli 1020

QY 1021 QABQTSQSDGNPCDMVK 1036  
DB 1021 qabqtsdsgnpncdmvk 1036

RESULT 5  
AAR33553  
ID AAR33553 standard; Protein; 1091 AA.  
XX AAR33553;  
XX AC  
XX DT 30-JUN-1993 (first entry)  
XX DE Sequence of the alpha 2 human calcium channel subunit.  
XX KW Human calcium channel subunit; diagnosis; agonist; antagonist;  
XX KW Lambert Eaton syndrome.  
XX OS Homo sapiens.  
XX PN WO9304083-A.  
XX PD 04-MAR-1993.  
XX PF 14-AUG-1992; 92WO-US06903.  
XX PR 15-AUG-1991; 91US-0745206.  
XX PR 10-APR-1992; 92US-0868354.  
XX PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
XX PI Williams ME;  
XX DR WPI: 1993-093936/11.  
XX DR N-PSDB; AAQ37821.  
XX PT DNA encoding specific human calcium channel sub-units - used for  
XX PT identifying calcium channel agonists and antagonists and  
XX PT diagnosing Lambert Eaton syndrome  
XX PS Disclosure; Page 134-138; 150pp; English.  
XX CC DNA encoding a human neuronal calcium channel alpha 2 subunit was  
XX CC isolated from a human genomic DNA library probed under low and high  
XX CC stringency conditions with a fragment of DNA encoding the rabbit  
XX CC skeletal muscle calcium channel alpha 2 subunit. The fragment  
XX CC included nucleotides having a sequence corresponding to the  
XX CC nucleotide sequence between nucleotides 43 and 272 inclusive of  
XX CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.  
XX CC PCR analysis identified splice variants of the human calcium alpha  
XX CC 2 subunit transcript. In particularly preferred embodiments, the  
XX CC DNA encoding the alpha 2 subunit is produced by alternative  
XX CC processing of a primary transcript that includes DNA encoding the  
XX CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted  
XX CC between nucleotides 1624 and 1625 of AAQ37821.  
XX SQ Sequence 1091 AA;

Query Match 99.9%; Score 5437; DB 14; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSYGNQLVDI 60  
DB 1 maagcllaltltlqsligpsseepfppsavtikswdkmqedlvtlaktasgynqlvdi 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVOAAHQRDFASN 120  
DB 61 yekyqdltyvepnarqlveiaardieklslsnrskalvslaleaeekvqaahqrdfasn 120

QY 121 EVVYNAKDDLDPEKNDSPGSGRIKPVIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
DB 121 evvynakddldpekndspgsgrikpviedanfgrqisyqhaahvhiptdiyegstivl 180  
QY 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASFWVDSNRTPNKIDLYDVR 240  
DB 181 nelnwtalsidevfkknreedpsllwqvfgsatglaryypasfwvdsnrtpnkidlydvr 240  
QY 241 RPWYIQAASPKDMLILVDVSGVSGLTLEKLRISYSEMLETSDDDFVNVSFNSNAQD 300  
DB 241 rpwyiqgaaspkdmlilvdvsgvsgltleklrirtsysemletlsdddfvnvsfnsnaqd 300  
QY 301 VSCFQHLVQANVRNKKVLDKADANNITAKGIDYKKGFSAFQQLLNYNVSRANCKNIIML 360  
DB 301 vscfqlhvanvrnkvlkdavnnitakgidykkgfsafqqlnynvsranckniiml 360  
QY 361 FDTGGEERAQEIFENKYNKDKKVRFRFSVQGNHYERGPQIOWACENKGYIYIPSGAIR 420  
DB 361 ftdggeeraqeifenkynkdkkvrfrfsvqgnhyergpqiowacenkgyyeipsgair 420  
QY 421 INTOEYLDVLRPMVLGAKAKOVQWTVNYLDALGLVITGTLPVFNITGOFENKTNLK 480  
DB 421 intoeylvlrpmvlgakakovqwtvnyldalglvitgtlvpfnitgofenktnlk 480  
QY 481 NQILGVMGVDSLEIDIKRLTPRFTLPCPNGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
DB 481 nqilgvmgvdsleidikrltpftlpcpngyfaidpngyvllhpnlpknpsqepvtl 540  
QY 541 DFLDALENDIKVEIRNKMIDGESGEKTRTLVKSDERYIDKGNFTYTWTPVNGTDYSL 600  
DB 541 dfldaelendikveirnkmidgesgektftrlvksderyidkgnftytwtvpngtdysl 600  
QY 601 ALVLPYSYVYIKAKLEETITQARSKKGMKDSSETLKPONFEESGVTFTAPRDYCNDAKI 660  
DB 601 alvlpysyvyikakleetitqarskkgmkssetlkpofeesgvtftaprdycondaki 660  
QY 661 SDNTEFLNFEIDRKTTPNPNPCNADILNRLVDAGFTNELVQWYKQNIKGVKAR 720  
DB 661 sdnteflnfeidrkttpnpnpncnadilnrvldagftnelvqwykqnikgvkar 720  
QY 721 FVYTDGGITRVYPKEAGENQENPEYEDSFYKRSJLDNDNYVFTAPYFNKSGPGAYESGI 780  
DB 721 fvytdggitrvyypkeagenqenpeyedsfykrslndndnyvftapyfnksgpgayesgi 780  
QY 781 MYSKAVEIYIQGLKPAVVGKIDVNSHNIENFTKTSIRDPCAGPYCDCKRNSDVMDCVI 840  
DB 781 mvskaveiyyiqglkpvvgkldvnsnienftktsirdpcagpycdckrnsdvmdcvi 840  
QY 841 LDGQGLLANHDDYNTQIRFPFGEIDPSLMRLHVNISVYAFNKSVDYQSVCEPGAAPKQ 900  
DB 841 ldggglmanhddyntqirffgeidpslmrlhvnisvafnksydyqsvcepgaaapkq 900  
QY 901 GAGHRSAYVPSVADILQIGWATAAAMSILQOFLSLTTPRLEAVEMEDDDFTASLSKQ 960  
DB 901 gaghreayvpsvadilqigwataaamsilqflsltprrleavemedddftaslskq 960  
QY 961 SCITEOTQYFFDNDKSFSGVLDGNCNCSIFRCEKLMNHLNLFIMVESKGTCPDTRILLI 1020  
DB 961 sciteotqyffndksfsgvldgncncsifhgekilmnlnlhfimveskgtcpdtrilli 1020  
QY 1021 QAEQTSDDGPNPCDMVK 1036  
DB 1021 qaeqtsdgpnpdcmvk 1036  
RESULT 6  
ID AAW63148  
XX AAW63148 standard; Protein; 1110 AA.  
AC AAW63148;  
XX AAW63148;  
DT 12-OCT-1998 (first entry)  
XX

DE Human calcium channel alpha-2 subunit.  
XX Alpha-2 subunit; human; calcium channel; assay; detection;  
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
XX Homo sapiens.  
XX US5792846-A.  
XX 11-AUG-1998.  
XX 31-MAY-1995; 95US-0455543.  
XX 04-APR-1994; 94US-0223305.  
PR 04-APR-1988; 88US-0176899.  
PR 04-APR-1989; 89US-0603751.  
PR 04-APR-1989; 89WO-US01408.  
PR 20-FEB-1990; 90US-0482384.  
PR 30-NOV-1990; 90US-0620250.  
PR 15-AUG-1991; 91US-0745206.  
PR 31-MAY-1995; 95US-0455543.  
XX (STBI-) STBIA NEUROSCIENCES INC.  
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
PI Williams ME;  
XX WPI: 1998-456192/39.  
DR N-FSDB; AAV42694.  
XX DNA encoding human calcium channel alpha 1B sub:unit protein -  
PT useful for recombinant production of the channel for screening of  
PT its modulators, and diagnosis of Lambert Eaton Syndrome  
XX Disclosure; Columns 131-138; 166pp; English.  
XX The present sequence represents the alpha-2 subunit of a human calcium  
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
CC that allow controlled entry of calcium ions into cells. This leads  
CC to depolarisation events required for muscle contraction. The recombinant  
CC subunit, when expressed with nucleic acids encoding the complete calcium  
CC channel, can be used in assays for the detection and characterisation of  
CC compounds that modulate the channel. The DNA encoding the subunits can  
CC be alternatively spliced when transcribed, giving more than one form of  
CC the protein from the same transcript, each having slightly different  
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
CC molecules from the serum of an individual with Lambert Eaton Syndrome  
CC (LES) can be used as a diagnostic for the disease.  
XX Sequence 1110 AA;  
QY Query Match 99.6%; Score 5423.5; DB 19; Length 1110;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 19; Gaps 1;  
QY 1 MAAGCLLATLTLLFQSLILGPSSSEEPFSAVTIKSVWQKMOEDLVTLAKTASGNOLVDI 60  
DB 1 maagcllatltllfqsllilgpssseepfsavtiksvwkmqedlvltaktasvnglvdI 60  
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLSNRKSLVSLALEAEKVQAHAHQWREDFASN 120  
DB 61 yekyqdytvepnnarqlveiaardieklslsrkslvsaleaeqvqaahqwrdfasn 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSGRIKPVIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
DB 121 evvynakddldpekndsepgsgrikpviedanfgrqisyqhaahvhiptdiyegstivl 180  
QY 181 NELNWTSAIDVEFKKNEEDPSLLWQVFGSATGLARYYPASFWVDSNRTPNKIDLYDVR 240  
DB 181 nelnwtalsidevfkknreedpsllwqvfgsatglaryypasfwvdsnrtpnkidlydvr 240  
QY 241 RPWYIQAASPKDMLILVDVSGVSGLTLEKLRISYSEMLETSDDDFVNVSFNSNAQD 300  
DB 241 rpwyiqgaaspkdmlilvdvsgvsgltleklrirtsysemletlsdddfvnvsfnsnaqd 300

|||||  
Db 241 rpwyiqgaaspkdmllilvdvsgsvglklkirtssemlctlsdddfvnvasfnsgd 300  
Qy 301 VSCFOHLVQAVNRNKKVLKDAVNNTAKGIDYKKGFSFAFQQLNYSRANCNKIIML 360  
Db 301 vscfghlvqanvrnkvlkdavnntakgldydkgfsfafeqllnynvsnrncnkliiml 360  
Qy 361 FTDGGEERAQEIFNKYKDKKVRFRFSGVGHNYERGIOWMACENKGYYYEIPSIGAIR 420  
Db 361 ftdggeeraqeflnkynkdkkvrfrfsvghnyergplqwmacenkgyyyelipsigair 420  
Qy 421 INTQBYLDVLRPMVLADGKAKQVQWTVNYLDALGLVITGTLFVFNITGOFENKTNLK 480  
Db 421 intqeyldvlgprpmvladgkakqvwtvnyldalelgvltgtlpvfnitgqfenktnlk 480  
Qy 481 NQILGVNGVDVSLIEDIKRLPRFTLCPNGYFFAIDPNGYVLLHLPNLOPK----- 530  
Db 481 nqililgvngvdsledikrlprftlcpngyffaidpnygvllhlpnlpkplvgvpiptin 540  
Qy 531 -----NPKSQBPVTLDFDLAELENDIKVEIRNKMIDGESGEKTPRTLKVSQDERYI 581  
Db 541 lrkrpnlqnpksgpevtldfldaelendikveirnkmidgesgektfirtlvksqderyi 600  
Qy 582 DKGNRTYTWTPVNGTDYSLALVLPYSFYIKAKLEETITQARSKKGKMKDSETLKPDNF 641  
Db 601 dkgnrtycwtpvngtdyslalvlpysfyikakleetitqarskkgkmdsetlkpdnf 660  
Qy 642 EESGYTFIAPDYCNLDKISDNNTFLNFEFIDRKPNNPNSCNADLTNRVLIDAGFTN 701  
Db 661 eesgytfiapdycndlkisdnteflnfeidrkptnpsncnadlnrvlldagftn 720  
Qy 702 ELVQYNSQKNIKGVKARFVVTVGGITRVYPKEAGENQENPETYDSFYKRSLDNDNY 761  
Db 721 elvqywsqkniqvkarfvtvtdggitrvypkeagenqenpetyedsfykrsldndny 780  
Qy 762 VFTAPYFNKSGPGAYESIMVSKAVEIYIQGLKLPVAVGKIDYNSWIENFTKSIDRP 821  
Db 781 vftapyfnksgpgayesimvskaveiyiqgklkpvavvgkldvnswieftksirdp 840  
Qy 822 CAGPVCDCKRNSVMDCVILDDGGFLMANHDDYTNQIRFFGEIDPSLMRHLNVISYA 881  
Db 841 cagpvcdckrnsvmdcvilddggflmanhddytngirffgeidpslmrhlvnisyva 900  
Qy 882 FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASWILQOFLSLTTPR 941  
Db 901 fnksydyosvcepgaapkgaghrsayvpsvadilqigwataaawslqgflslttfpr 960  
Qy 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDSKFSVLDGCGNCSRFHGEKLMNTNL 1001  
Db 961 lleavemedddftaslskqsciteqtqyffdnndskfsvldgcnscrfhgekilmntnl 1020  
Qy 1002 IFIMVESKGTCPDTRLLIQAEQTSQSDGNPCDMVK 1036  
Db 1021 ifimveskgtcpdtrlliqaeqtsqsdgnpcdmvk 1055

## RESULT 7

ID AAR71013 standard; Protein; 1086 AA.

XX AAR71013;

XX 01-DEC-1995 (first entry)

XX Human neuronal calcium channel subunit alpha 2c.

XX Calcium channel subunit; antagonist; agonist; diagnosis;  
XX Lambert Eaton Syndrome.

XX Homo sapiens.

XX W09504822-A.

XX

16-FEB-1995.  
XX 11-AUG-1994; 94WO-US09230.  
XX 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
PI WPI; 1995-090900/12.  
XX N-PSDB; AAQ84667.  
XX DNA encoding human calcium channel sub-unit(s) - used for  
PT developing prods. for studying calcium channels, e.g. for  
PT obtaining agonists and antagonists  
XX  
PS Disclosure; Page 237-242; 285pp; English.  
XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
CC differentially processed in skeletal muscle, aorta, and CNS in  
CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
CC tissues. Five alternatively spliced variant transcripts that differ  
CC in the presence or absence of one to three different portions of  
CC this region. There are three sequences involved (see AAQ84664 FT  
CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
CC alpha 2 encoding transcripts from the different tissues include  
CC different combinations of the three sequences, except for one of  
CC the alpha 2 transcripts expressed in aorta which lacks all three  
CC sequences. The five alpha 2 forms identified are (1) a form that  
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
CC expressed in aorta and (5) one that lacks sequences 1 and 3  
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
CC are set forth in AAQ84666-084669 and AAR71012-R71015 respectively.  
XX  
SQ Sequence 1086 AA;

Query Match 99.3%; Score 5403.5; DB 16; Length 1086;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 MAAGCLLALTTLFOSLLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60

Db 1 maagcllalttlfoslilgspseepfpavtikswvdkmqedlvclaktaagvnlvdi 60

Qy 61 YEKYQDLYTVEPNARQLVEIARAARDIEKLLNSRKALVSLALEAEKVQAAHQRDFASN 120

Db 61 yekyqdltyvepnnarqlveiaardieklkllnsrkalsvslaleaeqvqaahqrdfasn 120

Qy 121 EVVYVNAKDDLDPEKNSEPSQRIKPVFIEDANFGROIHQHAAVHIPTDIYEGSTVL 180

Db 121 evvyvnaakddldpeknsepsqrikpvfiedanfgroisqhaavhiptdiyegstvl 180

Qy 181 NELNWTSSALDEVFKNREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTPNKIDLYDVR 240

Db 181 nelnwtssaldevfknreedpsllwqvfgsatglaryypasppwvdsnrtpnkidlydvr 240

Qy 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300

Db 241 rpwyiqgaaspkdmllilvdvsgsvgltklirtsvsemlletlsdddfvnvasfnsgd 300

Qy 301 VSCFOHLVQAVNRNKKVLKDAVNNTAKGIDYKKGFSFAFQQLNYSRANCNKIIML 360

Db 301 vscfghlvqanvrnkvlkdavnntakgldydkgfsfafeqllnynvsnrncnkliiml 360

Qy 361 FTDGGEERAQEIFNKYKDKKVRFRFSGVGHNYERGIOWMACENKGYYYEIPSIGAIR 420

Db 361 ftdggeeraqeflnkynkdkkvrfrfsvghnyergplqwmacenkgyyyelipsigair 420



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QY 421 INTQEVLDVLRPMVLGADKAKQVQWTVNYLDALGLVITGLTPVENITGQFENKTLK 480
DB 421 intqeyldvlgprpmvlagadkakqvqwnvldalelgvltgclpvnitgqfentknlk 480
QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYGYFAIDPNQYVLLHPNLQPKPKSQEPVTL 540
DB 481 nqlilgvmgvdsledikrltprftlcpgngyyfaidpnyvllhpnlpk-----epvtl 535
QY 541 DFLDAELENDIKVEIRNKMIDGSEKFTRTLVLKSDERYIDKGNRTYTWTPVNGTDSL 600
DB 536 dfldaelendikveirnmidgesektfttlvksgderyidkgnrtwtwtpvngtdysl 595
QY 601 ALVLPYFYIYAKLEETITQARSKGKMKDSETLKPDNFEESGYFTIAPRDYCNDLKI 660
DB 596 alvlpysfyyiakleetitqarskkgmkdsetlkdpnfeesgytftiapr-dychnlki 655
QY 661 SNNTEFLNFEIDRTPNPNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720
DB 656 sdnntefllnfnfidrktppnpncnadlinrvlldagftnelvqnywskqknikgvkar 715
QY 721 FVYTDGGITRVYPKEAGENWQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
DB 716 fvytdggitrvyypkeagenwqenpeteysfykrsldndnyvftapyfnksgpgayesgi 775
QY 781 MYSKAVEIYIQGLLKPAVVGKIDVNSWNIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840
DB 776 myskaveiyiqgllkpvavvgikidvnswnienftktsirdpcagpvcdcckrnsdvmcvi 835
QY 841 LDGGFLLMANHDDVTNQIGRFFGEIDPSLMRLHVNISVYAFNKSVDYQSVCEPGAAPRQ 900
DB 836 ldggfllmanhddvtngqgrffgeidpslmrhlvnisvyafrnksydyqsvcepgaapq 895
QY 901 GAGHRSAYVPSVADILQIGMWATAAAWSTLQOFLSLTPRLEAVEMEDDDFTASLSKQ 960
DB 896 gaghrsayvpsvadilqigwataaawstlqofllsltprrleavedddftaslskq 955
QY 961 SCITEQTQYFFNDKSFSGVLDGNCRSRIFHGEKLMNTNLIIFIMVESKGTGCPDTRLII 1020
DB 956 sciteqtqyffndksfsgvldgncsrifhgeklmntnliifimveskgtpcdtrlli 1015
QY 1021 QAEQTSDGPNPCDMVK 1036
DB 1016 qaeqtsdgnpcdmvk 1031

RESULT 8
AAW63153
ID AAW63153 standard; Protein; 1086 AA.
AC AAW63153;
XX
DT 12-OCT-1998 (first entry)
XX
DE Human calcium channel alpha-2c subunit.
XX
KW Alpha-2 subunit; human; calcium channel; assay; detection;
KW Characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX
OS Homo sapiens.
XX
PN US5792846-A.
XX
PD 11-AUG-1998.
XX
PF 31-MAY-1995; 95US-0455543.
XX
PR 04-APR-1994; 94US-0223305.
PR 04-APR-1988; 88US-0176899.
PR 04-APR-1989; 89US-0603751.
PR 04-APR-1989; 89WO-US01408.
PR 20-FEB-1990; 90US-0482384.
PR 30-NOV-1990; 90US-0620250.
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PR 15-AUG-1991; 91US-0745206.
PR 31-MAY-1995; 95US-0455543.
XX
FA (STBI-) SIBIA NEUROSCIENCES INC.
XX
PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI Williams ME;
XX
XX WPI; 1998-456192/39.
DR N-PSDB; AAV42702.
XX
XX DNA encoding human calcium channel alpha 1B subunit protein -
PT useful for recombinant production of the channel for screening of
PT its modulators, and diagnosis of Lambert Eaton Syndrome
XX
XX Claim 3; Columns 293-300; 166pp; English.
XX
XX The present sequence represents the alpha-2c subunit of a human calcium
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC that allow controlled entry of calcium ions into cells. This leads
CC to depolarisation events required for muscle contraction. The recombinant
CC subunit, when expressed with nucleic acids encoding the complete calcium
CC channel, can be used in assays for the detection and characterisation of
CC compounds that modulate the channel. The DNA encoding the subunits can
CC be alternatively spliced when transcribed, giving more than one form of
CC the protein from the same transcript, each having slightly different
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC molecules from the serum of an individual with Lambert Eaton Syndrome
CC (LES) can be used as a diagnostic for the disease.
XX
SQ Sequence 1086 AA;
XX
Query Match 99.3%; Score 5403.5; DB 19; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 1 MAAGCLLALTITLFSLLIGPSSEPPFSAVTIKSWDKMQEDVTLAKTAGVNLVDI 60
DB 1 maagcllaltitlfglligpsseepfsvatikswdkmgdvltlaktasgvnqlvdi 60
QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN 120
DB 61 yekyqdytvepnnaqlveiaardieklslsrskalvslaleaeekvqaahqwrdefasn 120
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISQHOAAVHIPTDIYEGSTIVL 180
DB 121 evvynakddldpekndsepgsqrikpvfiedanfgrqisqhaavhiptdiyegstivi 180
QY 181 NELNWTSAALDEVFKKNREEDPSLLAQVFGSATGLARYYPASPVDNSRTPNKIDLYDVR 240
DB 181 nelnwtasaldevfkknreedpsllwqvfgsatglaryypaspvwnsrtpnkidlydvrr 240
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETSDDDFVNVASFNSNAQD 300
DB 241 rpwyiqgaaspkdmlilvdvsgsvgltklirtsvsemletisdddfrvnvasfnnaqd 300
QY 301 VSCFOHLVQAVNRNKKVLDVNNITAKGIDYKKGFSFAFQQLLNYNVSRANCNKIIML 360
DB 301 vscfchlvanvrnkklvdavnnitakgidtykkgfsfafqqlnynvsrancnkiiml 360
QY 361 FTDGGEERAQEIFNKYNDKKVYRFRFVSQHOHNYERGPQIOWMACENKGYIYIPSTGATR 420
DB 361 ftdggeeraqeilfnkynkdkkvyrrfrfvsqhoynyergpiqwmacenkgyyieipstgatr 420
QY 421 INTQEVLDVLRPMVLGADKAKQVQWTVNYLDALGLVITGLTPVENITGQFENKTLK 480
DB 421 intqeyldvlgprpmvlagadkakqvqwnvldalelgvltgclpvnitgqfentknlk 480
QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYGYFAIDPNQYVLLHPNLQPKPKSQEPVTL 540
DB 481 nqlilgvmgvdsledikrltprftlcpgngyyfaidpnyvllhpnlpk-----epvtl 535
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QY 541 DFLDAELENDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWPVNGTDYSL 600
DB 536 dfldaeendikveirkmkidgesgkftltlksqderidkgnrtytwpvngtdysl 595
QY 601 ALVLPYSYIYKAKLEETITQARSKKGMKDSKSETLKPDNFESGTYFFIAPRDCNDLKI 660
DB 596 alvlpysyiykakleetitqarskkgmkdssetlkpdnfesgtyffiaprdcndlki 655
QY 661 SDNTEFLNFNEDIDRKTNNPCNADLNIRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
DB 656 sdnteflnfnedidrktnnpncnadlnirvlldagftnelvqywskqknikgvkar 715
QY 721 FVYTDGIRVYPKEAGENKQENPEYERYSFRRSDNDNRYFTAPYFNKSGPGAYESGI 780
DB 716 fvytdgirtvypkeagenkqenpeyedyfrrsldndnryftapyfnksgpgayesi 775
QY 781 MVSKEVEIYIQGLKPAVVGIIKIDVNSWIENTFTKTSIRPCAGPVCDCKRNSDVMDCVI 840
DB 776 mvskaveiyiqglkpvvgiikidvnswnientftktsirpcagpvcdckrnsdvmdcvi 835
QY 841 LDGSGFLMANHDDYTNQIGRFFGEIDPDSLMRHLVNIYSYAFNKSXYDQSVCEPGAAPKQ 900
DB 836 ldgsgflmanhdynqigrffgeidpslmrhlvnisyafnksxydyqsvcepgaapkq 895
QY 901 GAGHRSAVPSVADIIQIGWATAAASIIQQFLSLTTPRLLAEVEMEDDDFTASLSKQ 960
DB 896 gaghrsavpsvadliqigwataaasliqqflsltprllaevememdddfatlaslskq 955
QY 961 SCITEGTYFFDNDKSFSGVLDCGCSRIFFHGEKLMNTNLIIFIMVESKGTCTCPDTRLLI 1020
DB 956 scitegtqyffndksfsgvlcdgcsrfffhgeklmntnliifimveskgtctcpdtrlli 1015
QY 1021 QABQTSQGNPCDMVK 1036
DB 1016 qabqtsqgnpcdmvk 1031

RESULT 9
AAB10587
ID AAB10587 standard; Protein; 1086 AA.
AC AAB10587;
XX
XX
DT 22-DEC-2000 (first entry)
DE Human calcium channel alpha-2c subunit; protein.
KW Human; calcium channel; calcium channel subunit; diagnosis;
XX Lambert Eaton Syndrome; calcium channel subunit alpha-2c.
OS Homo sapiens.
XX
XX
PN US6096514-A.
XX
PD 01-AUG-2000.
XX
XX PF 25-MAY-1995; 95US-0450562.
XX
XX 04-APR-1988; 88US-0176899.
PR 02-FEB-1990; 90US-0482384.
PR 08-NOV-1990; 90US-0603751.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
PR 10-APR-1992; 92US-0868354.
PR 13-JUL-1992; 92US-0914231.
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
PR 07-FEB-1994; 94US-0193078.
PR 11-AUG-1994; 94US-0223305.
PR 23-SEP-1994; 94US-0290012.
PR 28-SEP-1994; 94US-0311363.
PR 07-NOV-1994; 94US-0314083.
PR 07-NOV-1994; 94US-0336257.
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PR 13-MAR-1995; 95US-0404950.
XX
XX (SIBI-) SIBIA NEUROSCIENCES INC.
PA
XX Ellis SB, Williams MB, McCue AF, Harpold MM;
PI
XX WPI; 2000-548230/50.
DR N-PSDB; AAA71725.
XX
XX Human calcium channel beta subunit polynucleotides, useful for
PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton
PT Syndrome
XX
XX Disclosure; Column 237-244; 153pp; English.
PS
XX
XX This invention describes a novel isolated DNA molecule (I) comprising a
CC sequence encoding a beta3-1 subunit of a human calcium channel.
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
CC beta3 subunit encoding DNA are useful for isolation and cloning of
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that
CC express heterologous calcium channel are useful for identifying compounds
CC that modulate calcium channel activity and in assays for identifying
CC agonists and antagonists of calcium channel activity in humans. Human
CC calcium channel subunit or eukaryotic cells expressing the channel are
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This
CC sequence represents the human calcium channel alpha-2c subunit which is
CC described in the method of the invention.
XX
XX Sequence 1086 AA;

Query Match 99.3%; Score 5403.5; DB 21; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLLALTLTFLQSLIGPSSEEPSPSAVTTKSWDKMQEDLVTLAKTAGSVNQVLVDI 60
DB 1 maagcllaltltlqslilgpsseepfpsavtlkswdkmqedlvtlaktasgvnqlvdi 60
QY 61 YEKYQDLTYVEPNNAQOLVIAARDIEKLLSNRSKALVSLALEAEKVQAQAHQWREDFASN 120
DB 61 yekyqdltyvepnnaqlveiaardieklksnrskalvslaleaeekvqaahqwrdfasn 120
QY 121 EYVYNAKDDLDPKNDSEPGSORIKPVFIEDANFGQISYQHAHVHPTDIIEGSIYV 180
DB 121 evvyynakddldpkndsepgsqrikpvfiedanfgqisqyhaavhptdiiegstivl 180
QY 181 NELNWTSAALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDNSRTNPKIDLYDVR 240
DB 181 nelnwtasaldevfknreedpsllwqvgatglaryypaspwvdnsrtpnkidlydvrr 240
QY 241 RPWYIOGAASPDKMLILVDYSGVSGLTLLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300
DB 241 rpwyiogaaspdkmllivdysgsvsgltklirtsvsemletisdddfvnvsfnasnaqd 300
QY 301 VSCFQHLVQANVRNKKVYLKDAVNNITAKGITYDKKGSFAFEQLLLNYSRANCNKIIML 360
DB 301 vscfqlhvqanvrnkvylkdavnnitakgitydkkgsfafeqllnysrancnkiiml 360
QY 361 FTDGGERAQEIENKYNKDKKRVFRFSGVGHNYERGPQIWMACENKGYEYIEPSIGAIR 420
DB 361 ftdggeeraqeiefnkynkdkkrrvfrfsvqghnyergpigmacenkgyyeiepsigair 420
QY 421 INTQEYLDVLGRPMVLAGDKAKOVQMTNVYLDALGLVITGTLPVFNITGQFENKYNLK 480
DB 421 intqeyldvlgrpmvlagdkakqvmtnvyldaleglvitgtlpvfnitgqfekenknlk 480
QY 481 NQLILGYMGVDVSLIEDIKRITPRTFLCPNGYYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
DB 481 nqlilgvmgvdvsledikritprftlcpngyyfaidpngyvllhpnlpknpsqepvttl 540
QY 541 DFLDAELENDIKVEIRKMKIDGESGKFTLTKSODERYIDKGNRTYTWPVNGTDYSL 600
DB 536 dfldaeendikveirkmkidgesgkftltlksqderidkgnrtytwpvngtdysl 595
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721 FVVDGGITRVYTPKEAGENWQENPETYEDSEYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
 714 fvtvdggitrvypkeagenwqenpetyedsfykrslndndnyvftapyfnksgpgayesgi 773  
 781 MYSKAVEIYIQGLKLPVAVGIRKIDVNSWIENFTKTSIRDPKAGPVCDCCKRNSDVMDCVI 840  
 774 mvsKaveIyIqgklllpavvgirkidvnsWienftktsirDpkagpvcDckrnSDvmDcvi 833  
 841 LDGCGFLMANHDDYTNOIGRFGEDIDPSLMRHLVNSVYAFNKSIDYQSVCEPGAAPKQ 900  
 834 lddgcfllmanhddytngirfgedidpslmrhlvnsVYafnksIdyQsvcePGAapKq 893  
 901 GAGHRSAYVPSVADILQIGWATAAASIIQOFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960  
 894 gaghrsayvpsvadilqigwataaasIIqoFLslTffPrlleAVemEDddftaslsKq 953  
 961 SCITPQTOYFFDNDKSKFSGLVDCGNCSPRIFHGEKLMNTNLIFFIMVESKGTCPDCTRLII 1020  
 954 sciteqtgyffDndksKfsGLvdcGncSPRifHgeKlMntnlIffImvesKgtcPDcTrlII 1013  
 1021 QAEQTSQGNPCDMVK 1036  
 1014 qaeqtsdgnpCDmVk 1029

RESULT 11  
 AA63155  
 ID AA63155 standard; Protein; 1084 AA.  
 AC AA63155;  
 XX  
 12-OCT-1998 (first entry)  
 XX Human calcium channel alpha-2e subunit.  
 DE  
 XX Alpha-2 subunit; human; calcium channel; assay; detection;  
 KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 XX Homo sapiens.  
 OS  
 XX US792846-A.  
 PN  
 XX 11-AUG-1998.  
 PD  
 XX 31-MAY-1995; 95US-0455543.  
 PF  
 XX 04-APR-1994; 94US-0223305.  
 PR 04-APR-1988; 88US-0176899.  
 PR 04-APR-1989; 89US-0603751.  
 PR 04-APR-1989; 89WO-US01408.  
 PR 20-FEB-1990; 90US-0482384.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 31-MAY-1995; 95US-0455543.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 PA Brenner R, Ellis SB, Feldman DH, Harpold MW, McCue AF;  
 PI Williams ME;  
 PI WPI; 1998-456192/39.  
 XX N-PSDB; AAV42704.  
 DR  
 DR DNA encoding human calcium channel alpha 1B sub:unit protein -  
 PT useful for recombinant production of the channel for screening of  
 PT its modulators, and diagnosis of Lambert Eaton Syndrome  
 PT  
 XX Claim 3; Columns 305-310; 166pp; English.  
 PS The present sequence represents the alpha-2e subunit of a human calcium  
 XX channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 CC that allow controlled entry of calcium ions into cells. This leads  
 CC to depolarisation events required for muscle contraction. The recombinant

CC subunit, when expressed with nucleic acids encoding the complete calcium  
 CC channel, can be used in assays for the detection and characterisation of  
 CC compounds that modulate the channel. The DNA encoding the subunits can  
 CC be alternatively spliced when transcribed, giving more than one form of  
 CC the protein from the same transcript, each having slightly different  
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 CC molecules from the serum of an individual with Lambert Eaton Syndrome  
 CC (LES) can be used as a diagnostic for the disease.

XX Sequence 1084 AA;

Query Match 99.0%; Score 5386.5; DB 19; Length 1084;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;  
 QY 1 MAAGCLLATLTTLFOSLLIGPSSEPPFPSPATYKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
 DB 1 maagcllatlttlfoslIlgpsseepfpSpatYkswDKmqEDlvTLaktagvgnqlvdi 60  
 QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHOWREDFASN 120  
 DB 61 yekyQdlytvePnnarqlveiaardiekllsnrSkalvslaleaekvqaahQwredfaSn 120  
 QY 121 EYVYNKADDDLPKNDSEPGSORIKPVFIEDANFGRIQISYQHAHVHPTDIYEGSTIVL 180  
 DB 121 evvynakddldpEkndsepgsOrIkpvfiEDanfgriqisYqhaahVhptdiYegstivl 180  
 QY 181 NELNWTSAIDVEPKNREEDPSLLIQVFGSATGLARYYPASPWPVDSRTNKIDLYDVR 240  
 DB 181 nelnWtsaIdvePKnreedpsllIQvfgsatGLaryypaspWPvdsrtnkIdlydvr 240  
 QY 181 nelnWtsaIdvefknreedpsllwqyfgsatGLaryypaspWPvdsrtnkIdlydvr 240  
 QY 241 RPWYIQGAASPDKMLILVDVSGSVSGTLKIRTSVSEMLETLSDDDDFNVASFNNAQD 300  
 DB 241 rpwyIqgaaspkDmlilvdvsgsvsgtlkIrtsvseMLEtlSDdddfnvafsnnaqd 300  
 QY 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGITDYKKGFSFAFEQLLNNVSRANCKIIML 360  
 DB 301 vscfqlhvqanvrnkKvylkdavnntakgitdyKkgfsafaEQllnnvSrancnkiIml 360  
 QY 361 FTDGGEARAEIFNKYNDKKVRFVRFVSGHNYERGPQIWMACENKGYEYIEPSIGAIR 420  
 DB 361 ftdgGearaeIfnkYndkKvrfvrfvsgHnyerGPqiWmacenKgyeYiepsigair 420  
 QY 421 INTQYLDVIGRPMVLGAKAKOVQNTVYLDALGLVITGTPLPVFNITGOFENKTNLK 480  
 DB 421 intqeyldvIgrpmvlgakakOvqntvYldalglvITgtPlpvfnitgOfenktnlk 480  
 QY 481 NQILGVMGVDVSLSDIKRLTPFTLCPNGYFAIDPNGYVLLHPLNLPKPKSQEPVTL 540  
 DB 481 nqilgvmgvdvslSDIKrltPftlcpngyYfaIdpNgYvllhplnlpkpkSqepvtl 540  
 QY 541 DFIDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600  
 DB 541 dfidaeleNDIKveIRnkmIDgesgkftftlvksQdeRYidKgnrtYtTPvngtdySl 600  
 QY 601 ALVLPYTSFYIIRAKLEETITQARSKKGKMKDSETLPKDNFEESGYFTIAPRDYCNLDKI 660  
 DB 601 alvlpYtsfYiIRakleETITqARskKgkMKdsetLPkdnFEesgyfTiaprDYcndlki 660  
 QY 661 SDNTEFLLNFEIDRKTNPNSCNADLINRVLLDAGFTNELVQNVYWSKOKNIKGVKAR 720  
 DB 661 sdnTEfllnfeIdrKtNPNsCNadlinrvllDagftnELvqnvYwsKoknikgvkar 720  
 QY 721 FVVDGGITRVYTPKEAGENWQENPETYEDSEYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 714 fvtvdggitrvypkeagenwqenpetyedsfykrslndndnyvftapyfnksgpgayesgi 773  
 QY 781 MYSKAVEIYIQGLKLPVAVGIRKIDVNSWIENFTKTSIRDPKAGPVCDCCKRNSDVMDCVI 840  
 DB 774 mvsKaveIyIqgklllpavvgirkidvnsWienftktsirDpkagpvcDckrnSDvmDcvi 833  
 QY 841 LDGCGFLMANHDDYTNOIGRFGEDIDPSLMRHLVNSVYAFNKSIDYQSVCEPGAAPKQ 900

Db 834 lddggfillmanhdytngigrfgeidpslmrhlvnisvafnksydyqsvcepgaaapk 893  
 QY 901 GAGHSAVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db 894 gaghhsayvpsvaddilqigwataaawilqgflsltfprlleavemedddftaslskq 953  
 QY 961 SCITPQTOYFFDNDKSPSGVLDGNCNCSRIFFHGEKLMNTNLIFFIMVESKGTCPDTRLLI 1020  
 Db 954 sciteqtqyffondsksfsgvldcncncriffhgeklmtnliffimveskgtpcdtrlli 1013  
 QY 1021 QAEQTSQDGNPCDMVK 1036  
 Db 1014 qaeqtsdgnpcdmvk 1029

## RESULT 12

AAB10589  
 ID AAB10589 standard; Protein; 1084 AA.

XX AC AAB10589;

XX DT 22-DEC-2000 (first entry)

XX Human calcium channel alpha-2e subunit protein.

XX Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2e.

XX OS Homo sapiens.

XX PN US6096514-A.

XX PD 01-AUG-2000.

XX PF 25-MAY-1995; 95US-0450562.

XX PR 04-APR-1988; 88US-0176899.

XX PR 02-FEB-1990; 90US-0482384.

XX PR 08-NOV-1990; 90US-0603751.

XX PR 30-NOV-1990; 90US-0620250.

XX PR 15-AUG-1991; 91US-0745206.

XX PR 10-APR-1992; 92US-0868354.

XX PR 13-JUL-1992; 92US-0914231.

XX PR 11-AUG-1993; 93US-0105536.

XX PR 05-NOV-1993; 93US-0149097.

XX PR 07-FEB-1994; 94US-0193078.

XX PR 04-APR-1994; 94US-0223305.

XX PR 11-AUG-1994; 94US-0290012.

XX PR 23-SEP-1994; 94US-0311363.

XX PR 28-SEP-1994; 94US-0314083.

XX PR 07-NOV-1994; 94US-0336257.

XX PR 13-MAR-1995; 95US-0404950.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX PA Ellis SB, Williams ME, McCue AF, Harpold MM;

XX PI WPI; 2000-548230/50.

XX DR N-PSDB; AAA1727.

XX Human calcium channel beta subunit polynucleotides, useful for

XX PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton

XX PT Syndrome

XX FS Disclosure; Column 253-260; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a

XX sequence encoding a beta3-1 subunit of a human calcium channel.

XX Nucleic acid probes comprising 14-30 contiguous nucleotides of

XX beta3 subunit encoding DNA are useful for isolation and cloning of

XX calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that

XX express heterologous calcium channel are useful for identifying compounds

CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit or eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2e subunit which is  
 CC described in the method of the invention.

XX SQ Sequence 1084 AA;

Query Match 99.0%; Score 5386.5; DB 21; Length 1084;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTTLTFLQSLLIGPSSSEPPPSAVTIISWVDKMOEDLVTLAKTASGVNQLVDI 60

Db 1 maagcllalttlifqslilgspseepfapsavtikswvdkmedlvtlaktasgvnqlvdi 60

QY 61 YEKYQDLYTVPEPNAROLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRDFAFN 120

Db 61 yekyqdlytvepnarqlveilaardieklslsrakalvslaleaeakvqaahqrredfasn 120

QY 121 EYVYNKADDLDPKNDSEPGSQRIKPVFIEDANFGROIYSYQHAHVHIPTDIYEGSTIVL 180

Db 121 evvynakddldekndsepgsqrikpvfiedanfgroisqyghaavhiptdiyegstivl 180

QY 181 NELNWTLSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240

Db 181 nelnwtlsaldevfkknreedpsllwqvfgsatglaryypaspwdnsrtpnkidlydvr 240

QY 241 RPWYIQGAASPDKMLILVDVSGVSGLTCLKIRTSVSEMLETSLDDDFNVASFNQAQD 300

Db 241 rpwyiqgaaspdkmlilvdvsgvsgltklirtsvsemlletloddvfnvasfnasqd 300

QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDKKGSFAFEQLLNVNVRANCKNIIML 360

Db 301 vscfqlhvqanvrnkvlkdavnnitakgitydkkgsfafeqllnvnvrancnkilm 360

QY 361 FTDCGEERAQEIFNKYKNDKKRVFRSVGOHNERGPIOMACENKGYVYEISIGAIR 420

Db 361 ftdggeeraqeifnknkdkkrrvfrsvgqnyergpigmacenkgyyeipsgair 420

QY 421 INTQEYLDVLGRPMVLAKQVQWTVNYLDALGLVITGTLVPFNITQGFENKTLK 480

Db 421 intqeyldvlgrpmvlagdkakqvqwtvnyldaleglvitgtlpvfnitqgfektnlk 480

QY 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYVFAIDPNGYVLLHPNLQPKNPKSOEPTL 540

Db 481 nqlilgvmgvdvsledikrltpftlcpngyyfaidpnyvllhpnlpkpkpksepvtl 540

QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRYITWTVPVNGTDSL 600

Db 541 dfldaeelndikveirnmidgesgektftrlvksqderiyidkgnrtyitwtvpvngtdysl 600

QY 601 ALVLPYTFYVYIKAKLEETITQARSKKMKDSETLPDNEEESGYTFIAPRDCNDLKI 660

Db 601 alvlpysfyvikakleetitqary-----setlpdnfeesgytfiaprdcndkli 653

QY 661 SDNNTFLLNFEIDRKTNNPCNADLINRVLLDAGFTNELVQNTYWSKQKNGVKAR 720

Db 654 sdntefllnfeidrktnpnpcnadinrvlldagftnelvqnywskqknkngvkar 713

QY 721 FVYTDGGITRVYPKEAGENQENPETVEDSFYKSLDNDNYVFTAPYFNKSGPGAYESGI 780

Db 714 fvytdgggitrvypkeagenqenpetyedsfykrslndndnyvftapyfnksgpgayesgi 773

QY 781 MYSKAVIYIQQGLLKPAVVGKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840

Db 774 mvskaiveiyqgllkpaavgikidvnswieftktsirdpcagpvcdcckrnsdvmdcvi 833

QY 841 LDGGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNTSVYAFNKSVDYQSVCEPGAAPKQ 900

Db 834 ldgggflmanhddytngigrfgeidpslmrhlvnisvafnksydyqsvcepgaaapk 893

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Query Match 98.68; Score 5367; DB 16; Length 1103;  
 Best Local Similarity 97.48; Pred. No. 0;  
 Matches 1028; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

1 MAAGCLLALTTLTQSLIGPSSEPPFSAVTIKSWDKMEDLVTLAKTAGVNLVDI 60  
 1 maagcllalttlqsligpsseepfipavtikswdkmedlvtlaktagsvnlvdi 60  
 61 YEKYODLYTVPNNARQVETAAARIEKLLNRSKALYSALAEAKVQAAHQWREDFASN 120  
 61 yekyodlytvpnnarqlveetaardiekllnsrskalysalaeakvqaahqwrdfasn 120  
 121 EYVYNNAKDDLPKNDSEPGSQRIPKPFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
 121 evvynnakddlpeknsepgsqrikpiefdanfgrqisyqhaavhptdiyegstivl 180  
 181 NELNWTSAIDVFKKNREDDPSLLWQVFGSATGLARYYPASPVWDSRPNKIDLYDVR 240  
 181 nelnwtসাaidvfkknreedpsllwqvfgsatglaryypaspvwdsrpnkidlvdvrr 240  
 241 RPWYIQAASPKDMLILVDVSGVSGITLKIITSVSEMLETSLDDDFVNVASFNSNAQD 300  
 241 rpywigaaaspkdmlilvdvsgvsgitlkiirtsvsemlletlstdddfvnvafnsnaqd 300  
 301 VSCFQHLVQANVRNKKVLDVNNITAKGTDYKKGFSFAFEQLLNYNVSRANCNKIIML 360  
 301 vscfqlhvlqanvrnkvlkdvnnitakgtidykkgfsfafeqllnynvsrancnkiml 360  
 361 FTDCGEERAQEIFPNKYNKDKRVFRFVSGOHNTERGPIQWACENKGYEYIEPSIGAIR 420  
 361 ftdggeeraqeifpnkynkdkrvfrfsvgohntergpiqwacenkgyeyiepsigair 420  
 421 INTQEYLDVGLRPMVLADGKAKOVWNTVYLDALGLVITGTLFVFNITQGFENKTNLK 480  
 421 intqeyldvlgprpmvlagdkakovwntvyldaleglvitgtlfpvfnitqgfektnlk 480  
 481 NQILGVMGVDVSLIEDIKRLTPRETLCPNGYFAIDPNGYVLLHNPLOPK----- 530  
 481 nqilgvmgvdsledikrltpretlcpngyfaidpnyvllhnplopk----- 530  
 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKFTILVKSQDERYI 581  
 531 -----npskqepvtldfdaelendikveirnkmidgesgektftrlvksqderyi 581  
 541 LRKRRPNIGNPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKFTILVKSQDERYI 600  
 541 lrkrrpnignpkseqpvtldfdaelendikveirnkmidgesgektftrlvksqderyi 600  
 582 DKGNTTYTTPVNGTDYSIALVLPYTSFYIRAKLEETITQARSKKGMKDSSETLKPDNF 641  
 582 dkgnttyttpvngtdysialvlpysfyirakleetitqarskkgmkdsetlkdndf 641  
 601 DKGNTTYTTPVNGTDYSIALVLPYTSFYIRAKLEETITQARSKKGMKDSSETLKPDNF 653  
 601 dkgnttyttpvngtdysialvlpysfyirakleetitqarskkgmkdsetlkdndf 653  
 642 EESGYTFIAPRDYCNLDKISDNTEFLNFEIDRKTNNPCNADLINRVLLDAGFTN 701  
 642 eesgytfiaprdycnldkisdntefllnfeidrktnnpcnadinrvlldagftn 701  
 654 EESGYTFIAPRDYCNLDKISDNTEFLNFEIDRKTNNPCNADLINRVLLDAGFTN 713  
 654 eesgytfiaprdycnldkisdntefllnfeidrktnnpcnadinrvlldagftn 713  
 702 ELVQNTYWSKOKNIGVKARFVVDGGITRVYKPEAGENWQENPETVEDSFYKSLDNDNY 761  
 702 elvqntywskoknigvkarfvvdggitrvykpeagenwqenpetvedsfykrslndny 761  
 714 ELVQNTYWSKOKNIGVKARFVVDGGITRVYKPEAGENWQENPETVEDSFYKSLDNDNY 773  
 714 elvqntywskoknigvkarfvvdggitrvykpeagenwqenpetvedsfykrslndny 773  
 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGKIDVNSWNIENFTKTSIRDP 821  
 762 vftapyfnksgpgayesgimvskaveiyiqglklpvavgkiddvnswnienftktsirdp 821  
 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGKIDVNSWNIENFTKTSIRDP 833  
 774 vftapyfnksgpgayesgimvskaveiyiqglklpvavgkiddvnswnienftktsirdp 833  
 822 CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTQIGRFFGEIDPSLMHLYNISVYA 881  
 822 cagpvcdcrnsdvmcdvildddggflmanhddytqigrffgeidpslmhlynisvya 881  
 834 CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTQIGRFFGEIDPSLMHLYNISVYA 893  
 834 cagpvcdcrnsdvmcdvildddggflmanhddytqigrffgeidpslmhlynisvya 893  
 882 FNKSYDYQSVCEPAGAPKOGAGHRSAAYVPSVADIILQIGWATAAAWSILQOFLSLTFFR 941  
 882 fnksydyqsvcepagapkogaghrsaayvpsvadiilqigwataaawsilqofllstffr 941  
 894 FNKSYDYQSVCEPAGAPKOGAGHRSAAYVPSVADIILQIGWATAAAWSILQOFLSLTFFR 953  
 894 fnksydyqsvcepagapkogaghrsaayvpsvadiilqigwataaawsilqofllstffr 953  
 942 LLEAVEMEDDDFTASLQKSCITEQYQFEEDNDSKFSGLDCGNCSTRIFHGEKLMNTNL 1001  
 942 lleavemedddftaslqksciteqyqfeedndskfsgldcgcncsrifhgeklmntnl 1001  
 954 LLEAVEMEDDDFTASLQKSCITEQYQFEEDNDSKFSGLDCGNCSTRIFHGEKLMNTNL 1013  
 954 lleavemedddftaslqksciteqyqfeedndskfsgldcgcncsrifhgeklmntnl 1013  
 1002 IFIMVESKGTCPCDTLLIQAQETSDGNPCDMVK 1036  
 1002 ifimveskgtcpcdtllliqaqetsgdnpcdmvk 1036

901 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLSLTFFRLLLEAVEMEDDDFTASLSKQ 960  
 901 gaghrsayvpsvadilqigwataaawsilqofllstffrllleavemedddftaslskq 960  
 953 GAGHRSAYVPSVADILQIGWATAAAWSILQOFLSLTFFRLLLEAVEMEDDDFTASLSKQ 953  
 953 gaghrsayvpsvadilqigwataaawsilqofllstffrllleavemedddftaslskq 953  
 961 SCITEQYQFEEDNDSKFSGLDCGNCSTRIFHGEKLMNTNLIFIMVESKGTCPCDTRLII 1020  
 961 sciteqyqfeedndskfsgldcgcncsrifhgeklmntnlifimveskgtcpcdtrlli 1020  
 1013 SCITEQYQFEEDNDSKFSGLDCGNCSTRIFHGEKLMNTNLIFIMVESKGTCPCDTRLII 1013  
 1013 sciteqyqfeedndskfsgldcgcncsrifhgeklmntnlifimveskgtcpcdtrlli 1013  
 1021 QAEQTSDDGNPCDMVK 1036  
 1021 qaeqtsddgnpcdmvk 1036  
 1014 QAEQTSDDGNPCDMVK 1029  
 1014 qaeqtsddgnpcdmvk 1029

RESULT 13  
 AAR71012  
 ID AAR71012 standard; Protein; 1103 AA.  
 AC AAR71012;  
 DT 01-DEC-1995 (first entry)  
 DE Human neuronal calcium channel subunit alpha 2a.  
 XX Calcium channel subunit; antagonist; agonist; diagnosis;  
 KW Lambert Eaton Syndrome.  
 KW Homo sapiens.  
 OS W09504822-A.  
 PN 16-FEB-1995.  
 PD 11-AUG-1994; 94WO-US09230.  
 PF 11-AUG-1994; 94WO-US09230.  
 XX 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
 PI WPI; 1995-090900/12.  
 DR N-PSDB; AAQ84666.  
 XX DNA encoding human calcium channel sub-unit(s) - used for  
 PT developing prods. for studying calcium channels, e.g. for  
 PT obtaining agonists and antagonists  
 XX Disclosure; Page 231-236; 285pp; English.  
 PS Human neuronal alpha 2 coding sequence (AAQ84666) transcript is  
 CC differentially processed in skeletal muscle, aorta, and CNS in  
 CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
 CC tissues. Five alternatively spliced variant transcripts that differ  
 CC in the presence or absence of one to three different portions of  
 CC this region. There are three sequences involved (see AAQ84664 FT  
 CC and AAQ84665 FT), sequence 1, sequence 2, and sequence 3. The five  
 CC alpha 2 encoding transcripts from the different tissues include  
 CC the alpha 2 transcripts expressed in aorta which lacks all three  
 CC different combinations of the three sequences, except for one of  
 CC sequences. The five alpha 2 forms identified are (1) a form that  
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
 CC (2) one that lacks sequences 1 and 2 called alpha 2b, expressed in  
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
 CC expressed in aorta and (5) one that lacks sequences 1 and 3  
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
 CC are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.  
 XX Sequence 1103 AA;  
 SQ

Db 1014 ifimvesgtcpcdtrlllqaeqtsdgnpcdmvk 1048  
|||||

RESULT 14  
AAW63151  
ID AAW63151 standard; Protein; 1103 AA.

XX AC AAW63151;

DT 12-OCT-1998 (first entry)

XX DE Human calcium channel alpha-2a subunit.

XX KW Alpha-2 subunit; human; calcium channel; assay; detection;  
XX KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.

XX OS Homo sapiens.

XX PN US5792846-A.

XX PD 11-AUG-1998.

XX PF 31-MAY-1995; 95US-0455543.

XX PR 04-APR-1994; 94US-0223305.

XX PR 04-APR-1988; 88US-0176899.

XX PR 04-APR-1989; 89US-0603751.

XX PR 20-FEB-1990; 90US-0482384.

XX PR 30-NOV-1990; 90US-0620250.

XX PR 15-AUG-1991; 91US-0745206.

XX PR 31-MAY-1995; 95US-0455543.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;

XX PI Williams ME;

XX DR WPI; 1998-456192/39.

XX DR N-PSDB; AAW42700.

XX PT DNA encoding human calcium channel alpha 1B subunit protein -

XX PT useful for recombinant production of the channel for screening of

XX PT its modulators, and diagnosis of Lambert Eaton Syndrome

XX PS Claim 3; Columns 287-294; 166pp; English.

XX CC The present sequence represents the alpha-2a subunit of a human calcium  
XX CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
XX CC that allow controlled entry of calcium ions into cells. This leads  
XX CC to depolarisation events required for muscle contraction. The recombinant  
XX CC subunit, when expressed with nucleic acids encoding the complete calcium  
XX CC channel, can be used in assays for the detection and characterisation of  
XX CC compounds that modulate the channel. The DNA encoding the subunits can  
XX CC be alternatively spliced when transcribed, giving more than one form of  
XX CC the protein from the same transcript, each having slightly different  
XX CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
XX CC molecules from the serum of an individual with Lambert Eaton Syndrome  
XX CC (LES) can be used as a diagnostic for the disease.

XX SQ Sequence 1103 AA;

Query Match 98.6%; Score 5367; DB 19; Length 1103;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1028; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLATLTTLFQSLTGPSSEFPSPAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
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Db 1 maagcilaatlftlfgallgppssefpfpavtikswdkmqedlvltlaktasgvnqlvdi 60  
|||||

QY 61 YEKYQDLYTVEPNARQLVEIARDEIKLLSNRSKALVSALAEAKVQAQHWREDFASN 120  
|||||

Db 61 yekyqdytvepnarqlveiaardiekllsnrskalvsalaeakvqaahqwfedfasn 120  
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QY 121 EVYYNAKDDLDPEKNDSEPGSRIKPVFTIEDANFRQISVQHAHVHPTDIYEGSGIVL 180  
|||||

Db 121 evyyanakddldpekndsepgsrikpvfiedanfrqisyqhaavhlpdciyegstivl 180  
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QY 181 NELNWTSAALDEVFKKREEDPSLLMQVFGSATGLARYYPASPWWYDNRTPNKIDLYDVR 240  
|||||

Db 181 nelnwtasaldevfkknreedpsllmqvfgsatglaryypaspwwydnrtpnkldlydvr 240  
|||||

QY 241 RPWYIOGAASPDKMLILVDYSGVSGSLTTLKIRTSVSEMLETLSDDDFVNVASNSNAQD 300  
|||||

Db 241 rpwyiogaaspdkmliilvdysgsvsglttlkirtsvsemletlsdddfvnvasnnaqd 300  
|||||

QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFEOQLLYNVSRANCKLIIML 360  
|||||

Db 301 vscfqlhvanvrnkklvldavnnitakgtdykgkfsfafeoqllynvsrcanckliiml 360  
|||||

QY 361 FTDGGEERAQEIFNKYNKDKKRVFRFSVGOHNYERPIQWACENKGYVEIPSIGAIR 420  
|||||

Db 361 ftdggeeraqeifnknkdkkrrvfrfsvgohnyerpiqwmacenkgyyeipsigair 420  
|||||

QY 421 INTQEYLDVLGRPMVLAKQVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480  
|||||

Db 421 intqeyldvlgrpmvlagkakqvqntnvyldaleglvltgtpvfnitgqfenktnlk 480  
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QY 481 NQILGVMGVDSLEIDIKRLTPFTLCPNGYYPADPNGVYLLHPNLQPK----- 530  
|||||

Db 481 nqilgvmgvdsleidikrltpftlcpngyyfaldpnngvyllhpnlpkpgvigtin 540  
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QY 531 -----NPKSQEPVTLDFDAELENDIKVIRNKMIDGESGEKTFRLVKSQDERYI 581  
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Db 541 lkrtrpniqnpsqevptldfdaelendikveirnmkidgesgektfrclvksqderiy 600  
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QY 582 DKGNRRTYTWTPVNGTDYSLALVPTYFYIYKAKLEETITQARSKKGMKDSLTLPDNF 641  
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Db 601 dkgnrtytwtpvngtdyslalvptyfyiykakleetitqary-----setlkdnpf 653  
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QY 642 EESGYTFIAPROYCNDLKISDNNTEFLNFEFIDRKTNNPSCNADLINRVLLDAGFTN 701  
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Db 654 eesgytfiaproycndlkisdnnfeflnfnefidrktnpnpscnadlinrvlldagftn 713  
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QY 702 ELVQNTWSQKNIKGVKARFVWTDGGITRVYPKEAGENQENPETVEDSFYKSLDNDNY 761  
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Db 714 elvqnywsqkniqgvkarfvtdggitrvypkeagenqenpetyedsfykrsldndny 773  
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QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRD 821  
|||||

Db 774 vftapyfnksgpgayesgimvskaveiyioqkllkpavvgikidvnswiensfctksirdp 833  
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QY 822 CAGPYCDCKRNSDVMDCVTLDDGGFLLMANHDDYTNQIGRFGFGEIDPSLMRHLVNI SVYA 881  
|||||

Db 834 cagpycdckrnsdvmcdvcllddggfllmanhddytnqigrffgeidpslmrhlvnsvya 893  
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QY 882 FNKSYDYQSVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAAWSILQOFLSLTEPR 941  
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Db 894 fnksydyqsvcepagapkgaghrsayvpsvadilqigwataaawslilqffllstlfr 953  
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QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDCGNCSTRIFHGKLMNTNL 1001  
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Db 954 lleavemedddftaslskqsciteqtqyffdnkskfsfgvldcgncsrifhgkclmntnl 1013  
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QY 1002 IFIMVESGTCPDTRLLIQAQTSDDGNPCDMVK 1036  
|||||

Db 1014 ifimvesgtcpcdtrlllqaeqtsdgnpcdmvk 1048  
|||||

RESULT 15

AAAB10586

ID AAB10586 standard; Protein; 1103 AA.

XX

AC AAB10586;



Mon Jul 23 08:36:22 2001

XX 22-DEC-2000 (first entry)  
 XX Human calcium channel alpha-2a subunit protein.  
 DE Human; calcium channel; calcium channel subunit; diagnosis;  
 XX Human; calcium channel; calcium channel subunit alpha-2a.  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2a.  
 XX Homo sapiens.  
 OS US6096514-A.  
 PN 01-AUG-2000.  
 PD 01-AUG-2000.  
 XX 25-MAY-1995; 95US-0450562.  
 XX 04-APR-1988; 88US-0176899.  
 PR 02-FEB-1990; 90US-0482384.  
 PR 08-NOV-1990; 90US-0603751.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 10-APR-1992; 92US-0868354.  
 PR 13-JUL-1992; 92US-0914231.  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 PR 07-FEB-1994; 94US-0193078.  
 PR 04-APR-1994; 94US-0223305.  
 PR 11-AUG-1994; 94US-0290012.  
 PR 23-SEP-1994; 94US-0311363.  
 PR 28-SEP-1994; 94US-0314083.  
 PR 07-NOV-1994; 94US-0336257.  
 PR 13-MAR-1995; 95US-0404950.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX Ellis SB, Williams ME, McCue AF, Harpold MM;  
 PI WPI; 2000-548230/50.  
 DR N-PSDB; AAA71724.  
 XX Human calcium channel beta subunit polynucleotides, useful for  
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
 PT Syndrome -  
 XX Disclosure; Column 229-236; 153pp; English.  
 XX This invention describes a novel isolated DNA molecule (I) comprising a  
 CC sequence encoding a beta3-1 subunit of a human calcium channel.  
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
 CC beta\_3 subunit encoding DNA are useful for isolation and cloning of  
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 CC express heterologous calcium channel activity and in assays for identifying  
 CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit or eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2a subunit which is  
 CC described in the method of the invention.  
 XX Sequence 1103 AA;  
 SQ  
 Query Match 98.6%; Score 5367; DB 21; Length 1103;  
 Best Local Similarity 97.4%; Pred. No. 0;  
 Matches 1028; Conservative 0; Mismatches 1; Indels 26; Gaps 2;  
 QY 1 MAACCLALATLITLQSLIGSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
 DB 1 maagcllaltlilqslilgsspeppsaavtikswdkmqedlvtlaktasgvnqlvdi 60  
 QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLNSRKALVSLAEAEKVQAAHQWREDFASN 120  
 DB 61 yekyqdltyvepnnarqlveiaardiekllnsrkalslaleakvqaahqwredfasn 120

QY 121 EVVYNAKDDLDPEKNDSEPGSQRKPKVFIEDANFGROISYOHAAVHIPTDIYEGSTIVL 180  
 DB 121 evvynakddldpekndsepgsqrikpvfiedanfgroisynaavhahptdiyegstivl 180  
 QY 181 NELNWTSALEDEVFKNREDEPSLLAQVTSATGLARYYPASVPWDSNRTPNKIDYDVR 240  
 DB 181 nelnwtalsaledevfknredepssllaqvtsatglaryypasvpwdsnrtpnkidydvir 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGSVSLTLKLIRTSVSEMLETISDDDFVNVASFNSNAOD 300  
 DB 241 rpwyiogaaspkdmlilvdvsgsvsltlklirtsvsemlletisdddfvnnvasfnag 300  
 QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFECOLLNYSRANCNKIIML 360  
 DB 301 vscfqlhvcanvrnkklvdavnnitakitdykkkfsfafecollnynsrancnkiml 360  
 QY 361 FTDGGEERAQEIFNKYNKDKKVFVRFSGOHNRYERGPIQWMACENKGYIYEIPSGAIR 420  
 DB 361 ftdggeeraqeifnknkdkkvvrfvrfsgohnyergpqlqwmacenkgyyiyeipsigair 420  
 QY 421 INTQEVLDVLRPMVLGADRAKQVQWNTNLYDALEGLVITGTLVPVNTGQFENKTNLK 480  
 DB 421 intqeyldvlrmpvlgadkakqvwntnlydalelglvitgtlvpvntgqfenktnlk 480  
 QY 481 NQILGYMGVDVSLIEDIKRLTPRTLCPNGYIFAIDPNGYVLLHPNLQPK ----- 530  
 DB 481 nqilgymgvdsledikrltprtlcpngyifaidpngyvvllbpnlpqkpgvgiptin 540  
 QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNMIDGESKEKFTTLVKQSDERYI 581  
 DB 531 lrkxrpnlqnpksqepvtldfdaelendikveirnmidgeskektfttlvkqsderiy 600  
 QY 582 DKGRTYTWTPVNGTDYSLALVLPYSPYIYKAKLEETITQARKKKGMKMOSEILKPNDF 641  
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 QY 601 DKGRTYTWTPVNGTDYSLALVLPYSPYIYKAKLEETITQARKKKGMKMOSEILKPNDF 653  
 DB 601 dkgrrtytwtpvngtdyslalvlpyspyiakaleetitoarkkkgmkmoseilkpndf 653  
 QY 642 EESGYTFIAPRDYCNLDKISDNNTTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 701  
 DB 642 eesgytfiaprdydcndlkisdntteflnfefidrktppnpscnadlinrvlldagftn 713  
 QY 654 EESGYTFIAPRDYCNLDKISDNNTTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 761  
 DB 654 elvqnywskqknikgkavrfvtdggitrvypkeagenwoenpetyedsfyrksldndny 773  
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 DB 702 elvqnywskqknikgkavrfvtdggitrvypkeagenwoenpetyedsfyrksldndny 821  
 QY 762 VTTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDP 833  
 DB 762 vttapyfnkspgpayesgimvskaveiyiqglklpavvgikidvnswieftktsirdp 833  
 QY 822 CAGPVCDCRRNSDVMDCVITLDDGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNSVYA 881  
 DB 822 cagpvcdcrrnsdvmcvtildgflmlanhddytqigrffgeidpslmrhlvnsvya 893  
 QY 882 FNKSYDYQVCEPGAAPKQAGHRSAYVSVADILQIGWATAAASIIQQFLLSTFPR 941  
 DB 882 fnksydyqvcepgaapkqaghrsayvsvadilqigwataaasiiqqfllstfpr 953  
 QY 894 FNKSYDYQVCEPGAAPKQAGHRSAYVSVADILQIGWATAAASIIQQFLLSTFPR 953  
 DB 894 fnksydyqvcepgaapkqaghrsayvsvadilqigwataaasiiqqfllstfpr 1001  
 QY 942 LLEAVEMEDDDFTASLSKQSCITEQYQYFPDNDKSPFSGVLDCGNCSPRIFHGKLMNTNL 1001  
 DB 942 lleavemedddftaslskqsciteqyqyfpdndkspfsgvlDCGNCSPRIFHGKLMNTNL 1013  
 QY 1002 IFIMVESKGTCPDTRILLIQAEQTSFGPNCDMVK 1036  
 DB 1014 ifimveskgtcpdtrilliqaeqtsfgpnpcdmvk 1048

Search completed: July 23, 2001, 07:36:44  
 Job time: 485 sec



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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:38:46 ; Search time 37.55 Seconds  
(without alignments)  
555.788 Million cell updates/sec

Title: US-09-397-548-16  
Perfect score: 5443  
Sequence: 1 MAAGCLLALTFLFQSLIG.....RLLIQAEQISDGNPCDMWK 1036

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgnl\_7/ptodata/1/iaa/5A-COMB.pap.\*
- 2: /cgnl\_7/ptodata/1/iaa/5B-COMB.pap.\*
- 3: /cgnl\_7/ptodata/1/iaa/6A-COMB.pap.\*
- 4: /cgnl\_7/ptodata/1/iaa/6B-COMB.pap.\*
- 5: /cgnl\_7/ptodata/1/iaa/PCTUS-COMB.pap.\*
- 6: /cgnl\_7/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5443	100.0	1091	1	US-07-745-206A-25
2	5443	100.0	1091	1	US-08-455-543A-52
3	5443	100.0	1091	2	US-08-223-305C-52
4	5443	100.0	1091	2	US-08-311-363-25
5	5439	99.9	1091	3	US-08-713-118-4
6	5439	99.9	1091	4	US-09-452-007-4
7	5403.5	99.3	1086	1	US-08-455-543A-54
8	5403.5	99.3	1086	2	US-08-223-305C-54
9	5386.5	99.0	1084	1	US-08-455-543A-56
10	5386.5	99.0	1084	2	US-08-223-305C-56
11	5367	98.6	1103	1	US-08-455-543A-53
12	5367	98.6	1103	2	US-08-223-305C-53
13	5347	98.2	1079	1	US-08-455-543A-55
14	5347	98.2	1079	2	US-08-223-305C-55
15	5229.5	96.1	1106	1	US-08-435-675B-5
16	5211.5	95.7	1106	1	US-08-336-257A-8
17	4978.5	91.5	1086	6	5386025-8
18	2581.5	47.4	508	1	US-08-435-675B-6
19	182	3.3	885	3	US-09-074-579-5
20	182	3.3	885	4	US-09-388-774-5
21	159.5	2.9	946	3	US-09-074-579-3
22	159.5	2.9	946	4	US-09-388-774-3
23	154	2.8	903	1	US-08-021-601-12
24	154	2.8	903	1	US-08-082-849B-12
25	154	2.8	903	5	PCT-US94-01624-12
26	152.5	2.8	789	1	US-08-471-033-32
27	152.5	2.8	789	2	US-08-471-044-32

28	152.5	2.8	789	2	US-08-463-483A-32	Sequence 32, Appl
29	152.5	2.8	789	2	US-08-471-046A-32	Sequence 32, Appl
30	152.5	2.8	789	2	US-08-470-566B-32	Sequence 32, Appl
31	152.5	2.8	789	2	US-08-838-219B-4	Sequence 4, Appl
32	152.5	2.8	789	2	US-08-469-334-32	Sequence 32, Appl
33	152.5	2.8	789	3	US-09-300-529-32	Sequence 32, Appl
34	152.5	2.8	789	3	US-09-233-336A-4	Sequence 4, Appl
35	152.5	2.8	789	4	US-09-233-732A-4	Sequence 4, Appl
36	150.5	2.8	789	4	US-08-960-780-6	Sequence 6, Appl
37	150.5	2.8	789	4	US-09-073-898-6	Sequence 6, Appl
38	148.5	2.7	790	4	US-08-960-780-4	Sequence 4, Appl
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40	147.5	2.7	746	2	US-08-838-219B-6	Sequence 6, Appl
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44	145.5	2.7	790	4	US-09-073-898-8	Sequence 8, Appl
45	141.5	2.6	789	1	US-08-471-033-29	Sequence 29, Appl

#### ALIGNMENTS

RESULT 1  
US-07-745-206A-25  
; Sequence 25, Application US/07745206A  
; Patent No. 5429921  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: McCue, Ann  
; APPLICANT: Feldman, Daniel  
; TITLE OF INVENTION: Human Calcium Channel Compositions and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Fitch, Even, Tabin & Flannery  
; STREET: 135 S. LaSalle  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/745,206A  
; FILING DATE: 19910815  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Feder, Scott B  
; REFERENCE/DOCKET NUMBER: 51504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-372-7842  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-745-206A-25

Query Match 100.0%; Score 5443; DB 1; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTFLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTFLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYODLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
DB 61 YEKYODLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIPKVFIEDANFRQISQYQAAVHIPTDIIYEGSTIVL 180  
DB 121 EVVYNAKDDLDPEKNDSEPGSQRIPKVFIEDANFRQISQYQAAVHIPTDIIYEGSTIVL 180  
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DB 181 NELNWTSAIDVEFKKNEEDPSLLWQVFSATGLARYYPASPWVNSRTPNPKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNSNAQD 300  
DB 241 RPWYIOGAASPKDMLILDVSGVSLTLKLRISYSEMLETLSDDDFYNVASFNSNAQD 300  
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLNLYNVRANCKNIIML 360  
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLNLYNVRANCKNIIML 360  
QY 361 FTDGGEERAQELFNKYNKDKVRFVFSVGOHNYERGPIQWACENKGYEYIPISGAIR 420  
DB 361 FTDGGEERAQELFNKYNKDKVRFVFSVGOHNYERGPIQWACENKGYEYIPISGAIR 420  
QY 421 INTQYLDVLGRPMVLADKAKQVQWNTVYLDALBGLVITGLPVENITGOFENKTNLK 480  
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QY 481 NOLILGVNGVDVSLDIKRLTPRTCLPNGYFFAIDPNGYVLLHPNLPKPKSOEPTVL 540  
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QY 541 DFLDAELNDIKVEIRNKMIDGSEKTFRLVKSQDERYDKGNRTYVTPVNGTDYSL 600  
DB 541 DFLDAELNDIKVEIRNKMIDGSEKTFRLVKSQDERYDKGNRTYVTPVNGTDYSL 600  
QY 601 ALVLPYSFYIYKAKLEETIQAORSKKGKMDSETLKPDPNFEESGYFFIAPRDYCNDLKI 660  
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QY 721 FVYTDGGITRVPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
DB 721 FVYTDGGITRVPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MVSQAVIYIYQGLLPAVVGIKIDVNSWIENTFKTSIRDPACAGPCDCKRNSDVMDCVI 840  
DB 781 MVSQAVIYIYQGLLPAVVGIKIDVNSWIENTFKTSIRDPACAGPCDCKRNSDVMDCVI 840  
QY 841 LDGDFLLMANHDDYTNQIGRFGEIDPDLMLRHLNVSIVAFNKSVDYQSVCEPGAAPKQ 900  
DB 841 LDGDFLLMANHDDYTNQIGRFGEIDPDLMLRHLNVSIVAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAWSILQOFLSLTPRLLAEVEMEDDDFTASLSQ 960  
DB 901 GAGHSAYVPSVADILQIGWATAAWSILQOFLSLTPRLLAEVEMEDDDFTASLSQ 960  
QY 961 SCITEQYFFNDNKSFSGLVDCGNCISRFHGEKLMNTNLIIFIMVESKGTGCPCTRLLI 1020  
DB 961 SCITEQYFFNDNKSFSGLVDCGNCISRFHGEKLMNTNLIIFIMVESKGTGCPCTRLLI 1020  
QY 1021 QAEQTSQDGNPCDMVK 1036  
DB 1021 QAEQTSQDGNPCDMVK 1036

RESULT 2  
US-08-455-543A-52  
; Sequence 52, Application US/0845543A

; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,543A  
; FILING DATE: May 31, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/223,305  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-52517  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-455-543A-52

Query Match 100.0%; Score 5443; DB 1; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLATLTFLQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60

Db 1 MAAGCLLALTTLFQSLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Qy 61 YEKYODLYTPNNARQJUEIARDIEKLLNSRKALYSLEAEKQVAAHQRWEDFASN 120  
Db 61 YEKYODLYTPNNARQJUEIARDIEKLLNSRKALYSLEAEKQVAAHQRWEDFASN 120  
Qy 121 EVVYNNAKDDLDPEKNDSEPSQRKPKFIEDANFGROISVQHAHVHPTDIYEGSTIVL 180  
Db 121 EVVYNNAKDDLDPEKNDSEPSQRKPKFIEDANFGROISVQHAHVHPTDIYEGSTIVL 180  
Qy 181 NELNWTLSALDEVFKNREDESLLMQVFGSATGLARYYPASPVWDSNRTPNKIDLYDVR 240  
Db 181 NELNWTLSALDEVFKNREDESLLMQVFGSATGLARYYPASPVWDSNRTPNKIDLYDVR 240  
Qy 241 RPWYIQAASPKMDLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVASFNSAQD 300  
Db 241 RPWYIQAASPKMDLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVASFNSAQD 300  
Qy 301 VSCFOHLVQANRNKVKLDAVNNITAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360  
Db 301 VSCFOHLVQANRNKVKLDAVNNITAKGIDYKKGFSFAFEQLLNYSRANCNKIIML 360  
Qy 361 FTDGGEERAQEIFNKYKNDKVRVFRFVSGOHNYERGPQIOWMACENKGYEYIPEISGAI 420  
Db 361 FTDGGEERAQEIFNKYKNDKVRVFRFVSGOHNYERGPQIOWMACENKGYEYIPEISGAI 420  
Qy 421 INTQBYDLVLRPMVLAGDAKQVQWNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480  
Db 421 INTQBYDLVLRPMVLAGDAKQVQWNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480  
Qy 481 NOLILGVNGVDVSLIEDIKRLPRFTLCNGYFFAIDPNGYVLLHNPQPKPSQEPVTL 540  
Db 481 NOLILGVNGVDVSLIEDIKRLPRFTLCNGYFFAIDPNGYVLLHNPQPKPSQEPVTL 540  
Qy 541 DFLDAELENDIKVEIRNKMIDGSEKFTRLVKSQDERYIDKGNRTYTWPVNGTDSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGSEKFTRLVKSQDERYIDKGNRTYTWPVNGTDSL 600  
Qy 601 ALVLPYTFYIYKAKLETITQAKSKGKMDSETLPKDPNFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIYKAKLETITQAKSKGKMDSETLPKDPNFEESGYTFIAPRDYCNLDKI 660  
Qy 661 SDNNTFELNNEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720  
Db 661 SDNNTFELNNEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720  
Qy 721 FVVTDDGTRVYPKAENWQENPETYEDSFYKSLDNDNVYFTAPYFNKSGPGAYESGI 780  
Db 721 FVVTDDGTRVYPKAENWQENPETYEDSFYKSLDNDNVYFTAPYFNKSGPGAYESGI 780  
Qy 781 MYSKAVEIYIOGKLLKPAVGIKIDVNSWENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVGIKIDVNSWENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840  
Qy 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLRHLNVSIVAFNKSIDYQSVCEPAAAPKQ 900  
Db 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLRHLNVSIVAFNKSIDYQSVCEPAAAPKQ 900  
Qy 901 GAGHRSATVPVADLIQGWATAAWSILOQFLLSLFPRLLEAVEMEDDDFTASLSQK 960  
Db 901 GAGHRSATVPVADLIQGWATAAWSILOQFLLSLFPRLLEAVEMEDDDFTASLSQK 960  
Qy 961 SCITEQTQYFFDNDKSPSGVLDGNCNCSIFHGEKLMNTNLIIFIMVESKGCPCDTRLLI 1020  
Db 961 SCITEQTQYFFDNDKSPSGVLDGNCNCSIFHGEKLMNTNLIIFIMVESKGCPCDTRLLI 1020  
Qy 1021 QAEQTSQGNPCDMVK 1036  
Db 1021 QAEQTSQGNPCDMVK 1036

RESULT 3

US-08-223-305C-52  
; Sequence 52, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-223-305C-52

Query Match 100.0%; Score 5443; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTTLFQSLIGSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
|||||

Db 1 MAAGCLLALTTLTFLFOSLLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
Db 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
QY 121 EVVYNNAKDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYNNAKDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSALEDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
Db 181 NELNWTSALEDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300  
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNINVSANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNINVSANCNKIIML 360  
QY 361 FTDCGEERAQOEIFNKNKDKVRVRESVQGHNYERGIOWMACENKGYIYEIPSGAIR 420  
Db 361 FTDCGEERAQOEIFNKNKDKVRVRESVQGHNYERGIOWMACENKGYIYEIPSGAIR 420  
QY 421 INTOEYLDVLRPMVLAGDKAKQVQWNTNVDLDALEGLVITGTLPVFNITGQFENKTNL 480  
Db 421 INTOEYLDVLRPMVLAGDKAKQVQWNTNVDLDALEGLVITGTLPVFNITGQFENKTNL 480  
QY 481 NQLILGVMGVDVSLIEDIKRTPFTLPCNGYYPFAIDPBGVLLHPNLPKNPKSQBPVTL 540  
Db 481 NQLILGVMGVDVSLIEDIKRTPFTLPCNGYYPFAIDPBGVLLHPNLPKNPKSQBPVTL 540  
QY 541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIIKAKLEETITQARSKKGMKSETLKPONFESSGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIIKAKLEETITQARSKKGMKSETLKPONFESSGYTFIAPRDYCNLDKI 660  
QY 661 SDNTEFLNFEFIDRKPNNPSCNADLINRVLLDAGFTNELVQWYWSKQNKIKGVKAR 720  
Db 661 SDNTEFLNFEFIDRKPNNPSCNADLINRVLLDAGFTNELVQWYWSKQNKIKGVKAR 720  
QY 721 FVYTDGGITRVTPKEAGENWQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVTPKEAGENWQENPETEYDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLLMANHDDVTNQGIFRFGGIDPSLMRHLVNI SYAFNKSVDYQSCVCEPAAAPKQ 900  
Db 841 LDDGGFLLMANHDDVTNQGIFRFGGIDPSLMRHLVNI SYAFNKSVDYQSCVCEPAAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTOYFFDNDKSGSVGLDCGNCRIHFHGEKLMNTNLI FIMVESKGRCPDTRLLI 1020  
Db 961 SCITEQTOYFFDNDKSGSVGLDCGNCRIHFHGEKLMNTNLI FIMVESKGRCPDTRLLI 1020  
QY 1021 QAEQTSQDGNPCDMVK 1036  
Db 1021 QAEQTSQDGNPCDMVK 1036

RESULT 4

US-08-311-363-25

; Sequence 25, Application US/08311363  
; Patent No. 5876558  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: Human Calcium Channel Compositions and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,363  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-51506  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-311-363-25

Query Match 100.0%; Score 5443; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTTLTFLFOSLLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTTLTFLFOSLLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
Db 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
QY 121 EVVYNNAKDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYNNAKDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSALEDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
Db 181 NELNWTSALEDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300  
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNINVSANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNINVSANCNKIIML 360

361 FTGGEERAQIEFNKYNKDKKVRFRFVSGQHNYERGPQIOMACENKGYIYEIPSGAIR 420  
Db 361 FTGGEERAQIEFNKYNKDKKVRFRFVSGQHNYERGPQIOMACENKGYIYEIPSGAIR 420  
QY 421 INTQEVLDVLRPMVLGADKAKOVQNTNLYDLAELGLVITGLPVENITGQENKTNLK 480  
Db 421 INTQEVLDVLRPMVLGADKAKOVQNTNLYDLAELGLVITGLPVENITGQENKTNLK 480  
QY 481 NQILGVMGVDVSDLEIKRLTPFTLCPNGYFAIDPBGVYLLHPNLQPNKPSQEPVTL 540  
Db 481 NQILGVMGVDVSDLEIKRLTPFTLCPNGYFAIDPBGVYLLHPNLQPNKPSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDNFEEGTYFFIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDNFEEGTYFFIAPRDYCNLDKI 660  
QY 661 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNWYWSKQNIKGVKAR 720  
Db 661 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNWYWSKQNIKGVKAR 720  
QY 721 FVYTDGIGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
Db 721 FVYTDGIGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MVSQAVIYIQLKLLPAPVIGIKIDVNSWIENFTKTSIRPCACGPVDCRNSDVMDCVI 840  
Db 781 MVSQAVIYIQLKLLPAPVIGIKIDVNSWIENFTKTSIRPCACGPVDCRNSDVMDCVI 840  
QY 841 LDGSGFLMANHDDYTNQIGRFFGEIDPDLMLRLVNI SVYAFNKSVDYQSVCPGAPKQ 900  
Db 841 LDGSGFLMANHDDYTNQIGRFFGEIDPDLMLRLVNI SVYAFNKSVDYQSVCPGAPKQ 900  
QY 901 GAGHSAYVPSVADIIQIGWATAAASWILQQLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADIIQIGWATAAASWILQQLLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTYFFDNDKSFSGVLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCTCDTRLLI 1020  
Db 961 SCITEQTYFFDNDKSFSGVLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCTCDTRLLI 1020  
QY 1021 QAEQTSQGNPCDMVK 1036  
Db 1021 QAEQTSQGNPCDMVK 1036

## RESULT 5

US-08-713-118-4  
; Sequence 4, Application US/08713118  
; Patent No. 6040436  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suey, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118  
; FILING DATE: 16-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-713-118-4

Query Match 99.9%; Score 5439; DB 3; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLIALTLTFLQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLIALTLTFLQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNARQOLVEIAARDIEKLSNRKSKALVSIALALEAEKVQAAHONREDFASN 120  
Db 61 YEKYQDLYTVEPNARQOLVEIAARDIEKLSNRKSKALVSIALALEAEKVQAAHONREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQAAVHIPDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQAAVHIPDIYEGSTIVL 180  
QY 181 NELNWSALDEVKPKNREEDPSLLMQVFGSATGLARYYPASPVWDNSRTNPKIDLYDVR 240  
Db 181 NELNWSALDEVKPKNREEDPSLLMQVFGSATGLARYYPASPVWDNSRTNPKIDLYDVR 240  
QY 241 RPVYIOGAASPKDMLILVDVSGVSGVGLTKLIRTSVSEMLETSDDDFVNVASFNNAQD 300  
Db 241 RPVYIOGAASPKDMLILVDVSGVSGVGLTKLIRTSVSEMLETSDDDFVNVASFNNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQLLNVSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQLLNVSRANCNKIIML 360  
QY 361 FTGGEERAQIEFNKYNKDKKVRFRFVSGQHNYERGPQIOMACENKGYIYEIPSGAIR 420  
Db 361 FTGGEERAQIEFNKYNKDKKVRFRFVSGQHNYERGPQIOMACENKGYIYEIPSGAIR 420  
QY 421 INTQEVLDVLRPMVLGADKAKOVQNTNLYDLAELGLVITGLPVENITGQENKTNLK 480  
Db 421 INTQEVLDVLRPMVLGADKAKOVQNTNLYDLAELGLVITGLPVENITGQENKTNLK 480  
QY 481 NQILGVMGVDVSDLEIKRLTPFTLCPNGYFAIDPBGVYLLHPNLQPNKPSQEPVTL 540  
Db 481 NQILGVMGVDVSDLEIKRLTPFTLCPNGYFAIDPBGVYLLHPNLQPNKPSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGSGEKTFTLVKSDQERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDNFEEGTYFFIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIIRAKLEETITQARSKKGMKDSSETLKPDNFEEGTYFFIAPRDYCNLDKI 660  
QY 661 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNWYWSKQNIKGVKAR 720  
Db 661 SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNWYWSKQNIKGVKAR 720  
QY 721 FVYTDGIGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780



Db 721 FVTDGGITRVYKPEAGENWQENPEYEDSFYKRSNDNDNYVFTAPIFNKSGPGAYESGI 780  
QY 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP CAGPVCDCKRNSDVMDCVI 840  
Db 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP CAGPVCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAASWLTQOFLSLTFEPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAASWLTQOFLSLTFEPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTYFFDNDKSKFSGLVDCGNCGRIFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
Db 961 SCITEQTYFFDNDKSKFSGLVDCGNCGRIFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
QY 1021 QAEQTS DGNPCDMVK 1036  
Db 1021 QAEQTS DGNPCDMVK 1036

## RESULT 6

US-09-452-007-4  
; Sequence 4, Application US/09452007  
; Patent No. 6140485  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Al Ru  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09452,007  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118  
; FILING DATE: 16-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-452-007-4

Query Match 99.9%; Score 5439; DB 4; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYODLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
Db 61 YEKYODLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
QY 121 EVVYNNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 EVVYNNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEVFKKNREDDPSLLMQVFGSATGLARYYPASVPWVNSRTPNPKIDLYDVR 240  
Db 181 NELNWTSSALDEVFKKNREDDPSLLMQVFGSATGLARYYPASVPWVNSRTPNPKIDLYDVR 240  
QY 241 RPWYTOGAASPKDMLILVDVSGVSGLTCLKIIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPWYTOGAASPKDMLILVDVSGVSGLTCLKIIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGITDYKKGFSFAFEQLLNYSRANCKIIML 360  
Db 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGITDYKKGFSFAFEQLLNYSRANCKIIML 360  
QY 361 FTDGEERAQEIENKYNKDKKRVFRFVSGOHNYERGPIONMACENKGYEYIPIPSIGAIR 420  
Db 361 FTDGEERAQEIENKYNKDKKRVFRFVSGOHNYERGPIONMACENKGYEYIPIPSIGAIR 420  
QY 421 INTOEYLDVLGRPMVLAGDKAKQVQWNTNVYLDALDELGLVITGTLPVFNITGQFENKTLK 480  
Db 421 INTOEYLDVLGRPMVLAGDKAKQVQWNTNVYLDALDELGLVITGTLPVFNITGQFENKTLK 480  
QY 481 NQLILGVMGVDVSLIEDIKRLTPRTLPNGYFFAIDPNGYVLLHPNLPKPKSOEPTVL 540  
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTLPNGYFFAIDPNGYVLLHPNLPKPKSOEPTVL 540  
QY 541 DFLDAELENDIKVEIRNMIDGESGKFTFLVKSODRYDKGNRTVTWTPVNGTDYSL 600  
Db 541 DFLDAELENDIKVEIRNMIDGESGKFTFLVKSODRYDKGNRTVTWTPVNGTDYSL 600  
QY 601 ALVLTYSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFEESGYTFIAPRDCNDLKI 660  
Db 601 ALVLTYSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFEESGYTFIAPRDCNDLKI 660  
QY 661 SDNTEFLNFEIDRKTNNPCNADLINRVLLDAGFTNVLQVYWSKOKNKGKVKAR 720  
Db 661 SDNTEFLNFEIDRKTNNPCNADLINRVLLDAGFTNVLQVYWSKOKNKGKVKAR 720  
QY 721 FVTDGGITRVYKPEAGENWQENPEYEDSFYKRSNDNDNYVFTAPIFNKSGPGAYESGI 780  
Db 721 FVTDGGITRVYKPEAGENWQENPEYEDSFYKRSNDNDNYVFTAPIFNKSGPGAYESGI 780  
QY 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP CAGPVCDCKRNSDVMDCVI 840  
Db 781 MVS KAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP CAGPVCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAASWLTQOFLSLTFEPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAASWLTQOFLSLTFEPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTYFFDNDKSKFSGLVDCGNCGRIFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
Db 961 SCITEQTYFFDNDKSKFSGLVDCGNCGRIFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
QY 1021 QAEQTS DGNPCDMVK 1036  
Db 1021 QAEQTS DGNPCDMVK 1036

RESULT 7  
US-08-455-543A-54  
; Sequence 54, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,543A  
; FILING DATE: May 31, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/223,305  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-52517  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1086 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-455-543A-54

Query Match 99.3%; Score 5403.5; DB 1; Length 1086;

Best Local Similarity 99.5%; Pred. No. 0;									
Matches 1031; Conservative 0; Mismatches 0; Indels 5; Gaps 1;									
QY	1	MAAGCLLALTLTLFQSL	IGPSSSEPPPSAVTIKSWDK	QMOEDLVTLAKTASGYNQLVDI	60				
DB	1	MAAGCLLALTLTLFQSL	IGPSSSEPPPSAVTIKSWDK	QMOEDLVTLAKTASGYNQLVDI	60				
QY	61	YKQYDLYTVEPNARQ	LVIAARDIEKLLSNRSKALVSLA	LEAEKVAQAAHOWREDFASN	120				
DB	61	YKQYDLYTVEPNARQ	LVIAARDIEKLLSNRSKALVSLA	LEAEKVAQAAHOWREDFASN	120				
QY	121	EVVYNAKDDLDPKND	SEPGSQRIPVFIEDANFGQIS	YQHAHVHTPTDIYEGSTVL	180				
DB	121	EVVYNAKDDLDPKND	SEPGSQRIPVFIEDANFGQIS	YQHAHVHTPTDIYEGSTVL	180				
QY	181	NELNWTSDALDEVFK	KNEEDPSLLQVFGSATGLARY	PASPWDNSRTPNKIDLYDVR	240				
DB	181	NELNWTSDALDEVFK	KNEEDPSLLQVFGSATGLARY	PASPWDNSRTPNKIDLYDVR	240				
QY	241	RPWYIQGAASPKDML	ILVDVSGSVGLTLKIRTSV	SEMLETLSDDDFVNVASNSNAQD	300				
DB	241	RPWYIQGAASPKDML	ILVDVSGSVGLTLKIRTSV	SEMLETLSDDDFVNVASNSNAQD	300				
QY	301	VSCFOHLVQANVRN	KVYLKDAVNITAGITDYKKG	SFAFEQLLNKNSRANCKIIML	360				
DB	301	VSCFOHLVQANVRN	KVYLKDAVNITAGITDYKKG	SFAFEQLLNKNSRANCKIIML	360				
QY	361	FTDGEERAQEIFNK	YNKDKKRVFRFVSQGHNYER	GPIQMACENKGYIYEIFSIGAIR	420				
DB	361	FTDGEERAQEIFNK	YNKDKKRVFRFVSQGHNYER	GPIQMACENKGYIYEIFSIGAIR	420				
QY	421	INTQEYLDVLGRPM	VLAGDRAKQVQWNTNVLDA	LEGLVITGTLPVNITQGFENKLNK	480				
DB	421	INTQEYLDVLGRPM	VLAGDRAKQVQWNTNVLDA	LEGLVITGTLPVNITQGFENKLNK	480				
QY	481	NQLILGVMGVDVSL	EIKRLTPRETLCPNGYFPAID	PNGVYLLHPNLPKPKSOEPTVL	540				
DB	481	NQLILGVMGVDVSL	EIKRLTPRETLCPNGYFPAID	PNGVYLLHPNLPKPKSOEPTVL	540				
QY	541	DFLDAELENDIKV	EIRNMIDGESGKTFRTLVK	SQDERYIDKGNRTYTTPVNGTDYSL	600				
DB	536	DFLDAELENDIKV	EIRNMIDGESGKTFRTLVK	SQDERYIDKGNRTYTTPVNGTDYSL	595				
QY	601	ALVLPYTSFYIYI	KAKLEETIQARSKKGMKD	SETLPDNPFEESGYTFIAPRDYCNLDKI	660				
DB	596	ALVLPYTSFYIYI	KAKLEETIQARSKKGMKD	SETLPDNPFEESGYTFIAPRDYCNLDKI	655				
QY	661	SDNTEFLANFNE	IDRKTNNPCNADLINRVLL	DAGFTNELVQNTWSKOKNKGVKAR	720				
DB	656	SDNTEFLANFNE	IDRKTNNPCNADLINRVLL	DAGFTNELVQNTWSKOKNKGVKAR	715				
QY	721	FVYTDGGITRVYP	KEAGENQENPETYEDSFYK	SRSLDNDNYFTAPYFNKSGPGAYESGI	780				
DB	716	FVYTDGGITRVYP	KEAGENQENPETYEDSFYK	SRSLDNDNYFTAPYFNKSGPGAYESGI	775				
QY	781	MVSKAVEIYQGLK	LPVAVGIIKIDVNSWIENFT	KTSIRDPACGPDCKRNSDVMDCVI	840				
DB	776	MVSKAVEIYQGLK	LPVAVGIIKIDVNSWIENFT	KTSIRDPACGPDCKRNSDVMDCVI	835				
QY	841	LDGGFLLMANHDD	YTNOIGRFCEIDPSLMRHL	VNTSVYAFNKSVDYQSVCEPGAAPKQ	900				
DB	836	LDGGFLLMANHDD	YTNOIGRFCEIDPSLMRHL	VNTSVYAFNKSVDYQSVCEPGAAPKQ	895				
QY	901	GAGHRSAYVPSAD	ILQIGMWATAAAMSILQO	FLSLTFPRLLEAVEMEDDDFTASLSKQ	960				
DB	896	GAGHRSAYVPSAD	ILQIGMWATAAAMSILQO	FLSLTFPRLLEAVEMEDDDFTASLSKQ	955				
QY	961	SCITEQTYFFDND	SKSFGVLDGCGNCSRI	PHGKLMNTNLIIFIMVSKGTCPCDTRLII	1020				
DB	956	SCITEQTYFFDND	SKSFGVLDGCGNCSRI	PHGKLMNTNLIIFIMVSKGTCPCDTRLII	1015				
QY	1021	QAEQTSQGNPCD	MAVK 1036						

Db 1016 QAEQTS DSGNPNCDMVK 1031

RESULT 8

US-08-223-305C-54

; Sequence 54, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; City: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/223,305C

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/176,899

; FILING DATE: 04-APR-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 52516 (P519739)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)238-0999

; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 54:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1086 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: Internal

US-08-223-305C-54

Query Match

Best Local Similarity 99.3%; Score 5403.5; DB 2; Length 1086;

Pred. No. 0;

	Matches	1031;	Conservative	0;	Mismatches	0;	Indels	5;	Gaps	1;				
QY	1	MAAGCLLALTTLT	FQSLLIGPSEEP	PSAVTIKSWYDKMQ	EDLVTLAKTAGSV	QNLV	DI	60						
Db	1	MAAGCLLALTTLT	FQSLLIGPSEEP	PSAVTIKSWYDKMQ	EDLVTLAKTAGSV	QNLV	DI	60						
QY	61	YEKYQDLTYV	EPNNARQLVEIA	ARDIEKLLSNRS	KALVSALAEK	VQAAH	QWREDFASN	120						
Db	61	YEKYQDLTYV	EPNNARQLVEIA	ARDIEKLLSNRS	KALVSALAEK	VQAAH	QWREDFASN	120						
QY	121	EVYYNAKDDLD	PEKNDSEPGSQ	RKPKVPFIEDAN	FGROI	SYQOHA	AVHPTDIE	BGSGTIVL	180					
Db	121	EVYYNAKDDLD	PEKNDSEPGSQ	RKPKVPFIEDAN	FGROI	SYQOHA	AVHPTDIE	BGSGTIVL	180					
QY	181	NELNWT	SALDEVFKKN	REDDPSLLWQ	VFGSATGL	ARYYPAS	PWVNSRTPNK	IDLDYDVR	240					
Db	181	NELNWT	SALDEVFKKN	REDDPSLLWQ	VFGSATGL	ARYYPAS	PWVNSRTPNK	IDLDYDVR	240					
QY	241	RPWYIOGA	ASPDKMLIL	VDVSGVSGT	LKLR	TSVSEMLET	LSDDDFVNV	AFSNSNAQ	300					
Db	241	RPWYIOGA	ASPDKMLIL	VDVSGVSGT	LKLR	TSVSEMLET	LSDDDFVNV	AFSNSNAQ	300					
QY	301	VSCFQHL	YQANVRNKK	VLKDAVNNIT	AKGIDYK	KGFSFAF	QOLLNYSR	ANCNKIIML	360					
Db	301	VSCFQHL	YQANVRNKK	VLKDAVNNIT	AKGIDYK	KGFSFAF	QOLLNYSR	ANCNKIIML	360					
QY	361	FTDGE	ERAQEIFN	KYKDKVR	FPFSVQ	HNRYERG	PIQWMACEN	KGYEIP	SIGAIR	420				
Db	361	FTDGE	ERAQEIFN	KYKDKVR	FPFSVQ	HNRYERG	PIQWMACEN	KGYEIP	SIGAIR	420				
QY	421	INTQEY	LDVLGRPM	VLAGDKAK	QVQWNT	YLDAL	ELGLVITGT	LPVNTIG	QFENKYNLK	480				
Db	421	INTQEY	LDVLGRPM	VLAGDKAK	QVQWNT	YLDAL	ELGLVITGT	LPVNTIG	QFENKYNLK	480				
QY	481	NQLIL	GVMGVDV	SLEDIKRL	TPFTLCP	NGYFAID	PNGYVLL	HPNLQPNK	SOEPTVL	540				
Db	481	NQLIL	GVMGVDV	SLEDIKRL	TPFTLCP	NGYFAID	PNGYVLL	HPNLQPNK	SOEPTVL	540				
QY	541	DFLDA	ELENDIK	VEIRNKM	DGESG	EKTRTLVK	SODERYIDK	GNRTYTW	TPVNGT	DYSL	600			
Db	536	DFLDA	ELENDIK	VEIRNKM	DGESG	EKTRTLVK	SODERYIDK	GNRTYTW	TPVNGT	DYSL	595			
QY	601	ALVLP	TSFYIY	YKAKLE	ETITQ	ARSKKG	KMDSETL	KPDNFE	ESGYTFT	IAPR	CNDLKI	660		
Db	596	ALVLP	TSFYIY	YKAKLE	ETITQ	ARSKKG	KMDSETL	KPDNFE	ESGYTFT	IAPR	CNDLKI	655		
QY	661	SDNTE	FLNFEF	IDRKT	PNNP	SCNADLIN	RVLLDAG	FTNELV	QYWSKQ	KNIKGVKAR	720			
Db	656	SDNTE	FLNFEF	IDRKT	PNNP	SCNADLIN	RVLLDAG	FTNELV	QYWSKQ	KNIKGVKAR	715			
QY	721	FVVT	DGGITRVY	PKEAGEN	QWNPETY	EDSFYKRS	LNDNNTYV	ETAPYFNK	SGPGAY	ESGI	780			
Db	716	FVVT	DGGITRVY	PKEAGEN	QWNPETY	EDSFYKRS	LNDNNTYV	ETAPYFNK	SGPGAY	ESGI	775			
QY	781	MYSKA	VEIYIOG	KLKPAV	VYTKID	VNSIENFT	KTSIRD	PCAGP	VCDCR	NSDVMDCVI	840			
Db	776	MYSKA	VEIYIOG	KLKPAV	VYTKID	VNSIENFT	KTSIRD	PCAGP	VCDCR	NSDVMDCVI	835			
QY	841	LDDG	GFLMAN	HDDYTN	QIGR	FFGEID	PSLMRHL	NISVYAF	NKSVDY	OSVCEP	GGAAPKQ	900		
Db	836	LDDG	GFLMAN	HDDYTN	QIGR	FFGEID	PSLMRHL	NISVYAF	NKSVDY	OSVCEP	GGAAPKQ	895		
QY	901	GAGH	SAYVPS	VADILQ	IGW	WATAA	WSILQ	QFLLSL	TPR	LEAVEM	EDDDFTAS	LSKQ	960	
Db	896	GAGH	SAYVPS	VADILQ	IGW	WATAA	WSILQ	QFLLSL	TPR	LEAVEM	EDDDFTAS	LSKQ	955	
QY	961	SCITE	QVFF	FNDSK	SFSG	VLDG	CNCSR	IFHG	CKLM	NNTLIF	IMVESK	GTCPD	TRLLI	1020
Db	956	SCITE	QVFF	FNDSK	SFSG	VLDG	CNCSR	IFHG	CKLM	NNTLIF	IMVESK	GTCPD	TRLLI	1015
QY	1021	QAEQ	TS	DSGN	PNC	DMVK		1036						
Db	1016	QAEQ	TS	DSGN	PNC	DMVK		1031						

RESULT 9  
US-08-455-543A-56  
Sequence 56, Application US/08455543A  
Patent No. 5792846  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1084 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-56

Query Match 99.0%; Score 5386.5; DB 1; Length 1084;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;  
Qy 1 MAAGCLLALTLTTLFOSLLIGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTLTTLFOSLLIGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60  
Qy 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120  
Db 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120  
Qy 121 EYVYNKADDDLPKNDSEPGSQRIKPFIEDANFGRIQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 EYVYNKADDDLPKNDSEPGSQRIKPFIEDANFGRIQISYQHAHVHPTDIYEGSTIVL 180  
Qy 181 NELNWTALDEYFKKNREDDPSLLAQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
Db 181 NELNWTALDEYFKKNREDDPSLLAQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
Qy 241 RPYIQQGAASPKDMLILVDVSGVSLTLKLIKRTSVSEMLETSLDDDFVNVASFNSNAO 300  
Db 241 RPYIQQGAASPKDMLILVDVSGVSLTLKLIKRTSVSEMLETSLDDDFVNVASFNSNAO 300  
Qy 301 VSCFQHLVQANVRNKKVLDAVNNTAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDAVNNTAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360  
Qy 361 FTDGGEERAQEIFNKYKDKKRVFRFSGVQHNRYERGPTQWACENKGYIYEPSIGAIR 420  
Db 361 FTDGGEERAQEIFNKYKDKKRVFRFSGVQHNRYERGPTQWACENKGYIYEPSIGAIR 420  
Qy 421 INTQEYLDVLGRPMVLGADKAKOVQNTNVLDALGLVITGLPVFNITGQFENKTNL 480  
Db 421 INTQEYLDVLGRPMVLGADKAKOVQNTNVLDALGLVITGLPVFNITGQFENKTNL 480  
Qy 481 NQILGVMGVDVSLDIKRLTPRTILCPNGIYFAIDPNGVYLHPNLPKNPKSQBPVTL 540  
Db 481 NQILGVMGVDVSLDIKRLTPRTILCPNGIYFAIDPNGVYLHPNLPKNPKSQBPVTL 540  
Qy 541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTPVNGTDYSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTPVNGTDYSL 600  
Qy 601 ALVLPYSFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNLKI 660  
Db 601 ALVLPYSFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNLKI 660  
Qy 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSKOKNKGKVKAR 720  
Db 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSKOKNKGKVKAR 720  
Qy 721 FVTDGGITRVYPKEAGENQENPETEYDSFYKBSLNDNVFTAPYFNKSGPGAYESGI 780  
Db 721 FVTDGGITRVYPKEAGENQENPETEYDSFYKBSLNDNVFTAPYFNKSGPGAYESGI 780  
Qy 773 FVTDGGITRVYPKEAGENQENPETEYDSFYKBSLNDNVFTAPYFNKSGPGAYESGI 773  
Db 773 FVTDGGITRVYPKEAGENQENPETEYDSFYKBSLNDNVFTAPYFNKSGPGAYESGI 773  
Qy 781 MYSKAVEIYIQQKLLKPAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
Db 781 MYSKAVEIYIQQKLLKPAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
Qy 841 LDDGGFLMANHDDYTNOIGRFFGEIDPDLMRHLNVISVYAFNKSIDYQSCVCEGAAAPKQ 900  
Db 841 LDDGGFLMANHDDYTNOIGRFFGEIDPDLMRHLNVISVYAFNKSIDYQSCVCEGAAAPKQ 900  
Qy 893 LDDGGFLMANHDDYTNOIGRFFGEIDPDLMRHLNVISVYAFNKSIDYQSCVCEGAAAPKQ 893  
Db 893 LDDGGFLMANHDDYTNOIGRFFGEIDPDLMRHLNVISVYAFNKSIDYQSCVCEGAAAPKQ 893  
Qy 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFPRLLLEAVEMDDDFASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFPRLLLEAVEMDDDFASLSKQ 960  
Qy 953 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFPRLLLEAVEMDDDFASLSKQ 953  
Db 953 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFPRLLLEAVEMDDDFASLSKQ 953  
Qy 961 SCITEQTOYFFDNDKSKFSGLVDCGNCNRIFHGEKLMNTNLIIFIMVESKGTCPDCTRLLI 1020  
Db 961 SCITEQTOYFFDNDKSKFSGLVDCGNCNRIFHGEKLMNTNLIIFIMVESKGTCPDCTRLLI 1020  
Qy 954 SCITEQTOYFFDNDKSKFSGLVDCGNCNRIFHGEKLMNTNLIIFIMVESKGTCPDCTRLLI 1013  
Db 954 SCITEQTOYFFDNDKSKFSGLVDCGNCNRIFHGEKLMNTNLIIFIMVESKGTCPDCTRLLI 1013  
Qy 1021 QAEQTS DGP N FCDMYK 1036  
Db 1021 QAEQTS DGP N FCDMYK 1036

Db 1014 QAEQTS DGNPCDVK 1029

## RESULT 10

US-08-223-305C-56

; Sequence 56, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/223,305C

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/176,899

; FILING DATE: 04-APR-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 52516 (P519739)

; TELEPHONE: (619)238-0999

; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 56:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1084 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

US-08-223-305C-56

Query Match 99.0%; Score 5386.5; DB 2; Length 1084;

Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1028; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTTLTFLQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNLVDI 60  
DB 1 MAAGCLLALTTLTFLQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNLVDI 60  
QY 61 YEKYQDLTYVEPNNAQVVEIAARDIEKLLSNRSLKALVSLAEAEKVAQAAHQWREFASN 120  
DB 61 YEKYQDLTYVEPNNAQVVEIAARDIEKLLSNRSLKALVSLAEAEKVAQAAHQWREFASN 120  
QY 121 EYVYNAKDDLDPEKNDSPGSGORIKPVFIEDANFGROIYSYQHAHVHPTDIYEGSTIVL 180  
DB 121 EYVYNAKDDLDPEKNDSPGSGORIKPVFIEDANFGROIYSYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240  
DB 181 NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKLTISVSEMLETISDDDFYNVASFNSNAQD 300  
DB 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKLTISVSEMLETISDDDFYNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITYKKGFSAFEOLLNYSRANCKNIIML 360  
DB 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITYKKGFSAFEOLLNYSRANCKNIIML 360  
QY 361 FTDGGEERAQEIFNKYKDKVFRFSGQHNRYERGIQWMACENKGYEYIPEISGAIR 420  
DB 361 FTDGGEERAQEIFNKYKDKVFRFSGQHNRYERGIQWMACENKGYEYIPEISGAIR 420  
QY 421 INTQEYLDVLGRPMVLGAKAQVQNTNYLDALGLVITGTLPVFNITGOFENKTLK 480  
DB 421 INTQEYLDVLGRPMVLGAKAQVQNTNYLDALGLVITGTLPVFNITGOFENKTLK 480  
QY 481 NOLILGVMGVDVSLIEDIKRLTPRFLCPNGYFAIDPNGYVLLHPNLQPKNSQBPVTL 540  
DB 481 NOLILGVMGVDVSLIEDIKRLTPRFLCPNGYFAIDPNGYVLLHPNLQPKNSQBPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600  
DB 541 DFLDAELENDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLTYSFYIYKAKLEETITQARSKKGMKDSITLKPDPNFESGYFTIAPRDCNDLKI 660  
DB 601 ALVLTYSFYIYKAKLEETITQARSKKGMKDSITLKPDPNFESGYFTIAPRDCNDLKI 660  
QY 661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNKGVKAR 720  
DB 661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNKGVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
DB 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIQGLLKPAVVGKIDVNSIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
DB 781 MYSKAVEIYIQGLLKPAVVGKIDVNSIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDVTNOIGRFFGEIDPSLMRHLNYSVYAFNKSVDYOSVCEPGAAPQ 900  
DB 841 LDDGGFLMANHDDVTNOIGRFFGEIDPSLMRHLNYSVYAFNKSVDYOSVCEPGAAPQ 900  
QY 901 GAGHRSAYVPSVADILIQGWATAAASLIQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
DB 901 GAGHRSAYVPSVADILIQGWATAAASLIQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTQYFFDNDKSPFSGVLDGCNCSRFHGEKMLNTNLIIFIMVESKGTCPDCTRLLI 1020  
DB 961 SCITEQTQYFFDNDKSPFSGVLDGCNCSRFHGEKMLNTNLIIFIMVESKGTCPDCTRLLI 1020  
QY 1021 QAEQTS DGNPCDVK 1036  
DB 1021 QAEQTS DGNPCDVK 1036

Db 1014 QAEQTSDBNCPDMVK 1029

RESULT 11

US-08-455-543A-53

; Sequence 53, Application US/08455543A

; Patent No. 5792846

GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; METHODS

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,543A

; FILING DATE: May 31, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/223,305

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/176,899

; FILING DATE: 04-APR-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 6362-52517

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)238-0999

; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1103 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-455-543A-53

Query Match	98.6%;	Score 5367;	DB 1;	Length 1103;
Best Local Similarity	97.4%;	Pred. No. 0;		
Matches 1028;	Conservative	0;	Mismatches	1; Indels 26; Gaps 2;
QY	1	MAAGCLLALTLTQSLIGPSSEPPFSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI	60	
DB	1	MAAGCLLALTLTQSLIGPSSEPPFSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI	60	
QY	61	YEKYODLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVAHAHQWREDFASN	120	
DB	61	YEKYODLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVAHAHQWREDFASN	120	
QY	121	EVVYVNAKDDLDPEKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL	180	
DB	121	EVVYVNAKDDLDPEKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL	180	
QY	181	NELNMTSALDEYFKKNREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR	240	
DB	181	NELNMTSALDEYFKKNREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR	240	
QY	241	RPWYIOGAASPKDMLILVDVSGVSGTLTKLIRTSYSEMLETLSDDDFVNVASFNSNAOD	300	
DB	241	RPWYIOGAASPKDMLILVDVSGVSGTLTKLIRTSYSEMLETLSDDDFVNVASFNSNAOD	300	
QY	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEOQLLNNYSRANCNKLIML	360	
DB	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEOQLLNNYSRANCNKLIML	360	
QY	361	FTDGEERAQEIFNKYKDKKVRFRFSVGOHNVERGPIOWMACENKGYEIPSGAIR	420	
DB	361	FTDGEERAQEIFNKYKDKKVRFRFSVGOHNVERGPIOWMACENKGYEIPSGAIR	420	
QY	421	INTQEYLDVLGRPMVLGADKAKQVQNTNVYLDALGLVITGTLPVENITGQENKTNLK	480	
DB	421	INTQEYLDVLGRPMVLGADKAKQVQNTNVYLDALGLVITGTLPVENITGQENKTNLK	480	
QY	481	NQILGVMGVDSVLEDIKRLTPRTLCPNGYYFAIDPNGYVLLHPNLOPK	530	
DB	481	NQILGVMGVDSVLEDIKRLTPRTLCPNGYYFAIDPNGYVLLHPNLOPK	530	
QY	531	-----NPKSQPPVTLDFDAELENDIKVEIRNKMIDGSEKTFRTLKVSQDERYI	581	
DB	531	-----NPKSQPPVTLDFDAELENDIKVEIRNKMIDGSEKTFRTLKVSQDERYI	581	
QY	541	LRKRRNPIONPKSQEPVTLDFDAELENDIKVEIRNKMIDGSEKTFRTLKVSQDERYI	600	
DB	541	LRKRRNPIONPKSQEPVTLDFDAELENDIKVEIRNKMIDGSEKTFRTLKVSQDERYI	600	
QY	582	DKNRTYTTPVNGTDYSLALVPTYFYIYKAKLEETITQARSKKGMKSEITLKPDNF	641	
DB	582	DKNRTYTTPVNGTDYSLALVPTYFYIYKAKLEETITQARSKKGMKSEITLKPDNF	641	
QY	601	DKNRTYTTPVNGTDYSLALVPTYFYIYKAKLEETITQARY	653	
DB	601	DKNRTYTTPVNGTDYSLALVPTYFYIYKAKLEETITQARY	653	
QY	642	EESGYTFIAPRDYCNLDKISDNTEFFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN	701	
DB	642	EESGYTFIAPRDYCNLDKISDNTEFFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN	701	
QY	654	EESGYTFIAPRDYCNLDKISDNTEFFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN	713	
DB	654	EESGYTFIAPRDYCNLDKISDNTEFFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTN	713	
QY	702	ELVQNYWSKQNKIKGVKARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSILDNDNY	761	
DB	702	ELVQNYWSKQNKIKGVKARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSILDNDNY	761	
QY	714	ELVQNYWSKQNKIKGVKARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSILDNDNY	773	
DB	714	ELVQNYWSKQNKIKGVKARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSILDNDNY	773	
QY	762	VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP	821	
DB	762	VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP	821	
QY	774	VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP	833	
DB	774	VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP	833	
QY	822	CAGPYVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYA	881	
DB	822	CAGPYVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYA	881	
QY	834	CAGPYVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYA	893	
DB	834	CAGPYVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYA	893	
QY	882	FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSITFFR	941	
DB	882	FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSITFFR	941	
QY	894	FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSITFFR	953	
DB	894	FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSITFFR	953	
QY	942	LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDKSKFSFGLDCGNCSTRIFHGEKLMNTNL	1001	
DB	942	LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDKSKFSFGLDCGNCSTRIFHGEKLMNTNL	1001	
QY	954	LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDKSKFSFGLDCGNCSTRIFHGEKLMNTNL	1013	
DB	954	LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDKSKFSFGLDCGNCSTRIFHGEKLMNTNL	1013	

QY 1002 IFIMVSKGTCPCDRLLIQAEQTS DGGPNPCDMVK 1036  
Db 1014 IFIMVSKGTCPCDRLLIQAEQTS DGGPNPCDMVK 1048

## RESULT 12

US-08-223-305C-53  
Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-53

Query Match 98.6%; Score 5367; DB 2; Length 1103;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1028; Conservative 0; Mismatches 1; Indels 26; Gaps 2;  
QY 1 MAAGCLALTLTFLQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
Db 1 MAAGCLALTLTFLQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
QY 61 YEKYQDLYTVEPNARQLVEAARDIEKLLSNRSKALVSLALEAEKVQAAHWRDFAFN 120  
Db 61 YEKYQDLYTVEPNARQLVEAARDIEKLLSNRSKALVSLALEAEKVQAAHWRDFAFN 120  
QY 121 EYVYNKADDDLPKNDSEPGSQRKPKVFIEDANFGROIISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EYVYNKADDDLPKNDSEPGSQRKPKVFIEDANFGROIISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWT SALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
Db 181 NELNWT SALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTCLKIRTSSVSEMLETSLDDDFNVASFNQAQD 300  
Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTCLKIRTSSVSEMLETSLDDDFNVASFNQAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCKNIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCKNIIML 360  
QY 361 FTDGEERAQEIFNKYKNDKKVRPRFSVGOHNYERGPDIQMACENKGYEIPISGAIR 420  
Db 361 FTDGEERAQEIFNKYKNDKKVRPRFSVGOHNYERGPDIQMACENKGYEIPISGAIR 420  
QY 421 INTQEYLDVLGRPMVLADKAKOVQNTNVDLDELGLVITGLPVENITGOFENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLADKAKOVQNTNVDLDELGLVITGLPVENITGOFENKTNLK 480  
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPK----- 530  
Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKPGVGIPTIN 540  
QY 531 -----NPKSQBPVTLDFDAELENDIKVEIRKMKIDGESGKTPRTLKVSQDERYI 581  
Db 541 LKRRPNIQNPKSQBPVTLDFDAELENDIKVEIRKMKIDGESGKTPRTLKVSQDERYI 600  
QY 582 DKGRTYTWTPVNGTDYSLALVLPYSEYIKAKLEETITQARSKKMKDSSETLKPONE 641  
Db 601 DKGRTYTWTPVNGTDYSLALVLPYSEYIKAKLEETITQARSKKMKDSSETLKPONE 653  
QY 642 EESGYTFIAPDYCNDLKI SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 701  
Db 654 EESGYTFIAPDYCNDLKI SDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 713  
QY 702 ELVQYWSKQKNIKGVKARFVVDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNY 761  
Db 714 ELVQYWSKQKNIKGVKARFVVDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNY 773  
QY 762 VETAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWENETKT SIRDP 821  
Db 774 VETAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWENETKT SIRDP 833  
QY 822 CAGPVCDCKRNSDVMDCVLLDDGGFLLMANHDDYTNQIGRFFEGEIDPSLMRHLVNI SYA 881  
Db 834 CAGPVCDCKRNSDVMDCVLLDDGGFLLMANHDDYTNQIGRFFEGEIDPSLMRHLVNI SYA 893  
QY 882 FNKSYDYQSVCEPGAAPKQAGHRSAIYVPSVADIQIGWATAAASLIQQFLLSLTTPR 941  
Db 894 FNKSYDYQSVCEPGAAPKQAGHRSAIYVPSVADIQIGWATAAASLIQQFLLSLTTPR 953  
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTOYEFNDNSFSFGLDCGNCRIFFHGEKLMNTNL 1001  
Db 954 LLEAVEMEDDDFTASLSKQSCITEQTOYEFNDNSFSFGLDCGNCRIFFHGEKLMNTNL 1013  
QY 1002 IFIMVSKGTCPCDRLLIQAEQTS DGGPNPCDMVK 1036



Db 1014 IFIMVESKGTCPDTRLLIQAEQTSDBGNPCDMVK 1048  
|||||  
RESULT 13  
US-08-455-543A-55  
; Sequence 55, Application US/0845543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08455,543A  
; FILING DATE: May 31, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/223,305  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-52517  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-455-543A-55

Query Match		98.2%	Score 5347;	DB 1;	Length 1079;
Best Local Similarity		98.7%	Pred. No. 0;		
Matches 1023;		Conservative	0;	Mismatches 1;	Indels 12;
					Gaps 2;
Qy	1	MAAGCLLALTLTLFOSLLIGSPSEPPFP	SAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60	
Db	1	MAAGCLLALTLTLFOSLLIGSPSEPPFP	SAVTIKSWDKMQEDLVTLAKTASGVNQLVDI	60	
Qy	61	YEKYQDLYTVEPNNAQOLVEIAARDIEK	LLSNRSKALVSLALEAEKVQAAHQRDEFSN	120	
Db	61	YEKYQDLYTVEPNNAQOLVEIAARDIEK	LLSNRSKALVSLALEAEKVQAAHQRDEFSN	120	
Qy	121	EVVYNKADDDLDPEKNDSEPGSQRIKPV	FIEDANFGRQISYOHAAVHIPTDIYEGSTIVL	180	
Db	121	EVVYNKADDDLDPEKNDSEPGSQRIKPV	FIEDANFGRQISYOHAAVHIPTDIYEGSTIVL	180	
Qy	181	NELNWTSSALDEVEFKKREEDPSLLMQV	FGSATGLARYYPASPWVDSNRTPNKIDLYDVR	240	
Db	181	NELNWTSSALDEVEFKKREEDPSLLMQV	FGSATGLARYYPASPWVDSNRTPNKIDLYDVR	240	
Qy	241	RPWYIQAASPKDMLILVDVSGVSLTTLK	LIRTSVSEMLETSSDDDFVNVASFNSNAOD	300	
Db	241	RPWYIQAASPKDMLILVDVSGVSLTTLK	LIRTSVSEMLETSSDDDFVNVASFNSNAOD	300	
Qy	301	VSCFQHLVQANVRNKKVLDKAVNNITAK	ITIDYKGFSAFAPOLLNRYNSRANCNKIIML	360	
Db	301	VSCFQHLVQANVRNKKVLDKAVNNITAK	ITIDYKGFSAFAPOLLNRYNSRANCNKIIML	360	
Qy	361	FTDGGEEAQAEIFNKYNKDKYVFRFSY	GHOHNERGPIOWMACENKGYEYIETPSIGAIR	420	
Db	361	FTDGGEEAQAEIFNKYNKDKYVFRFSY	GHOHNERGPIOWMACENKGYEYIETPSIGAIR	420	
Qy	421	INTQEYLDVLRPMVLGADKAKQVQNTN	YLDALGLVITGTPLVFNITGQENKTNLK	480	
Db	421	INTQEYLDVLRPMVLGADKAKQVQNTN	YLDALGLVITGTPLVFNITGQENKTNLK	480	
Qy	481	NQILGVMGVDVSLEDIKRLTPRTILCP	NGYYPADPNQVYLLHLPNPKNSQEPVTL	540	
Db	481	NQILGVMGVDVSLEDIKRLTPRTILCP	NGYYPADPNQVYLLHLPNPKNSQEPVTL	540	
Qy	541	DFLDAELENDIKVEIRNKMIDGESGKFT	RLVKSDERYIDKGNRTYTTPVNGTDYSL	600	
Db	541	DFLDAELENDIKVEIRNKMIDGESGKFT	RLVKSDERYIDKGNRTYTTPVNGTDYSL	600	
Qy	595	DFLDAELENDIKVEIRNKMIDGESGKFT	RLVKSDERYIDKGNRTYTTPVNGTDYSL	595	
Db	595	DFLDAELENDIKVEIRNKMIDGESGKFT	RLVKSDERYIDKGNRTYTTPVNGTDYSL	595	
Qy	601	ALVLPYTFYIIKAKLEETITQARSKK	MKDSETLKPDNFESGYTTFIAPROYCNDLKI	660	
Db	596	ALVLPYTFYIIKAKLEETITQARSKK	MKDSETLKPDNFESGYTTFIAPROYCNDLKI	648	
Qy	661	SDNTEFLNFEIDRKTNNPNSCNADLIN	RVLDDAGFTNQLVQVWYNSKOKNKGVKAR	720	
Db	649	SDNTEFLNFEIDRKTNNPNSCNADLIN	RVLDDAGFTNQLVQVWYNSKOKNKGVKAR	708	
Qy	721	FVYTDGGITRVYKEAGENQENPETEDS	FYKRSLDNDNVTFTAPYFNKSGPGAYESGI	780	
Db	709	FVYTDGGITRVYKEAGENQENPETEDS	FYKRSLDNDNVTFTAPYFNKSGPGAYESGI	768	
Qy	781	MVSKAVEIYIQGKLLKPAVVGVGKIDV	NSWIENFTKTSIRDPACGVCDCRNSDVMDCVI	840	
Db	769	MVSKAVEIYIQGKLLKPAVVGVGKIDV	NSWIENFTKTSIRDPACGVCDCRNSDVMDCVI	828	
Qy	841	LDDGGFLLMANHDDYTQIGRFFGEIDP	SLMRHLVNSVYAFNKSXYQSVCEPGAAPKQ	900	
Db	829	LDDGGFLLMANHDDYTQIGRFFGEIDP	SLMRHLVNSVYAFNKSXYQSVCEPGAAPKQ	888	
Qy	901	GAGHRSAYVPSVADILQIGMWATAA	WSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ	960	
Db	889	GAGHRSAYVPSVADILQIGMWATAA	WSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ	948	
Qy	961	SCITEQTYQFFDNDKSKFSGLDCGNC	SRIPHGBKLMNTNLIIFIMVESKGTCPDTRLLI	1020	
Db	949	SCITEQTYQFFDNDKSKFSGLDCGNC	SRIPHGBKLMNTNLIIFIMVESKGTCPDTRLLI	1008	

QY 1021 QAEOTSDGNPCDMVK 1036  
Db 1009 QAEOTSDGNPCDMVK 1024

## RESULT 14

US-08-223-305C-55  
; Sequence 55, Application US/08223305C  
; Patent No. 5851824

## GENERAL INFORMATION:

; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/223,305C

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/176,899

; FILING DATE: 04-APR-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Seigman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 52516 (P519739)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)238-0999

; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1079 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-223-305C-55

Query Match 98.2%; Score 5347; DB 2; Length 1079;  
Best Local Similarity 98.7%; Pred No. 0;  
Matches 1023; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

QY 1 MAAGCLLALTTLTFLQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTTLTFLQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALYSVLALEAEKVQAAHQRDFASN 120  
Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALYSVLALEAEKVQAAHQRDFASN 120  
QY 121 EVYYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYSYOHAAVHIPTDIYEGSTIVL 180  
Db 121 EVYYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYSYOHAAVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDVR 240  
Db 181 NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASVPWVDSNRTPNKIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRISVSEMLETSLDDDFYNVASFNSNAQD 300  
Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRISVSEMLETSLDDDFYNVASFNSNAQD 300  
QY 301 VSCFOHLYQANVRNKKVLKDAVNNTAKGITDYKKGFSFAPFQLLNLYNVRANCKNIIML 360  
Db 301 VSCFOHLYQANVRNKKVLKDAVNNTAKGITDYKKGFSFAPFQLLNLYNVRANCKNIIML 360  
QY 361 FTDGGEERAQEIFNKYNDKKYRVFRFSVQGHNYERGPQIOMACENKGYIYIPISGAIR 420  
Db 361 FTDGGEERAQEIFNKYNDKKYRVFRFSVQGHNYERGPQIOMACENKGYIYIPISGAIR 420  
QY 421 INTQYLDVLRPMVLGDKAKQVQWNTYLDALGLVITGTLVPFNITGTFENKTNLK 480  
Db 421 INTQYLDVLRPMVLGDKAKQVQWNTYLDALGLVITGTLVPFNITGTFENKTNLK 480  
QY 481 NOLILGVNGVDVSLIEDIKRLTPRFLCPNGYFAIDPNGYVLLHNPLOPKPKSEPTVL 540  
Db 481 NOLILGVNGVDVSLIEDIKRLTPRFLCPNGYFAIDPNGYVLLHNPLOPKPKSEPTVL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDRIYIDKGNRTYTWTPVNGTDYSL 600  
Db 536 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDRIYIDKGNRTYTWTPVNGTDYSL 595  
QY 601 ALVLPYTFYIYIKAKLEETITQARSKKMKDSEFLKPDNFEESGYTTFAPRDYCNLKI 660  
Db 596 ALVLPYTFYIYIKAKLEETITQARY-----SETLKPDNFEESGYTTFAPRDYCNLKI 648  
QY 661 SDNTEFLLNNEFTDRKTPNPNPCNADLINRVLDAGFTNELVONYSKOKNIKGVKAR 720  
Db 649 SDNTEFLLNNEFTDRKTPNPNPCNADLINRVLDAGFTNELVONYSKOKNIKGVKAR 708  
QY 721 FVVTGGITRVYPKEAGENWQENPETIEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780  
Db 709 FVVTGGITRVYPKEAGENWQENPETIEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGI 768  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTTSIRDPGAGVPCDCKRNSDWDVCI 840  
Db 769 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTTSIRDPGAGVPCDCKRNSDWDVCI 828  
QY 841 LDDGGFLMANHDDYTNOIGRFFGIDPSLMRHLNYSVYAEKNSYDYSVCEPGAAPKQ 900  
Db 829 LDDGGFLMANHDDYTNOIGRFFGIDPSLMRHLNYSVYAEKNSYDYSVCEPGAAPKQ 888  
QY 901 GAGHRSAYVPSVADILQIGWATAAASWILQOFLSLTFPRLEAVEMEDDDFTASLSKQ 960  
Db 889 GAGHRSAYVPSVADILQIGWATAAASWILQOFLSLTFPRLEAVEMEDDDFTASLSKQ 948  
QY 961 SCITEQTQYFFDNDKSKFSGLDCGNCRIHFHGEKMLNTLIFIMVESKGTGTCPCDTRLLI 1020  
Db 949 SCITEQTQYFFDNDKSKFSGLDCGNCRIHFHGEKMLNTLIFIMVESKGTGTCPCDTRLLI 1008

Qy 1021 QAEQTSQGNPCDMVK 1036  
Db 1009 QAEQTSQGNPCDMVK 1024

RESULT 15

US-08-435-675B-5  
; Sequence 5, Application US/08435675B  
; Patent No. 5710250  
; GENERAL INFORMATION:  
; APPLICANT: Ellis, Steven Bradley  
; APPLICANT: Williams, Mark E.  
; APPLICANT: Harpold, Michael Miller  
; APPLICANT: Schwartz, Arnold  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,675B  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/314,083  
; FILING DATE: 28-SEP-1994  
; APPLICATION NUMBER: US 07/914,231  
; FILING DATE: 13-JUL-1992  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 08-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-53193  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1106 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-435-675B-5

Query Match 96.1%; Score 5229.5; DB 1; Length 1106;  
Best Local Similarity 94.8%; Pred. No. 0;  
Matches 1003; Conservative 14; Mismatches 12; Indels 29; Gaps 4;

Qy 1 MAAGCLLTLTLFQS--LLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLV 58  
Db 1 MAAGRPLATLTLQAWLLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLV 60  
Qy 59 DIYEKYQDLYTEPPNARQLVEIARDEIKLLSNRSKALVSLALEAEKVQAAHQWREDEFA 118  
Db 61 DIYEKYQDLYTEPPNARQLVEIARDEIKLLSNRSKALVRLALEAEKVQAAHQWREDEFA 120  
Qy 119 SNEVYYNAKDLDPEKNDSEPGSQRIKPVFTEDANFRQVSYQHAHVHIPTDIYEGSTI 178

Db 121 SNEVYYNAKDLDPEKNDSEPGSQRIKPVFTEDANFRQVSYQHAHVHIPTDIYEGSTI 180  
Qy 179 VLNELNWTSALEDEPKKNREEDPSLLMQVFGSATGLARIYPASPPWVDSRTPNKKIDLYDV 238  
Db 181 VLNELNWTSALEDEPKKNREEDPSLLMQVFGSATGLARIYPASPPWVDSRTPNKKIDLYDV 240  
Qy 239 RRPWYIOGAASPDKMLILVDVSGVSGTLLKLRISVSEMLETSLDDDFVNVASFNSNA 298  
Db 241 RRPWYIOGAASPDKMLILVDVSGVSGTLLKLRISVSEMLETSLDDDFVNVASFNSNA 300  
Qy 299 QDVSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFEQQLLNINVRANCKII 358  
Db 301 QDVSCFQHLVQANVRNKKVLDVANNITAKGTDYKKGFSFAFEQQLLNINVRANCKII 360  
Qy 359 MLFTDGGGEERAQEIENKYNKDKVRVFRSVGOHNVREPIQWMACENKGYIYEISIGA 418  
Db 361 MLFTDGGGEERAQEIENKYNKDKVRVFRSVGOHNVREPIQWMACENKGYIYEISIGA 420  
Qy 419 IRINTQEYLDVLGRPMVLADGAKAKOVQWTVNVDLDALELGLVITGTLPVFNITGOFFENKTN 478  
Db 421 IRINTQEYLDVLGRPMVLADGAKAKOVQWTVNVDLDALELGLVITGTLPVFNITGOFFENKTN 480  
Qy 479 LKNQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIFAIDPNGYVLLHPNLQPK----- 530  
Db 481 LKNQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIFAIDPNGYVLLHPNLQPKPIGVGPT 540  
Qy 531 -----NPKSQEPVTLDFDALELNDIKVETRNKMDIGESGEKTFRTLVKSQDER 579  
Db 541 INLRKRRPNVQPKSQEPVTLDFDALELNDIKVETRNKMDIGESGEKTFRTLVKSQDER 600  
Qy 580 YIDKGNRTYTWTPVNGTDY-SIALVLTPTSYFYIKAKLEETITQARSKGKKMDSLTLP 638  
Db 601 YIDKGNRTYTWTPVNGTDYSSIALVLTPTSYFYIKAKIEETITQARY-----SETLKP 653  
Qy 639 DNFEESGYTFIAPRDYCNLDKISDNTNTEFLNPNEDIRKTPNPNPCNADLINRVLLDAG 698  
Db 654 DNFEESGYTFIAPRDYCNLDKISDNTNTEFLNPNEDIRKTPNPNPCNADLINRVLLDAG 713  
Qy 699 FTNELVQNYWSKOKNITGVKARFVVDGGITRVYKPEAGENMOENPETEYDSYKRSLDN 758  
Db 714 FTNELVQNYWSKOKNITGVKARFVVDGGITRVYKPEAGENMOENPETEYDSYKRSLDN 773  
Qy 759 DNYVFTAPYFNKSGPGAYESGIMVSKAVEYIOGKLLKPAVVGKIDVNSWIENFTKTSI 818  
Db 774 DNYVFTAPYFNKSGPGAYESGIMVSKAVEYIOGKLLKPAVVGKIDVNSWIENFTKTSI 833  
Qy 819 RDPGAGPVCDCRNSDVMDCVILDDGGFLIMANHDDYTQIGRFFGEIDPFLMRHLVNIS 878  
Db 834 RDPGAGPVCDCRNSDVMDCVILDDGGFLIMANHDDYTQIGRFFGEIDPFLMRHLVNIS 893  
Qy 879 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLT 938  
Db 894 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSIADILQIGWATAAANSILOQFLLSLT 953  
Qy 939 FPELLEAVEMEDDDFTASLSKQSCITEQTYFFDNDPSKFSFVLDGCGNCSRIHGEKLMN 998  
Db 954 FPRLEAADMEDDDFTASMSKQSCITEQTYFFDNDPSKFSFVLDGCGNCSRIHGEKLMN 1013  
Qy 999 TNLIFTWVESKGTCPCDTRLLIOAEQTSQGNPCDMVK 1036  
Db 1014 TNLIFTWVESKGTCPCDTRLLIOAEQTSQGNPCDMVK 1051

Search completed: July 23, 2001, 07:39:05  
Job time: 532 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:37:58 ; Search time 84.28 Seconds  
(without alignments)  
936.365 Million cell updates/sec

Title: US-09-397-548-16  
Perfect score: 5443  
Sequence: 1 MAACLLALTLTFLQSLIG.....RLLIQAQTSQGNPCDMVK 1036

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5443	100.0	1091	2 JH0565	calcium channel al
2	5234	96.2	1091	2 A44147	calcium channel pr
3	5224.5	96.0	1106	1 CHRBA2	calcium channel al
4	1085	19.9	1091	2 T30256	calcium channel al
5	607	11.2	734	2 S44617	C50C3.11 protein -
6	572	10.5	1148	2 T18770	probable calcium c
7	198	3.6	1450	2 C86880	hypothetical prote
8	194.5	3.6	886	2 S54355	inter-alpha-trypsi
9	185	3.4	885	2 S30350	inter-alpha-trypsi
10	164.5	3.0	889	2 JC5576	inter-alpha-trypsi
11	161	3.0	2706	2 T28155	variant-specific s
12	159	2.9	1984	2 A44396	p-type cation tran
13	157.5	2.9	575	2 D64998	hypothetical prote
14	155	2.8	1516	2 E71619	RAD2 endonuclease
15	155	2.8	2364	2 I40884	cytotoxin L - clos
16	154.5	2.8	946	1 IYH02	inter-alpha-trypsi
17	154.5	2.8	1315	2 T28679	fibrinogen-binding
18	153	2.8	932	2 JC5953	inter-alpha-inhibi
19	152	2.8	1291	2 S46431	botulinum neurotox
20	152	2.8	1291	2 A49777	botulinum neurotox
21	151.5	2.8	420	2 S76691	hypothetical prote
22	150.5	2.8	921	2 JC4625	inter-alpha-trypsi
23	150	2.8	634	2 A69856	methyl-accepting c
24	149	2.7	459	2 F64688	proteinase (ec 3.4
25	149	2.7	930	2 JX0368	inter-alpha-trypsi
26	148.5	2.7	2401	2 T28676	rhoptory protein -
27	148	2.7	964	2 S25855	DNA-directed DNA p
28	146.5	2.7	1285	2 E72420	hypothetical prote
29	146	2.7	4688	2 F82885	hypothetical prote

30	145.5	2.7	676	2 T47637	hypothetical prote
31	145.5	2.7	689	2 F84811	probable retroelem
32	145.5	2.7	5005	2 F82884	hypothetical prote
33	144	2.6	1087	1 S41797	cellulose 1,4-beta
34	144	2.6	1091	2 S33850	fibrinogen-binding
35	143	2.6	946	2 JC5575	inter-alpha-trypsi
36	143	2.6	1864	2 T18485	hypothetical prote
37	142.5	2.6	382	2 S44618	C50C3.10 protein -
38	142	2.6	1169	2 A64505	p115 homolog - Met
39	142	2.6	1599	2 S22737	glucosyltransferas
40	141	2.6	1252	2 B42771	reticulocyte-bind
41	140.5	2.6	2369	2 T28677	rhoptory protein -
42	140	2.6	2710	2 A37052	toxoin A - Clostrid
43	140	2.6	3305	2 T18358	apolipoprotein prec
44	139.5	2.6	764	2 I39934	protective antigen
45	139	2.6	1180	2 A26858	parasporal crystal

ALIGNMENTS

RESULT 1

JH0565  
calcium channel alpha-2b chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999  
C:Accession: JH0565  
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Vellicelebi, G.; Ellis, S.B  
Neuron 8, 71-84, 1992  
A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of  
A:Reference number: JH0564; MUID:92110010  
A:Accession: JH0565  
A:Molecule type: mRNA  
A:Residues: 1-1091 <WIL>  
A:Cross-references: GB:M76559; NID:gl79761; PIDN:AAA51903.1; PID:gl79762  
A:Experimental source: basal ganglia  
A:Note: several conflicts are found between GenBank submission, authors' translation  
C:Comment: This protein is a subunit of the voltage dependent calcium channel.  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: glycoprotein; phosphoprotein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>  
F:32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase  
F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #  
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca  
F:501/Binding site: phosphate (Thr) (covalent) #status predicted  
F:833/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 100.0%; Score 5443; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACLLALTLTFLQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60

Db 1 MAACLLALTLTFLQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGVNLVDI 60

QY 61 YEKYODLYTVEPNARQLVEITAARDIEKLSNRKALVSLALEAEKVQAQHWREDFASN 120

Db 61 YEKYODLYTVEPNARQLVEITAARDIEKLSNRKALVSLALEAEKVQAQHWREDFASN 120

QY 121 EYVYNKADDDPEKNDSEPGSQRIKPVIEDANFGROISYQHAHVHPTDIYEGSTIVL 180

Db 121 EYVYNKADDDPEKNDSEPGSQRIKPVIEDANFGROISYQHAHVHPTDIYEGSTIVL 180

QY 181 NELNWTSDALDEVFKKNREDEPSLLMQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240

Db 181 NELNWTSDALDEVFKKNREDEPSLLMQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR 240

QY 241 RPWTIQGAASPKDMILILVDVSGVSGGLTKLIRTSVSEMLETSLDDDDFVNVASFNSAQD 300

Db 241 RPWTIQGAASPKDMILILVDVSGVSGGLTKLIRTSVSEMLETSLDDDDFVNVASFNSAQD 300

301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNLYNVRANCKNIIML 360  
|||||  
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNLYNVRANCKNIIML 360  
|||||  
QY 361 FTDGGEERAQEIFNKNYKDKKVRVFRFVSGQHNRYERGPIQMACKENKGYIYBPSIGAIR 420  
|||||  
Db 361 FTDGGEERAQEIFNKNYKDKKVRVFRFVSGQHNRYERGPIQMACKENKGYIYBPSIGAIR 420  
|||||  
QY 421 INTQEYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLFVNITGOFENKTNLK 480  
|||||  
Db 421 INTQEYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLFVNITGOFENKTNLK 480  
|||||  
QY 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHHPNLPKPKSQEPVTL 540  
|||||  
Db 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHHPNLPKPKSQEPVTL 540  
|||||  
QY 541 DFLDAELENIDKVEIRNKMIDGESGEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
|||||  
Db 541 DFLDAELENIDKVEIRNKMIDGESGEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
|||||  
QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNLKI 660  
|||||  
Db 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNLKI 660  
|||||  
QY 661 SDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVKAR 720  
|||||  
Db 661 SDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVKAR 720  
|||||  
QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNRYFTAPYKPKSGPGAYESGI 780  
|||||  
Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNRYFTAPYKPKSGPGAYESGI 780  
|||||  
QY 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENTFTSIRDPKAGPVCCKRNSDVMDCVI 840  
|||||  
Db 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENTFTSIRDPKAGPVCCKRNSDVMDCVI 840  
|||||  
QY 841 LDGCGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIYAFNKSQYDQVCEPGAAPKQ 900  
|||||  
Db 841 LDGCGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIYAFNKSQYDQVCEPGAAPKQ 900  
|||||  
QY 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960  
|||||  
Db 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960  
|||||  
QY 961 SCITEQTYFFDNDKSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
|||||  
Db 961 SCITEQTYFFDNDKSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
|||||  
QY 1021 QAEQTSQDGNPCDMVK 1036  
|||||  
Db 1021 QAEQTSQDGNPCDMVK 1036  
|||||

RESULT 2  
A44147  
calcium channel protein alpha-2 chain precursor - rat  
N:Alternate names: dihydropyridine-sensitive L-type  
C:Contains: calcium channel alpha-2 chain  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 20-Aug-1999  
C:Accession: A44147  
R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.  
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992  
A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive  
A:Reference number: A44147; MUID:92228762  
A:Accession: A44147  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1091 <KIM>  
A:Cross-references: GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 96.28; Score 5234; DB 2; Length 1091;  
Best Local Similarity 95.78; Pred. No. 0;  
Matches 992; Conservative 24; Mismatches 19; Indels 2; Gaps 2;

QY 1 MAAGCLLALTTLTFLQSLTLPSSSEPPFPSPVTKSWDKMQEDLVTLAKTAGSGVNQLYDI 60  
|||||  
Db 1 MAAGCLLALTTLTFLQSLTLPSSSEPPFPSPVTKSWDKMQEDLVTLAKTAGSGVTQLADI 60  
|||||  
QY 61 YEKYQDLYTVPEPNARQLVEAARDIEKLLSNRSKALYSALAEAEKVOAAHQRDEFSAN 120  
|||||  
Db 61 YEKYQDLYTVPEPNARQLVEAARDIEKLLSNRSKALYSALAEAEKVOAAHQRDEFSAN 120  
|||||  
QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180  
|||||  
Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180  
|||||  
QY 181 NELNWTLSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
|||||  
Db 181 NELNWTLSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240  
|||||  
QY 241 RPWYTOGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDFVNVASFNSAQD 300  
|||||  
Db 241 RPWYTOGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDFVNVASFNSAQD 300  
|||||  
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNLYNVRANCKNIIML 360  
|||||  
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNLYNVRANCKNIIML 360  
|||||  
QY 361 FTDGGEERAQEIFNKNYKDKKVRVFRFVSGQHNRYERGPIQMACKENKGYIYBPSIGAIR 420  
|||||  
Db 361 FTDGGEERAQEIFNKNYKDKKVRVFRFVSGQHNRYERGPIQMACKENKGYIYBPSIGAIR 420  
|||||  
QY 421 INTQEYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLFVNITGOFENKTNLK 480  
|||||  
Db 421 INTQEYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLFVNITGOFENKTNLK 480  
|||||  
QY 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHHPNLPKPKSQEPVTL 540  
|||||  
Db 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHHPNLPKPKSQEPVTL 540  
|||||  
QY 541 DFLDAELENIDKVEIRNKMIDGESGEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYS - 599  
|||||  
Db 541 DFLDAELENIDKVEIRNKMIDGESGEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDYS - 599  
|||||  
QY 600 LALVLPYTSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNL 659  
|||||  
Db 600 LALVLPYTSFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCNL 659  
|||||  
QY 660 ISDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVKA 719  
|||||  
Db 660 ISDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELYQVYWSKQKNIKGVKA 719  
|||||  
QY 720 RFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNRYFTAPYKPKSGPGAYESG 779  
|||||  
Db 720 RFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNRYFTAPYKPKSGPGAYESG 779  
|||||  
QY 780 IMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENTFTSIRDPKAGPVCCKRNSDVMDCV 839  
|||||  
Db 780 IMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENTFTSIRDPKAGPVCCKRNSDVMDCV 839  
|||||  
QY 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIYAFNKSQYDQVCEPGAAPK 899  
|||||  
Db 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNIYAFNKSQYDQVCEPGAAPK 899  
|||||  
QY 900 OGAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLLEAVEMEDDDFTASLSK 959  
|||||  
Db 900 OGAGHSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLLEAVEMEDDDFTASLSK 959  
|||||  
QY 960 QSCITEQTYFFDNDKSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLL 1019  
|||||  
Db 960 QSCITEQTYFFDNDKSGVLDGCGNCSRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLL 1019  
|||||

Query Match 19.9%; Score 1085; DB 2; Length 1091;  
Best Local Similarity 28.7%; Pred. No. 1.9e-57;  
Matches 309; Conservative 222; Mismatches 416; Indels 128; Gaps 40;  
3 AGCLALATLTFQSLIGSSSEPPFSANTIKSWDKMEDLYTLAKTASGNOLVDIYE 62

QY	1	MAAGCLLALTILFOS--LLGPSSEEPFPANVIKSHWDKQEDLVLTAKTASGVOLV	58
		:	
		:	
Db	1	MAAGRPLAWTLTWQAWLITGPSSEEPFSAVTIKSWDKQEDLVLTAKTASGVOLV	60
		:	
QY	59	DIVERYQDLYTEVPNNARQLVEIARD:EKLLSNRSKALVSLEAEKVQAAHQRWDEFA	118
		:	
Db	61	DIVEKYQDLYTEVPNNARQLVEIAARD:EKLLSNRSKALVRLEAEKVQAAHQRWDEFA	120
		:	
QY	119	SNEVYYNAKDLDPEKNDSFGSORIPVFRTEDANFGROI:SYQHAAVHIPTDIYEGSTI	178
		:	
Db	121	SNEVYYNAKDLDPEKNDSFGSORIKPFVIDDANFRQVSYQHAAVHIPTDIYEGSTI	180
		:	
QY	179	VLNELNWTLSALDEVFKKKREEDPSLLWQVFGSATGLARIYPASPWWDSNRTPNKIDLYDV	238
		:	
Db	181	VLNELNWTLSALDDVPKKREEDPSLLWQVFGSATGLARIYPASPWWDSNRTPNKIDLYDV	240
		:	
QY	239	RRRPWTIQGAASPKMDLIIVDYSGSVSGITLKITRYSVSEMLETISDDDFVNVAJSFNNA	298
		:	
Db	241	RRRPWTIQGAASPKMDLIIVDYSGSVSGITLKITRYSVSEMLETISDDDFVNVAJSFNNA	300
		:	
QY	299	QDYSCFOHLVQAVNRNKVLKDAVNNTAKGITDYKKGFSFAFEQLLNVTWNSRANCNKII	358
		:	
Db	301	QDYSCFOHTVOAVNRNKVLKDAVNNTAKGITDYKKGFSFAFEQLLNVTWNSRANCNKII	360
		:	





probable calcium channel protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T18770; T25249  
R: Sulston, J.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z19019  
A:Accession: T18770  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1148 <WIL>  
A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6  
A:Experimental source: clone B0491  
R: Chui, C.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z20004  
A:Accession: T25249  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1148 <W12>  
A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6  
A:Experimental source: clone T24F1  
C:Genetics:  
A:Gene: CESP:T24F1.6  
A:Map position: 2  
A:Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.5%; Score 572; DB 2; Length 1148;  
Best Local Similarity 21.2%; Pred. No. 2.1e-26;  
Matches 238; Conservative 213; Mismatches 424; Indels 248; Gaps 41;  
QY 37 VDKMQEDLVTLA-----KTASGVNOLVDIYKDYQDYVPEPNARQLVEIAARDI 86  
DB 99 VDTIEEPASIAQFSANILKDFETQSFSLVQEEFKLPDIKSKKEDAEKLRVATEHL 158  
QY 87 EKLNSRSKALVSLALBAEQAQAHQWREDFASNEVYVYNAKDDLPDPEKNDSEPGQR-- 144  
DB 159 DRLVTRNVDALKKLASAEASAAVF-----DEYDQAVAVPOADKRCE 201  
QY 145 --IKPVFIEDANFORISYQH---AAVHIPTDIYEGSTIVLNELNWTSA--LDEVFKNR 197  
DB 202 AYMKMNESDMHFVSNM-VEHNSKSGIHITVESYQCDDPRVMRDFDTGTRKLEKTSMDNK 260  
QY 198 EEDPSLLMQVGSATGLARYYPASFPWDNSPTPNKIDLYDVRPRPYTOGAASPKDMLIL 257  
DB 261 EKAPEMGHQYIGTYSGLTRMYPRRHW-KVEPTPTIDLDPRFRFWFNAESVPKDIYVL 319  
QY 258 VDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD-VSCFQH-LVQANVRN 315  
DB 320 LDYSGSVKGPMTMLIKITMWTILSTLSPNDFFGVYFNHFNPIISCANRTFMPATTSNK 379  
QY 316 KYLKDANNITAKGTYDKKGSFAFOL---LVNVS-----RANCKIIMLFDGSEE 367  
DB 380 KYVEELGMLBEKQQAHAFTPLKSLDLVRLGNLDSNQSLADYRSEGHKLIIITDGVDE 439  
QY 368 RAQETFN---KYNKDKYRVFRFSGQHYERGPQWACENKGYIYEPISGAIKRIHQ 424  
DB 440 WPHQILDEEFQTRNSLIRIFGSMYGTSLPLQOQYACKSHGGYSEIDSIMVYKPSQR 499  
QY 425 EYLDVLRPMVLADGAK-----QVQWTVNYLDALGLVITGLPVFNITGOFENKT 477  
DB 500 TQONVLSQ---VRGDELKGTNAEKREPSWTQLYMETQGTGPIVTLSPILT-----SEQR 551  
QY 478 NLKNQILGVMGVDSLEDKRLTFRFLCPNGYFAIDPNGYVLLHPNLQ-PKNPK--- 533  
DB 552 IWRDQKLAGVAIDISIKETKHLR--TSSEQMGIYVDNNGMLIYHPQLQIPKTEVHCV 609  
QY 534 -----SQEPV-----TLDFDALENDIKVEIRN 557  
DB 610 RRSACYDAQOVKQKAGSLRVHYGFDERVRLVGLIDSIPITLDMDYDLEGDSIAIRDLRR 669  
QY 558 KMDGESGEKTFRTLVKYSQDERYIDKGNRTYTWTVPNGTDSLALV--LPTYFYIKAK 615

DB 670 -----RITTKCYEAAIKDNSKEYCHSHIKSPFTLVIVNNIQLKTVYDSDV 717  
QY 616 LEETITQ-----ARSKGKMKDSETLKPNFNBESGYTFIAPRDYC--NDLKISDNNT 665  
DB 718 QELGLTDNKLVTFFPRDVCQWKLEDAHAHRFRV--WSDISEKEICAQDDMLRPRAFT 775  
QY 666 BELLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNQLVNTYWSKQKNIKGVKARFVVD 725  
DB 776 KGLSWTQSNPKSDIEHTC-----LLAQYPENASVPHVNS-----FVHTR 817  
QY 726 GGITRVYKPEAGENQENPETVEDSFYKSLDNDNVTFATPYFNKSGPGAYESGIMVSKA 785  
DB 818 SKLTAFYPTCSHDMKAVNKFEDEI--RLTDNDNFV---QFSMR-----SESLIYRT 866  
QY 786 VEIYQGLKLLPAGVGIKIDVN---SWIENFTKTSIRDPAGVPCVCKRNSD-----VMD 837  
DB 867 IADYDNNRL---AVGTQWKNENFDQIFDNFT-----RQNPDKMKCKRQE 908  
QY 838 CVTLDDGGFLLMANHDYTNQIGRFFEGEIDPSLMRHLVNIISVYAFNKSVDYQVCEPGAA 897  
DB 909 CSITIRNGHVIASSAHRAHAHLAKF---DPQLFESLVKVLNVTNSWTVEQSECK--- 960  
QY 898 PKOGAGHRSAYVPSVADIQIGWATAA--AWSILOQFLLSLTFPRLLLEAVEMEDDDFTA 955  
DB 961 -----AKRVAPWSSAAGSGSSILRYFTSI-----FKLAKTSFWR 995  
QY 956 SLSKQSCITEQTQYFPDNDKSFSGVLDCGNC-SRIFHGKELMNTNLFIMVESKGTFC-- 1012  
DB 996 NLLESALTLLVDAQFSMTGTCTTQKIKPFRCFMKFFHYRMTLNTK-QLOLAGMSTCSR 1054  
QY 1013 -----PCDTRLLIOAEQTSQGNP-----CDMV 1035  
DB 1055 YAKLYPVPHTTLSLIADACRACQYRPRIFESEPRKLEKCDV 1097

RESULT 7

C86880  
hypothetical protein yvcC [imported] - Lactococcus lactis subsp. lactis (strain IL140  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: C86880  
R: Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh  
Genome Res. in press, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium.  
A:Reference number: A86625  
A:Accession: C86880  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1450 <STO>  
A:Cross-references: GB:AE005176; NID:g12725093; PIDN:AAK06141.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: yvcC

Query Match 3.6%; Score 198; DB 2; Length 1450;  
Best Local Similarity 21.0%; Pred. No. 0.0012;  
Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56;

QY 37 VDKMQEDLVTLAKTASGVNQLVDIYKDYQDYVPEPNARQLVEIAARDIEK-----L 89  
DB 69 INKTENDKELKLFEGNQPIEIEE--NESWTLKEKNT-----IISDFKENEKGIYL 120  
QY 90 LSNRSKALVSLAEAKVQAHAQWR---EDFA-----SNEVYVNA 127  
DB 121 RANNSISLNLLEIQADAKLIENDQEVISEDILAKKESTIFSILYIPENNKADSKKDNKNT 180  
QY 128 KDDLPEKNDSEPGSORIKP---VFIEDANFGRIQISYQHAHVH----- 167  
DB 181 EEVLNNSESQEFTVSQLKKDSQLAFSPNFGIKAGNLDLAQNYENISPEYRQDETGISP 240  
QY 168 ----IPTDIYEGSTIVLNELNWTSALEDFVKKNREEDPSLLMQVFGSATGLARYYPASPW 223

Db 241 NHTSPT---GNTVNVHQCWNSF-----SSQWDGVNSWN--GEATNLENSYIEVAG 287  
Qy 224 VDN-----SRTPNKIDLY-DVRRPWTIOGAASPOMLILVDVSGSGVGTU 270  
Db 288 VNNPVDFAIRKYAKETETPGDYLYLVNRGN---VQNPPIKPVDTVLVDMSGSGMOGAKET 344  
Qy 271 LIRTSVSMLETLSD--DENVN--ASFNSADQVSCFQHLQVQANRNKVLKD---A 321  
Db 345 AVROGVDFSLTQNTAYADVIVNGVIGVSPGNVYVGAAGYIIVPI--DKVSSSHVKS 402  
Qy 322 VNNITA---KGITDYKKGFSFAFOLLNINVRANCNKIIMLFTDGGEEAQAEIFNKYNK 378  
Db 403 INQALAPQFSGGTFTQLGRKGTEML---EQDSSDNQKMLMTDQ---VPTESYKVN 455  
Qy 379 DKVYR--VFRSVQVHNERG---PIQ---WMACENKGYEIEI-----PSIGAIRINTQOE 425  
Db 456 ASKYVDNVIYGQSFASRDEPGNTSKIOSPYVVDKINGSNIEIRDTWAATLGEAEISKQE 515  
Qy 426 YLDLGRPMVLGAD-----KAKQVQWTVNYLDLLEGLVITGTLVPVFNITGQFE 474  
Db 516 ISEHTLGIQLCNGSVLSQBEVKSRSLSIATTLGYQDANSAN-----DITDYLK 565  
Qy 475 NKTN-----LKNQILGYVMGVDSLEDIKRLTPRFTLCPNGYVYFAIDPENGYYLLHPN 526  
Db 566 NOANVLSRENTITNGLILDLPGAQFEYKDKF-----FEITSVG----- 604  
Qy 527 LQPNKPSQEPVTLDFDAELENDIKVEIRNKMIDGSGEKTFTTLVKSQDERVIDKGNR 586  
Db 605 -----EDSIDNLPKTGINKEGLEISLNTI--GKNOEQVQIHYQVRLNTETDDFKTNY 653  
Qy 587 TY-----TWTPVNGT--DYSALVLPTSPYIYKAKLE-----ETITQASKK 627  
Db 654 WYQNGETTLTP--NGSPNDKNVNGVSPKSGNINLEKQWLANSENIENVELLIGRR 712  
Qy 628 GKMDSE-----TLKPNFEBSGYFTIAPRDYCNLDKISDNNTFELNFEIDIRKTPNN 682  
Db 713 SAQISSDWTKVTLKEDDEWSQLENLPKYSILGEEFYIEYKDEIVLN--SEIYDWITIGE 771  
Qy 683 PSCNADLINRVLD-----AGFTNELVQWYNSKQKNIKGVKARFVVTGGITRVYPKAGE 738  
Db 772 DKTTTANIEKRLQILKITSNHDNEPLSEVEFVLKNSQGEEDKAVTN-----EKGE 822  
Qy 739 --NWOENPETYEDSYKSLDNDNVFTAPYENKSGPGAYESGIMVSK-----AVEIYIQ 791  
Db 823 ILFKTRLNRYGEEQLHEIKSPGHSLEGPWKIT---EFFENGQPIIKVDGQIALDSEHN 879  
Qy 792 GKLLKPAVVGKIDVNSWNIENFTKITSIRDPGAPVDCPKRNSVMDCVLD-----DG-- 844  
Db 880 KPMIS---LNTINDIN--VEEF-----RNSVTIDKRAVDSEKLDGAV 917  
Qy 845 -GFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQAG 903  
Db 918 FNLQIESVDDDELTLQKPL--EITNNLLPGL-----YALQESVSPNGYRDEV 964  
Qy 904 H--RSAYVPSVADILQIGWATAAWSILOQL-----LSLTFE- 939  
Db 965 HFRVKFNGSIVAIGSEG-----IDIPFDENSGKNGVLNBEENGDHLTLIFY 1015  
Qy 940 ----PRLLEAVEMEDDDFTASLSKQSC--ITEQTOYFFDNDS-----KPSFGVLDGCGNSRI 990  
Db 1016 NOAVPPLQLEVDKIDDDFTSLAGVSFELTRLGKSTDSVSKRINSFDRILKTFN--NE 1073  
Qy 991 FHGEKL--MNTNL 1001  
Db 1074 FTGETALKSNL 1085

RESULT 8

S54355

inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 04-Feb-2000

C:Accession: S54355  
R:Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.  
Biochem. J. 306, 505-512, 1995  
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mou  
A:Reference number: S54353; MUID:95194326  
A:Accession: S54355  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-886 <CHA>  
A:Cross-references: EMBL:X70393; NID:G695635; PIDN:CAA49843.1; PID:G695636  
C:Superfamily: Inter-alpha-trypsin inhibitor complex component II

Query Match 3.6%; Score 194.5; DB 2; Length 886;  
Best Local Similarity 19.9%; Pred. No. 0.00089;  
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;

Qy 27 FPSAVTIKSWVDKMOEDLVTLAKTAGSNQVLVDIYKYQDLTYVPEPNNARQLVIAARDI 86  
Db 98 YPGNVKEVAQKQYKAVSQGTAG---LVKASGRKLEKFTVSVNVAAGSKVTFELTY 153  
Qy 87 EKLNSRSKALVSLALEAEKVAQAAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSORIK 146  
Db 154 EELL-KRKNKGYEMLYKVPKQLVRHFEID-----AHIFEP-----Q 189  
Qy 147 PVFTEDANFGQISYQAAVHIPTDIYEGSTIVLNELNWTSALDEVFKKNREEDPSLLWQ 206  
Db 190 GIGMLDAE-----ASFYTNDL-LGSALTQSF----- 214  
Qy 207 VFGSATGLARIYPASPWVDNSRT--PNKID-----LYDVRRRP-----WYI-- 245  
Db 215 -----SGKKGHVSFKPSLDQORSCTCTDSLLNGDFTIVYDVNRESQNVQVNGYEVHF 269  
Qy 246 ---QG--AASPKDMLILVDVSGSVGLKLIRTSVSEMLETSLDDDDFVNVASFNSAQDV 301  
Db 270 FAPQGLFVVPKNIYFIVDVSGSMGRKIQTREALLKILDVDDKEDDYLNLFST---DV 326  
Qy 302 SCFO-HLVQAVNRNKKVYLDKAVNNITAKGTDYKKGFSFAPEQLNLYNVRAN-----C 354  
Db 327 TTWKDHLVQATPANKLEAKFVKNHQSMNTINDGLLKGIEML---NKAREDTVPERS 383  
Qy 355 NKIIMLTQD---GEERAQEIFNKYNK--DKKYRVFRFSVQGHNYERGPQWMACENKG 408  
Db 384 TSIIMLTQDGTANTGESRPEKIQENVRNAIGGKFPYLNGLFG--NNLNYNLETLEAHNG 442  
Qy 409 YYEIPISGAIRINTQYLDVLRPMVLGDKAKQVQWTVNYLDLLEGL--VTGILPV 466  
Db 443 LARRIYEDSDANLQLOGFYEEVANPLL-----TNVEVEYPENAILDLTRNSYPH 491  
Qy 467 FNITQFENKTNLKNQILGYVMGVDSLEDIKRLTPRFTLCPNGYVYFAIDPENGYYLLHPN 526  
Db 492 F-----YDG-----SEIVVAGRLVDRNDN-----PKADYKGGHGLN-- 523  
Qy 527 LQPNKPSQEPVTLDFDAELENDIKVEIRNKMIDGSGEK--TFTRLVKSQDERYIDKG 584  
Db 524 ---DLAFTTEVDMEEDAALK-----EGYIFGDYIERLMAYLTIEQLLEKKNKAG 572  
Qy 585 NRTVTWTPVNGTDSLAA--LVLPYISFYIYKAKLEEFITQARSKKGMKDSSET-----LK 637  
Db 573 DEKENIT-AEALDLSLKYHFVTPLTSMVVTKPEDNEQDTSTADNAGEAFAETMTSFLT 631  
Qy 638 PDNFEESGYFIAPRDYCNLDKISDNNTFELNFEIDRKTNNPNSCNADLINRVLLDA 697  
Db 632 TQSSQSPYIYV-----DGDPHFTIQI-----PKNDSICFNIDEKP 668  
Qy 698 GFTNELVQWYNSKQKNIKGVKARFVVTGGITRVYPKAGEWNOENPETYEDSYKSLD 757  
Db 669 GTVLRLLIQD-----PVT--GIT-VTGGIIGD-----KRS-- 694  
Qy 758 NDNVFTAPFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTS 817  
Db 695 NASSRTGKTGYFGKLGITNAWMDFRVEVTEKIIIG-----TGAEISTFSWLDVTVTQ 747

QY 818 IRDPCAGPVCDCKRNSDWDVCDG-GFLMAN-----HDDYTNQIGRFGEDIP 868  
 Db 748 -----TGLSVTNRKKNV-VSGDGSFVILHQVKKHVPVHDFLG-----FYVDS 795  
 QY 869 SLMRHLNIVSYAENKSYDYQSV-CEPGAAP 898  
 Db 796 HRMSAQTHGLGQFFQPFDFKVRGIRPGSDP 826

RESULT 9  
 S30350  
 Inter-alpha-trypsin inhibitor heavy chain 3 precursor - human  
 A:Alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy chain H3  
 C:Species: Homo sapiens (man)  
 C:Date: 03-May-1994 #sequence\_revision 20-Feb-1995 #text\_change 04-Feb-2000  
 C:Accession: S30350; S02141; D34245; A39079; S50133; B53642; A59167  
 R:Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin, Eur. J. Biochem. 212, 771-776, 1993  
 A:Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-acid sequence  
 A:Reference number: S30350; MUID:93215656  
 A:Accession: S30350  
 A:Molecule type: mRNA  
 A:Residues: 1-885 <BOU1>  
 A:Cross-references: ENBL:X67055; NID:g288562  
 R:Bourguignon, J. Submitted to the EMBL Data Library, June 1992  
 A:Reference number: S34123  
 A:Accession: S34123  
 A:Molecule type: mRNA  
 A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
 A:Cross-references: ENBL:X67055; NID:g288562; PIDN:CAA7439.1; PID:g288563  
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattei, M.G.; Passage, E.; Saller, Eur. J. Biochem. 179, 147-154, 1989  
 A:Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three chromosomes  
 A:Reference number: S02141; MUID:89137072  
 A:Accession: S02141  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIA1>  
 A:Cross-references: ENBL:X14690; NID:g35464; PIDN:CAA32821.1; PID:g35465  
 R:Engild, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G. J. Biol. Chem. 264, 15975-15981, 1989  
 A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alpha-trypsin inhibitor  
 A:Reference number: A92736; MUID:89380192  
 A:Accession: D34245  
 A:Molecule type: protein  
 A:Residues: 30-49 <ENGL>  
 R:Engild, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V. J. Biol. Chem. 266, 747-751, 1991  
 A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood protein alpha-1-antitrypsin  
 A:Reference number: A39079; MUID:91093267  
 A:Accession: A39079  
 A:Molecule type: protein  
 A:Residues: 631-647 <ENG2>  
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Boncompagni-Udelli, R. Biochem. Biophys. Acta 1219, 551-554, 1994  
 A:Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 genes  
 A:Reference number: S50132; MUID:95002176  
 A:Accession: S50133  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-27 <DIA2>  
 A:Cross-references: ENBL:X75318  
 R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J. Biochemistry 33, 7423-7429, 1994  
 A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex with hyaluronan  
 A:Reference number: A35642; MUID:94271799  
 A:Accession: B53642  
 A:Molecule type: protein  
 A:Residues: 30-34, 'X' <WIS>  
 R:Jessen, T.E.; Faarvang, K.L.; Ploug, M. FEBS Lett. 230, 195-200, 1988  
 A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a nd

A:Reference number: S02431; MUID:88167187  
 A:Accession: A59167  
 A:Molecule type: protein  
 A:Residues: 30-32, 'GEQEQAVDT' <JES>  
 C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondroitin-6-sulfate  
 C:Genetics: As  
 A:Gene: GDB:ITTH3  
 A:Cross-references: GDB:120109; OMIM:146650  
 A:Map position: 3p13-3p12  
 C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
 C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase 1  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-29/Domain: propeptide #status predicted <PRO>  
 F:30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M>  
 F:648-885/Domain: carboxyl-terminal propeptide #status predicted <CT>  
 F:87,576/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s

Query Match 3.4%; Score 185; DB 2; Length 885;  
 Best Local Similarity 20.9%; Pred. No. 0.0033;  
 Matches 137; Conservative 101; Mismatches 239; Indels 180; Gaps 34;

QY 27 FPSAVTIKSWDKMOEDLVTLAKTAGVGNQVLDIYEKYQDLYTVEPNNAQVLEIAARDI 86  
 Db 97 YFGNVKEKAVAKQYKAVSQGTAG-----LVKASGRKL 131  
 QY 87 EKLLSNRSKAL---VSLALEAEKVAQAAHQRDFASNEVVYVNAKDDLDPEKNDSPPG 143  
 Db 132 ERTFVSNNVAAAGSKVTFTYELLKRHKGK-----YEMYLKVPK-----Q 173  
 QY 144 RKPVFIEDANFGRQISYQAAHVPDIDYEGSTIVLNELNWTSDALDEKKNREEDPSL 203  
 Db 174 LVKHFEIE-----VDIFEQGI-----SMLD-----AEASFI 200  
 QY 204 LMQVFESA-----TGLARYYPASPVVDNRT-PNKID-----LYDVRRP----- 242  
 Db 201 TNDLIGSALTQSKGKGVHSPKSLDQORSCPTCTDSLLNGDFTITYDNRESPGNVQI 260  
 QY 243 ---WYI-----QG-AASPKDMILVDVSGVSGLTUKLIRTSVSEMLETSDDDDFVNVAS 293  
 Db 261 VNGYFVHFPAQGLPVVKNVAFVDSGMAKLEQTKALLRILEDQEDYLNFI 320  
 QY 294 FNSNAQDVSCF-QHLVQANRKKVLDVNNITAGITDYKKGFSAFEQLLNVNVR- 351  
 Db 321 FSG---DVSTWKEHLVQATPENLQEAQTFVKSMDGNTINDGLLRGISM---NKARE 374  
 QY 352 ----ANCKNIIMLFTDG---GEERAQEIFNKYNK--DKKVRVFRFSVGOHNYERGPIQ 400  
 Db 375 EHRIPERSTSIIVMLTDGDNVNGESPEKIQENVRNAGKFPYLNLFNG-NNLNINFELE 433  
 QY 401 WMACENKYYEIPSGATIRINQEVLDVGRPMVLGAKQVQVNTVYLDALD----- 455  
 Db 434 NMALENHGFARVIEDSDADLQGFYEEVANPL-LTGVEMEYPE--NAILDLTQNTYQH 490  
 QY 456 ----LGLVITGLPVENITQGENKTNLK-----NOLILGVMGVDVSLDEIKRLTPRFTL 506  
 Db 491 FYDGSSEIVVAGRL-VDEDNNSF--KADVKGHGATNOL---TTFEEVDMKEMEK-----AL 539  
 QY 507 CPNGYVFAIDPN-----GVVLIHPNLQPK---NPKSQEPVTLDFDAELNDIKVEIRN 557  
 Db 540 QERDYIFG---NVIERLWAYLTIEQLLEKKNHAGEKENLTARALDLSLKYHFVTPLT 596  
 QY 558 KMIDGESGEKFTLVKSDQERY-DKGNRTYTPVNV-GTDSYSLALVLPFTFYFYI 612  
 Db 597 MVYTKPE-----DNEDERAIDKPGDEAETVPSPAMSYLTSYQPPQNPYYV 644

RESULT 10  
 JC5576  
 Inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster  
 C:Species: Mesocricetus auratus (golden hamster)  
 C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 17-Mar-1999

Db	308	WFDEAAEFCEIRKI-----KLENVKKCRD-----EPNNKYCSGDGHCKRTYLLKDNITF	350
Qy	79	VEIAARDIEKLLNSRKALVSLALEAEKQAAHOWERDEAFASNEWVYVYNAKDDLDPEKNS	138
Db	359	IDLNCPCENACSNYK-----WIEQRQKQDKKK--YMEI---KTKTNSNNENDK	408
Qy	139	E-----PGSORIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVLNNELNWTLSALDE	191
Db	409	EFVENLDKGYSTIN-TFLESNHGKQC-----	438
Qy	192	VFKKNREDSLLWQVFGSATGLARYYPASP-----WVDSRTPNKI	233
Db	439	IDKKNKTFNNKL-ETFGP-----SGYCEACPIYGVKCSNEKTPVTENEMWNNRLPTDT	493
Qy	234	DLVDVRRRPWYIQGAASPKDMLILVDVSGVSGLTKLIRTSVSEMLETSLSDDDDFVNAS	293
Db	494	STRNLN-----ATNDMLVNDGIGNAI-----	515
Qy	294	FNSNAQDVSCFQHLVQANRNKK-----VLKDAVNNTITAGTIDYKKGFSFAFQELL	345
Db	516	--DNELEKNTKYGILKIGKQKQWOCYQNLNITDOCKINNVMNSGYFDNKIAFNVLFORWL	573
Qy	346	NYVVSRAKNCKIIMLFTDGEERAQELFNKYDKKVRFRPSVGQHNVERGPIQWACE	405
Db	574	RYFYRDHNRLL-----EKIDYCIKENINENICIKRCKTN-----CE	610
Qy	406	NKGYYEIPISGAIIRI-----NTQYELDVLGRPVLADGAKOVQNTVYDLDALEGLVIT	461
Db	611	CVGKWLKKBAEWKINQHVQKNRHHFILIPWITGFYEK-ITFPNDFFKALE-----DV	665
Qy	462	GTLPVFVITQOFENKTNLKNQILGVMDVSLIEDIKRLTPRFTLCPNGYIYFAIDPNGVY	521
Db	666	DTINVLDLKECOD-THCKIEKIRSI-DVDLKEILSWLQNKIEVCKS--HHDEKHEVC	721
Qy	522	LLHPNLQPNPKSQEPVTLDFDLAELENDIKVEIRKNMIDGSGEKT-----FFT	571
Db	722	C---DILPLQSVDDDEED-BEVDEEKESSQTTKRN--ISQKGGTKSACSVKGACAIKVG	775
Qy	572	LKVSODERYID---KGNRTYTW-----TPVNGTD-----YSLALVLPTYSF	609
Db	776	VLQOKSNGSIDCNKARKKNEWQCOKNTFVDGNEGVCMPPRKSCICHNLFLIEQTRNK	835
Qy	610	Y-----YIKAKLEET-ITOARSKKGMKDSETLK---PDNFEE--SGYFFIAPROYC--N	656
Db	836	YQLREAFIKAAKETLLMDKYKNDKNEAEELLKKGKIPEDFMRIMFYTFGDFROFCLEN	895
Qy	657	DL-----KISDNTTEFLNFEFIDRK-----TPNPFSC--NADLINRVLDAGFTNEL	703
Db	896	DMGKDVDKVKKNINKVFNNSKRGFKKIDPENWNNWNGPQIWNGLMCAIHAHTDKSDIKN	955
Qy	704	VQNY-----	723
Db	956	KDNYKYEKVILAKRDSNGMTLSEFAKPKFLRWFWVDDYCKERQKYLEVASTCKS	1011
Qy	724	TDGITRV-----YPKAEAGENQENPETYEDSPYKRSLDN-----DNYV-762	
Db	1016	IDGSQLKDRGCNKKDEYKKYWRKKKEEWNLDQKYKQKRENGKIDKGPIGLIVKDYVL	1071
Qy	763	-----FTAPYFNKSPGAYESGIVWYKAVEIYIOGKLLKPAVGIKIDVNSWI---810	
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Qy	811	-----ENEFKTSIRQPCAGPVCCK-----RNSDVMDCVIL	841
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C;Date:	10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000		
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R.; Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; Robson, K.J.  
J. Cell Biol. 120, 385-398, 1993  
A; Title: A family of cation Arape-like molecules from Plasmodium falciparum.  
A; Reference number: A44396; MUID: 93132070  
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QY	107	VOAAHQWREDFASNEVYVYNAKDDLPKND-----SEPGSRIKPVFIEDANFGROIS	160		
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QY	161	YQRAVHIPTDIYEGSTIVLNELNW-TSALDEVFKKNEEDPSLLWQVFGSATGLARYP	219		
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DB	273	-----YNNNNNNKKKKNLN-----FVKTYINSNDLLY-----	303		
QY	279	MLETSDDDFVNVAFSNAODVSGFOHLVQANVRNKVKLDVANNITAKGIDTYKKGFS	338		
DB	304	-----DDKIGVNIPE-----DVNNMKH--KFNORININYNNKDTNNL-----EYNNKHR	345		
QY	339	FAFEOOLLNYSRANCNKIIMLFTDGGERAQETFNKYNKDKVFRVSVQHNVERGP	398		
DB	346	YIYDCLLKVEAISOKKIY-----SNEIDNKY-----	374		
QY	399	IQWACENKGYEYEPSIGAIRINTQEYLDVLRPMVLG-----DKAKQV	444		
DB	375	-----MLYGGTVLSYNLNKYNKYNKEENRILGL-VIKGTFTTKGIVNNLYHKREL	429		
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QY	488	MGVDVSLIEDIKRLTPRFLCPNGYFA-----IDPNGYVLLHPNLO-----PKNPKSO	535		
DB	489	VGISIAISRLKKFSISCLCPHKINAGIOWPMVFDKTG-TLTENNLOFIIITQNKNNK	547		
QY	536	EPVTLDFDAELENDIKVEIRKNMIDGESGKFTFTLVKSQDERYIDKGNRTYITWTPVG	595		
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C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999					
A; Accession: D64998					
R.; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;					
A.; Rose, D.J.; Mau, B.; Shao, Y.					
Science 277, 1453-1462, 1997					
A; Title: The complete genome sequence of Escherichia coli K-12.					
A; Reference number: A64720; MUID: 97426617					
A; Accession: D64998					
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QY	131	LDPEKND-----SEPGSRIKPVFIEDANFGQISVQHAA---VHIPTDI	172		
DB	76	LOGRLQEAFTFAAKAKATHANEGTARYQOF---DDNPVQVAQNPLATSLDVGDS	132		
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QY	338	SFAEQLLNYSRANCNKIIMLFTDG-----GEERAQEIFNKYNKOKKVRVFRSVQ	391		
DB	297	ELAYQOATK-GFIKGINR-ILLATDGFNVGDIDDPKSTESVMVKQKQESGVTSTFGVGN	354		
QY	392	HNVERGPIONMACENKGYEYIPSGAINTQEYLDVLRPMVL--AGDKAKQVQ---	445		
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Qy	72	PNNARQLVEIARAIDIEKLKLSNRG-----KALVS-----LALAEKVOAAHQWRDEFSASNEW	123	
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Qy	124	YNAKD-----DLDPKNDSEPGSQRIKP-----VFTEANQGR-	157	
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Qy	158	QISQHAHVHIPTDIYEGSTIVLNEIWNLTSDALDEVPKKNREEDPSLLWQVFGSATGLARY	217	
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Qy	278	EMLETLDDDDFVNVAFSNNAQDVSCFHLVQANVRNKKVLKADVANNITAK---GITYIK	334	
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Qy	335	KGFSFAFEQLLNN-----VSRA-----NCNKIIMLFTD-----GGEERAQ	370	
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QY 421 INTQEYLDVLRPMVLGDKAKO-----VQWTVNYLDALELGLVITGTL 465
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Db 1565 ILKFMNNAKSALNTSNLNFLESINIK-----NIFYNNLDPNIEFILD 1609
QY 526 NQPKNPKSOEPTVTLDFLOAELENDIKVEIRKMDGEGEKTFRTLVKSQDERYIDKGN 585
Db 1610 NF-----IISGSNSIGQFE-LICDKKN-----1631
QY 586 RTYTPTVNGTDSLALVPTSYFYIKAKLETTIQAQRSKGKMKDSETLKPDNFEESG 645
Db 1632 -----IQP-----YFINKIKET-----SYTLYVGNRQN-- 1655
QY 646 YTFIAPRYCNDLKISDNTEFLNFNE-----FIDR---KTPNNPSCNADLIN----- 691
Db 1656 -LIVEPSYHLDD---SGNISSTVINFSQKLYGIDRVNKKVIAIAPNLYTDEINITPVYKP 1711
QY 692 -----RYLDAQTNE-----LVQNYW-----SKOKNIKGVKARFVVT 724
Db 1712 NYICPEVILLDANYINEKINVINLDIRVVDNDGSDLLILIANSEEDNQPVKIRFV-- 1769
QY 725 DGGITRVYPKEAGE-----NWQENPE-----TYEDSFYKR-----SLDNDNY 761
Db 1770 -----NVFKSDTAADKLSEFNSDKQDVSVSKIISTFSLAAYSDFEYFGLVSLDND-- 1822
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Db 1861 -----DGN-----KYFDPKSGAASIGEI-----TIDGKD 1886
QY 880 YAFNKSVDYOSVCEPGNAPKQAGHRSAYVPSVADILQIGWATAAWSILQOFLLSLTF 939
Db 1887 YTFN-----KOG-----ILOQGVINTSDG---LKYFAPAGTL 1915
QY 940 PRLEAVEME-----DDDFATSLKQSCITEQTOYFFDNDNDSKFSFGVLDG 985
Db 1916 DENLEGESVNFICKLNIDGKIYYFEDNYRAV-EWKLDDETYYFNPKTGEALKGLHQIG 1974
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Job time: 511 sec



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QY 421 INTQEVLDVLRPMVLADKAKQVQWNTVYLDALGLVITCTLPVFNITGOFENKTNLK 480  
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DT 01-OCT-2000 (Rel. 40, Last annotation update)  
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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RX MEDLINE-92228762; PubMed-1314383;  
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;  
RT "Rat brain expresses an alternatively spliced form of the  
R dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).  
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
CC EXCITATION-CONTRACTION COUPLING.  
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
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CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -1- PM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
CC A PRECURSOR FORM (BY SIMILARITY).  
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M86621; AAA41088.1; -;  
DR InterPro; IPR002035; -;  
DR Pfam; PF00092; vwa; 1.  
DR PROSITE; PS50234; VWFA\_DOMAIN; 1.  
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

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KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW Alternative splicing.
FT SIGNAL 1 24 POTENTIAL.
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FT FT (BY SIMILARITY).
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FT FT SIMILARITY).
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FT TRANSMEM 906 930 POTENTIAL.
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FT FT (BY SIMILARITY).
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Best Local Similarity 95.7%; Pred. No. 2.9e-293;
Matches 992; Conservative 24; Mismatches 19; Indels 2; Gaps 2;

QY 1 MAAGCLLATLTLFQSLLLGPSEEPFPAVNIKSWDKMQEDLVTLAKTASGVNGLVDI 60
DB 1 MAAGCLLATLTLFQSLWLLGPSEEPFPAVNIKSWDKMQEDLVTLAKTASGVTLADI 60
QY 61 YEKYQDLYVEPNNAQLVEIARDETEKLSNRKALVSLALEAEKVAQAQHWREDFASN 120
DB 61 YEKYQDLYVEPNNAQLVEIARDETEKLSNRKALVSLALEAEKVAQAQHWREDFASN 120
QY 121 EYVYNAKDDLPENKDSPEGSORIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPENKDSPEGSORIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSSALDEVEFKKNEEDPSLLWQVGSATGLARYYPASPWVDSRTPNKTIDLYDVR 240
DB 181 NELNWTSSALDEVEFKKNEEDPSLLWQVGSATGLARYYPASPWVDSRTPNKTIDLYDVR 240
QY 241 RPWYIGGAAPKMDLTLVDVSGVSLTLKLTSTVSEMLETSSDDFVNVASFNSNAOD 300
DB 240 RPWYIGGAAPKMDLTLVDVSGVSLTLKLTSTVSEMLETSSDDFVNVASFNSNAOD 300
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGIDYTKGFSFAFQLLNYSRANCNKIIML 360
DB 300 VSCFQHLVQANVRNKKVLDVANNITAKGIDYTKGFSFAFQLLNYSRANCNKIIML 360
QY 361 FTDGGERAQEIFENKYNKDKVRFVRFPSVGHNYERGPIQWACENKGYIETPSIGAIR 420
DB 360 FTDGGERAQEIFENKYNKDKVRFVRFPSVGHNYERGPIQWACENKGYIETPSIGAIR 420
QY 421 INTQEYLDVLRPMVLGAKQKQVQNTNYLDALGLVITGLPVFNITGQENKTNLK 480
DB 420 INTQEYLDVLRPMVLGAKQKQVQNTNYLDALGLVITGLPVFNITGQENKTNLK 480
QY 481 NOLILGVMGVDSLEDKRLTPRTFLCPNGYYPFADPNQVYLLHPNLQPKNPKSQBPVTL 540
DB 480 NOLILGVMGVDSLEDKRLTPRTFLCPNGYYPFADPNQVYLLHPNLQPKNPKSQBPVTL 540
QY 541 DFLDALENDIKVEIRNKMIDGESGKFTFLVKSDQERIDYKGNRTYTWTPVNGTDYR 599
```

J. Biol. Chem. 265:14738-14741(1990).

- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.

- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HETERODIMERS THAT ARE DISULFIDE-LINKED.

- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.

- TISSUE SPECIFICITY: SKELETAL MUSCLE.

- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM.

- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

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EMBL: M21948; AAA81562.1; -  
 PIR: S10579; CHRA2.  
 InterPro: IPR002035; -  
 Pfam: PF00092; vwa; 1.  
 PROSITE: PS0234; VWFA\_DOMAIN; 1.  
 Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Phosphorylation; Signal;  
 Alternative splicing.  
 SIGNAL 1 26  
 CHAIN 27 960  
 CHAIN 961 1106  
 TRANSMEM 448 471  
 TRANSMEM 921 945  
 TRANSMEM 1082 1101  
 CARBOHYD 94 94  
 CARBOHYD 138 138  
 CARBOHYD 186 186  
 CARBOHYD 326 326  
 CARBOHYD 350 350  
 CARBOHYD 477 477  
 CARBOHYD 606 606  
 CARBOHYD 615 615  
 CARBOHYD 678 678  
 CARBOHYD 784 784  
 CARBOHYD 827 827  
 CARBOHYD 891 891  
 CARBOHYD 898 898  
 CARBOHYD 988 988  
 CARBOHYD 1001 1001  
 MOD\_RES 503 503  
 MOD\_RES 848 848  
 SEQUENCE 1106 AA; 125042 MW; B00DE7F3C877B618 CRC64;

Query Match 96.08; Score 5224.5; DB 1; Length 1106;  
 Best Local Similarity 94.7%; Pred. No. le-292;  
 Matches 1002; Conservative 15; Mismatches 12; Indels 29; Gaps 4;

QY 1 MAAGCLLATLTFLQSS--LLIGPSEEPFPAVTKSWDKMQEDLVTLAKTASGVNOLV 58  
 DB 1 MAAGPLAWTLTLQWUWLLIGPSEEPFPAVTKSWDKMQEDLVTLAKTASGVHOLV 60

QY 59 DIYEKYQDLYVEPNNAQRLVEIARDEKLLSNRSKALVSLALEAEKVQAAHQWREDA 118  
 DB 61 DIYEKYQDLYVEPNNAQRLVEIARDEKLLSNRSKALVSLALEAEKVQAAHQWREDA 120

QY 119 SNEVYVYNAKDDLPDEKNDSEPFSGORIKPVFIEDANFRQISYQHAHVHIPTDIYEGSTI 178  
 DB 121 SNEVYVYNAKDDLPDEKNDSEPFSGORIKPVFIEDANFRQISYQHAHVHIPTDIYEGSTI 180

QY 179 VLNELNWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDNKRTPNKIDLYDV 238  
 DB 181 VLNELNWTSSALDEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDNKRTPNKIDLYDV 240  
 QY 239 RRRPWYIOGAASPDKMLILVDVSGSVGLTLKLRISVSEMLETLSDDDDFVNVASFNSNA 298  
 DB 241 RRRPWYIOGAASPDKMLILVDVSGSVGLTLKLRISVSEMLETLSDDDDFVNVASFNSNA 300  
 QY 299 QDVSCFQHLVQANVRNKKVYKDAVNNTAKGTDYDKKGFSAFQELLNTNVSRANCKII 358  
 DB 301 QDVSCFQHLVQANVRNKKVYKDAVNNTAKGTDYDKKGFSAFQELLNTNVSRANCKII 360  
 QY 359 MLFTDGGGERAGEIEFNKYNKKKRVRFESVGOHNVERGPIOMWACENKGYEIEPSIGA 418  
 DB 361 MLFTDGGGERAGEIEFNKYNKKKRVRFESVGOHNVERGPIOMWACENKGYEIEPSIGA 420  
 QY 419 IRTNQEYLDVLRPMVLAGDKAKQVMTNVYLDLLEGLVITGTLPVFNITGQGFENKTN 478  
 DB 421 IRTNQEYLDVLRPMVLAGDKAKQVMTNVYLDLLEGLVITGTLPVFNITGQGFENKTN 480  
 QY 479 LKNQILGVMGVDVLESDIKRLTPRTFLCPNGYYPFAIDPNGYVLLHPNLPQK----- 530  
 DB 481 LKNQILGVMGVDVLESDIKRLTPRTFLCPNGYYPFAIDPNGYVLLHPNLPQKPIGVGIPT 540  
 QY 531 -----NPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTRFLVKQSODER 579  
 DB 541 INLRKRRPNVQPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTRFLVKQSODER 600  
 QY 580 YIDKGNRTYTWTPVANGTDY-SLALVLPYTSFYIYKAKLEETITQARSKKGMKDSSELPK 638  
 DB 601 YIDKGNRTYTWTPVANGTDYSSSLALVLPYTSFYIYKAKLEETITQARY-----SETLAP 653  
 QY 639 DNFEESGYTFTAPRDYCNLDKISDNTEFLNPFIDRKTPNPNPCNADLNIRVLLDAG 698  
 DB 654 DNFEESGYTFTAPRDYCNLDKISDNTEFLNPFIDRKTPNPNPCNADLNIRVLLDAG 713  
 QY 699 FTNELVQNVWSKQKNIKGVKARFVTDGGITRVYKPEAGENQENPETVEDSFYKRLDN 758  
 DB 714 FTNELVQNVWSKQKNIKGVKARFVTDGGITRVYKPEAGENQENPETVEDSFYKRLDN 773  
 QY 759 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIQGKLLPAVVGIVKIDVNSWIENFTKTSI 818  
 DB 774 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIQGKLLPAVVGIVKIDVNSWIENFTKTSI 833  
 QY 819 RDPGAPVCDCKRNSDVMDCVILDDGFLMANHDDYTNQIGRFFGEIDPISLMRHLVNTS 878  
 DB 834 RDPGAPVCDCKRNSDVMDCVILDDGFLMANHDDYTNQIGRFFGEIDPISLMRHLVNTS 893  
 QY 879 VYAFNKSVDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGHWATAAASIIQQFLLSLT 938  
 DB 894 VYAFNKSVDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGHWATAAASIIQQFLLSLT 953  
 QY 939 FPRLEAEVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDCGNCGRIFHGEKLAN 998  
 DB 954 FPRLEAEVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDCGNCGRIFHGEKLAN 1013  
 QY 999 TNLIFIMVESKGTCPDTRLLIQAEQTSDDGNPCDMVK 1036  
 DB 1014 TNLIFIMVESKGTCPDTRLLIQAEQTSDDGNPCDMVK 1051

## RESULT 4

UN36\_CAEEL STANDARD; PRT; 734 AA.  
 AC P34374;  
 DT 01-FEB-1994 (Rel.: 28, Created)  
 DT 01-FEB-1994 (Rel.: 28, Last sequence update)  
 DT 01-OCT-2000 (Rel.: 40, Last annotation update)  
 DE UNC-36 PROTEIN.  
 GN UNC-36 OR UNC-72 OR C50C3.11.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,  
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,  
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 RA Watson R., Watson K., Weinstock L., Wilkinson-Sproat J.,  
 RA Wohlman P.;  
 RT \*2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.;  
 RL Nature 368:32-38(1994).  
 CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: L14433; AAA27969.1; -;  
 DR PIR: S44617; S44617.  
 DR WormPep: C50C3.11; CE00117.  
 DR InterPro: IPR002035; -;  
 DR Pfam: PF00092; vwa: 1.  
 DR PROSITE: PS0234; VWFA\_DOMAIN; 1.  
 DR Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;  
 KW Glycoprotein.  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 734 AA; 85034 MW; CCFB78C8DEB4B71F CRC64;  
 SQ  
 Query Match 11.2%; Score 607; DB 1; Length 734;  
 Best Local Similarity 26.6%; Pred. No. 1.3e-27;  
 Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;  
 QY 47 LAKTAGVQLVDYKQYQDLYTEPNARQLVEIAARDTEKLLSNRS----KALVSLAL 102  
 DB 36 MKETFSKISHETIKQYKXELVEEQDPPRAELKSKHRIEDYLVKRSQFAYRAKIS--L 93  
 QY 103 EAKVQAHHQWRDEFASNVYVYNAKDDLDPEK--NDSEPGSQRIK-----VFIEDANF 155  
 DB 94 EARSVRNDSTVNDPQSKSFREMSAKOGNDGTIYESNHLGKRLKVNKTSFNLTONANF 153  
 QY 156 -GROISVQHAHVHPTDYGSTIVLNELNWTALDEVFKNKREEDPSLLWQVFGSATGL 214  
 DB 154 YTLPTSSVSSAVHIPTPLDYDRNEDLLKIDW--SDIDAVYRTNREETDLAFQFCSEAGY 212  
 QY 215 ARYPASPFW--DNSRTNKTLDYVRRPWPYIQGAASPDKMLIIVDVSGVSGTLKLIR 273  
 DB 213 MRYTPAASWFWNDQ--DEHLDFDCRTEWYINSATNSKNVILNMDSGSMGLQRYEVAK 270  
 QY 274 TSVSEMLETSDDDFVNVAWSNSNA---QDVSCFOHLVQANRNKVKYLDKAVNNITAKGI 330  
 DB 271 QTTEAILETISHNDYFNIMTFKNTFLDCNGTNGTNGLLQATMRNKKALRKMDYQSEKG 330  
 QY 331 TDYKKGFSFAPEQLLYN-----YSRANCKNIIMLTGGEERAQAEIFKNYKNDKRVRF 385

Db 331 AEYEKALPIAFSVLLDINNGGDNRRGACENVIMLTGAPNAYKKIFDMYNADKKRVRF 390  
 QY 386 RFSVGQHNTERGPIQWMAKNGYIYEIPSGAIRINTQYEL----DVLGRPMVLAGDKA 441  
 Db 391 TFLVGDDEAIDFNEVREMACNNRGYMHVANNADVDEKIHYYIRMSRVVGRHYKESGOLS 450  
 QY 442 KQVQWNNVYLDLELGL--VITGTLPVFNITGQFENKTN----- 478  
 Db 451 ---WMTGVYRERLYRPEIFAEPVPITNQSFVAMNMKMSRRKIRLOKSPARSRMFTTV 507  
 QY 479 ---LKNOLLIGVMGVDSLEKRLTPRTFLCPNGYFFAIDPNGYVLLHPNLQPKNP-- 532  
 Db 508 SYPIVNEFTMGVAANNIPLEVAQKSHPANIGSKSYFFMLDQNGFVMTHPQLRPIDPFT 567  
 QY 533 --KSQEPVTLDFLD-----AELENDIKVEIRNMKID 561  
 Db 568 KYHKQNNNNMDLLELVGQNNVRSQSAVSDLVCEGANTYAECDLRLKAVRKMID 627  
 QY 562 GESGEKTRFLVKSQDERY---IDK---GNRTYTWTPVNGTDYSLALVLPYTSFYVKA 614  
 Db 628 CDNSD-----VOOLDVLYATELLDRVYPOTNTYAEICINHANFVLGLAVAKGDDYRVK 681  
 QY 615 KLEETITQARSKKGMK 631  
 Db 682 K-----QKKYDFGRVK 692  
 RESULT 5  
 ITH3\_MOUSE  
 ID ITH3\_MOUSE STANDARD; PRT; 886 AA.  
 AC Q61704;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY  
 DE CHAIN H3).  
 GN ITH3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6N; TISSUE=Liver;  
 RX MEDLINE=95194326; PubMed=7534067;  
 RA Chan P., Risler J.-L., Raguenez G., Salier J.-P.;  
 RT "The three heavy-chain precursors for the inter-alpha-inhibitor  
 RT family in mouse: new members of the multicopper oxidase protein group  
 RT with differential transcription in liver and brain".  
 RL Biochem. J. 306:505-512(1995).  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2  
 CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ITH3 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
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[illegible]



[illegible]

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434 NMALENHGFAARRIYEDSDADLQGFVEEVANPL-LTGVEMEYPE--NAILDLTQNTQGH 490
QY 456 ----LGLVTGTLPVNIHQFENKTNLK-----NOLLGVGVGDVSLDEDIKRLTPREFL 506
Db 491 FYDGSIEIVAGRL-VDEDMNSF--KADVGHGATNDL---TTFTEEDVMKEMEK-----AL 539
QY 507 CPNGXYFAIDPN-----GYVLHLPNLQPK--NPKSQBPVTLDFDLDAELENIDKIVEIRN 557
Db 540 QEDYIFG---NVIERLWAYLTTEQLLEKKNHAHGEKENLTARALDLSLYKHVFVTPLT 596
QY 558 KMIDGESGKFTFTLVKSODERYI-DKGNRTYTPVNW-GTDSYSLALVLPPTSFYII 612
Db 597 MVTKPE-----DNEDEIRAIDKPGSDAETVPSPAMSYLTGYPPQNPYYV 644

RESULT 7
ITIH3_RAT
ID ITIH3_RAT STANDARD; PRT; 887 AA.
AC Q63416;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3).
DE ITIH3.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RA Blom A., Fries E.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).
CC -! SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -! PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -! SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC
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CC
CC EMBL; X83231; CAA58233.1; -.
CC DR InterPro; IPR002035; -.
CC DR Pfam; PF00092; vwa: 1.
CC DR PROSITE; PS0234; VWFA_DOMAIN; 1.
CC KW Serine protease inhibitor; Repeat; Signal; Multigene family; Glycoprotein.
CC FT SIGNAL 1 21 POTENTIAL.
CC FT PROPEP 22 33 BY SIMILARITY.
CC FT CHAIN 34 647 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3.
CC
CC FT PROPEP 648 887 BY SIMILARITY.
CC FT DOMAIN 282 442 VWFA.
CC FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).

```



SQ SEQUENCE 1829 AA; 211875 MW; A113A8BC57EB9CB3 CRC64;

Query Match 3.0%; Score 161; DB 1; Length 1829;  
Best Local Similarity 20.1%; Pred. No. 0.21;  
Matches 172; Conservative 101; Mismatches 301; Indels 282; Gaps 39;

QY 16 SLLIGSPSEEPFPPS-----AVTIKSWV-----DKMQEDLVILA 48  
DB 229 TLLGDRKEHEPEKTHRMGDSFAVEIKGRIHFDLPVVRRTINLPTYTELEAVEVLGT 288  
QY 49 KTASGVNOLVDIYKQDL-----YVPEPNARQVLETAARDIEKLLSNRSKALVSLALE 103  
DB 289 KSKLGAEEAIAWETESMKLAQYSME--DARATYEL-----GFEPPMEAE 334  
QY 104 AEKVQAAHQWREDFAS--NEVVY-----NAKDDLDPEKNDSPEQSRIKPVFI----- 150  
DB 335 LAKLIGQSVMDVSSTGNLVEWYLLRVAYERNELAPNKPDEEYRRRLRTTYLGGYVKE 394  
QY 151 EDANFGROIISYQHAAVHIPTD--IYEGSTIV-----LNLNMTSALDEVFKNREEDPSL 203  
DB 395 PERGLWENIAYLDFRCH-PADTKVIVKGGIVNISDKGDIILGIDG----- 441  
QY 204 LMQVFGSATGLARYYPASPVNDSR---TPN-KIDLDYVRRRPWYIQAASPKDMLILVD 259  
DB 442 -WQ---RVKKVWKHYEGKLININGLKCTPNHKVPVVTENDROTRI-----RDSLAKSF 491  
QY 260 VSGSVGLTKLIRTSVSEMLETLSDDDFVNVSFNSN----- 297  
DB 492 LSGKVGK---KIITTKL-----PEKIAEFKPKPSEEEILKGELSGIILAEGTL 537  
QY 298 -AODVSCF-----QHLVQANV-RNKKVYLKDAV-----NNITAKG----- 329  
DB 538 LRKDEYFDSRRGKKRISHQYRVEITIGENEKELLERYIFDKLFGIRPSVKKKGDTNA 597  
QY 330 --ITDYKKGFSFAPEOLLNWNVRANCNKIIMLFTDGGEEAQAQEIFNKYKNDKKVRVERF 387  
DB 598 LKITTAKAVYLOIEELLK-NIESLYAPAVLRGF-----FERDATVVKIRS 642  
QY 388 SV---GOHNYERGPIQWACENKGY---YIEIPSGAIAINTQEVLDVILGRPMVLGDK 440  
DB 643 TVIVTQGTNNKKKIDIVAKLLDSLGIPSYRYEYKIENGKELKHILEITGRD----- 695  
QY 441 AKQVQMTNVYLDALGLVITGLPVFNITQGF-----NKTNNKQLILGVMGVD 491  
DB 696 -----GLILFQTLVGFISSEKNEALEKAIEVREMNRLKNSFNLTSTFE 739  
QY 492 VSLEDIKRLPRTFLCPNGYFAIDPNGYVLLHPNLPKPKSQEPVTLDFDLDALENDI 551  
DB 740 VSSEYKGEVYDLTLEGNPYFA---NG-ILTHNSLYPSIIVTHN-VSPDTLRE----- 789  
QY 552 KVEIRNMKIDGSEGEKFTRLVKSDERYIDKGNRTYVTPVNGTDSYSLVLPYTSFY 611  
DB 790 -----GCKNDVAPIVG--YKFKDFPG----F 811  
QY 612 IKAKLEETITQARSKKGMKMDSETLKPDPNFEEGY-----TFTAPRYCNDLKISD 662  
DB 812 IPSILGELITMRQEIKKMK--ATIDPIEKKMLDYRORAVKLLANSILPNW---LPIIE 866  
QY 663 NNTFLLNFNEFDIKRTPNPNPNSCNADLINRVLLDAGFTNVLQVWWSKQKIKGVKARFV 722  
DB 867 NGEVFKVIGEFIDRYMBEQDKVRTVDNTEVLEVDNITAFSLNKSSEKSEIKVKAL-- 924  
QY 723 VTDGTRVYYPEAGE 738  
DB 925 -----IRHKYKGEAYE 935

RESULT 10  
ATX1\_PLAFA  
ID ATX1\_PLAFA  
AC Q04956;  
DT 30-MAY-2000 (Rel. 39, Created)

QY 202 SLLMQVFGSATGLARYYPASPVNDSR--PNKID-----LYDVRRR-PWYIQA-- 248  
DB 208 SALTSGSGKGGHVSFKPS---LDQORSCPTCTDSSLNGDFTIYDVNRESFGNVQVYNG 264  
QY 249 -----ASPKDMLILVDYSGSVGLTKLIRTSVSEMLETLSDDDFVNVSFNS 296  
DB 265 YFVHFAPQGLPVVFNKNTVFVIDISGSMAGRKIQOTRVALLKILDDMKQDDYLNFILEST 324  
QY 297 NAQDVSCFQHLVQANVRNKKVYLKDAVNITAKGITDYKKGFSFAFEQLLN-----YVNSRA 352  
DB 325 GV--TTWDSLVQATPANLEARTVRSISDOGMTNINDGLLGRIMLTDAREQHTVPER 382  
QY 353 NGNKIIMLFTDG-----GEARQAEIFNKYKNDKKVRVRSVG-QHNYERGPIQWACENK 407  
DB 383 SFSIIIML-TDGDANTGESRPEKIQENVRKATEGRFPLYNLGGFNGLNFTMALENH 441  
QY 408 GYIYEIPSGAIRINTQEVLDVILGRPMVLGDKAKQVQMTNVYLD 452  
DB 442 GVARIYEDSDANLQGGVEEYVAPLL-----TNVEVE 475

RESULT 9  
DPOL\_THEST STANDARD; PRT; 1829 AA.  
AC O33845;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE DNA POLYMERASE (EC 2.7.7.7).  
GN POL.  
OS Thermococcus sp. (strain TY).  
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.  
OX NCBI\_TaxID=86030;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98094267; PubMed=94341178;  
RA Niehaus F., Frey B., Antranikian G.;  
RT "Cloning and characterization of a thermostable alpha-DNA polymerase  
from the hyperthermophilic archaeon Thermococcus sp. TY";  
RL Gene 204:153-158(1997).  
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =  
N PYROPHOSPHATE + DNA(N).  
CC -1- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES  
A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION  
(INTEINS), FOLLOWED BY PEPTIDE LIGATION.  
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.  
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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC EMBL; Y13030; CAA73475.1;  
CC InterPro; IPR002064;  
CC InterPro; IPR002203;  
CC Pfam; PF00136; DNA\_pol\_B; 4.  
CC PRINTS; PR00379; INTEIN.  
CC PROSITE; PS00116; DNA\_POLYMERASE\_B; FALSE\_NEG.  
CC PROSITE; PS00881; PROTEIN\_SPLICING; 3.  
KW Transferase; DNA-directed DNA polymerase; DNA replication;  
KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;  
KW Protein splicing.  
KW CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).  
FT CHAIN 410 769 INTEIN I.  
FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).  
FT CHAIN 856 1392 INTEIN II.  
FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).  
FT CHAIN 1442 1598 INTEIN III.  
FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).

DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE PROBABLE CATION-TRANSPORTING ATPASE 1 (EC 3.6.1.-).  
OS Plasmodium falciparum.  
OX Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
RN NCBI\_TaxID=5833;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=T9/96;  
RX MEDLINE=93132070; PubMed=8421054;  
RA Krishna S.; Cowan G.; Meade J.C.; Wells R.A.; Stringer J.R.,  
RT "A family of cation ATPase-like molecules from Plasmodium  
RT falciparum".  
RL J. Cell Biol. 120:385-398(1993).  
CC - CATALYTIC ACTIVITY: ATP + H<sub>2</sub>O -> ADP + ORTHOPHOSPHATE.  
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC - SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2  
ATPASES). SUBFAMILY V.  
CC  
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CC  
CC EMBL; X65738; CA44646.1; -  
DR InterPro; IPR001757; -  
DR Pfam; PF00122; E1-E2 ATPase; 4.  
DR PROSITE; PS00154; ATPASE\_E1\_E2; 1.  
KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.  
FT DOMAIN 1 35  
FT TRANSMEM 36 58  
FT DOMAIN 59 61  
FT TRANSMEM 62 80  
FT DOMAIN 81 407  
FT TRANSMEM 408 427  
FT DOMAIN 428 440  
FT TRANSMEM 441 462  
FT DOMAIN 463 1818  
FT TRANSMEM 1819 1837  
FT DOMAIN 1838 1845  
FT TRANSMEM 1846 1863  
FT DOMAIN 1864 1881  
FT TRANSMEM 1882 1905  
FT DOMAIN 1906 1928  
FT TRANSMEM 1929 1952  
FT DOMAIN 1953 1956  
FT MOD\_RES 496 496  
FT METAL 1760 1760  
FT METAL 1764 1764  
FT DOMAIN 246 251  
FT DOMAIN 252 256  
FT DOMAIN 937 941  
FT DOMAIN 1344 1347  
FT DOMAIN 1363 1372  
FT DOMAIN 1680 1684  
FT SEQUENCE 1956 AA; 230285 MW; AE708AAE99009335 CRC64;  
Query Match 2.9%; Score 159; DB 1; Length 1956;  
Best Local Similarity 17.1%; Pred. No. 0.3; Mismatches 359; Indels 366; Gaps 45;  
Matches 179; Conservative 144;  
QY 58 VDYEKQDYTYEPNNARQVIAARDIEKLNSR-----SKALVSALAEAK 106  
DB 100 INV-RNTSYISS-----ELVPGDIYEIKNNMTIPCDTIILSGSVTMSHMTGES 152  
QY 107 VQAAHWRDFASNEVYVYNAKDDLPKND-----SEPGSRIKPVFTEDANFGQIS 160  
DB 153 V-PHKRLPFEGNAIKNNKYDSNDEKDDYLRINYNNHASINMKRNHLIETLGGKDR 211

QY 161 YQAAVHIPTDIYEGSTIVLNLNW-TSALDEVFKNREDEPSLLMQVEGSGATGLARYYP 219  
DB 212 EYKSNTH-----DLCSMNKLCYINNTYDVMKNNKM----- 244  
QY 220 ASPWYDNRKTPNKKIDLYDVRRPWTIOGA-ASPDKMLILVDVSGSGVGLTKLIRTSVSE 278  
DB 245 ---YNNNNNNKKKKINLN---FVKGTYINSNLLY----- 275  
QY 279 MLETLSDDDFVNVAFSNSNAQDVSCFOHLVQAVNRKKVYLKDAVNNITAKGTDYKKGFS 338  
DB 276 -----DDKIGVNIPE---DDVNNMKH--KFNQRININYKNDTNL-----EYNNKHR 317  
QY 339 FAFEQLLNYSVRANCKIIMLTGGEERAQEIFNKYNKDKKRVFRFSVGOHNYTERGP 398  
DB 318 YIYDCLLKVEAISOKNLIY-----SNEDINKY----- 346  
QY 399 IOWMACENKGYEYEPSIGAIRINQOEYLDVLRPMVLAG-----DKAKQV 444  
DB 347 ----MLYGGTYVLSLYNINKIKYNNKEENRIIGL-VIKTGFTTKGIVNNILYHKKKEL 401  
QY 445 QWTVNYLDALEGLVITGTLPVNITGQFENKTNLKNQILG-----V 487  
DB 402 NLINDSYKFLII-LIYALFSVFIILYITLSNNEYTNHIIKCLDIITDAIPALPTILT 460  
QY 488 MGVDSVLEDIKRLTPRTTLCPPNGYIEFA-----IDPNGYVLLHPNLQ-----PKNPKSQ 535  
DB 461 VGIATAISRLKKKFSISCLCPHKINAGQINTVMFDKGT-TLTENNLFQIITQNKKNK 519  
QY 536 EPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRLVKSQDERYIDKGNRTYTWTPVNG 595  
DB 520 NMLS-DFIHK-----EMNTESIYHSKDDNMHNKN----- 549  
QY 596 TDYSLALVLTYSFYVYKAKLEETITQARSKGKMKD-----SETLKPDPNFEESG 645  
DB 550 -----SIIEYIKONMMNLTSSK-KKSITKERSNFIQVTKSCLLKDHYYKEKK 599  
QY 646 YTFIAPRDYCNLDKISDNN-TEFLN-----FNEF--IDRKTNNPNSCNADLINRVLLD 696  
DB 600 KEYTNTNYCNDLHINDSTCSSYLLANSETKDAYCEYVNIH-----LCD---INKNMD 650  
QY 697 AGFTNELVQNSKQKNIKGVKARFVVTTGGITRVYPKEAGENWQENPETEYDSFYKRS 756  
DB 651 INSKNELMGKYSKNELMGKTKNELM-----GKYSKNEL 684  
QY 757 DNDNYVFTAPYFNKSGGAYESGIMVSKAVEIYIOGKLLKPAVVG-----IKIDVNSWI 810  
DB 685 -----MGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNEL 737  
QY 811 ENFTKTSIRD-PCAGPVCDCKRNSDVMDCV-----ILDDGGFLLMANHDDYTNOIGRF--- 862  
DB 738 MNCNDNYNDYPCD---YNCNCCNDYHRLYHNINKNSFNIPPEKNKSYNNISEHIKI 794  
QY 863 -----FGEIDPSLMRHLNVSIVAF-----NKSDYQ 889  
DB 795 NYPLLFEALACCHTLKSVNNKIMGDVLEILMFNFTNCDMLINNNSFIKEKKKNCSDYFQ 854  
QY 890 SVCEPAAAPQAGAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFFRLLAEVEME 949  
DB 855 KI---DGDKNIGANDERCHLNN-----NLVSYNILKRF----- 884  
QY 950 DDDFTASLSKQSCITEQTQYFFDNDKS 977  
DB 885 --EFQRLQRMVIVKST-YGNNDNNDN 909  
RESULT 11  
YFBK\_ECOLI STANDARD; PRT; 575 AA.  
AC YFBK\_ECOLI  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)







PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.  
 DR KW INIT\_MET 0 0  
 FT CHAIN 1 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN.  
 FT CHAIN 449 1290 BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN.  
 FT METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT\_SITE 229 229 BY SIMILARITY.  
 FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT DISULFID 436 452 INTERCHAIN (PROBABLE).  
 FT CONFLICT 84 84 P -> T (IN REF. 2).  
 SQ SEQUENCE 1290 AA; 148734 MW; 71FBE379F97129E8 CRC64;  
 Query Match 2.8%; Score 152; DB 1; Length 1290;  
 Best Local Similarity 20.3%; Pred. No. 0.42;  
 Matches 205; Conservative 125; Mismatches 346; Indels 334; Gaps 54;  
 QY 106 KVOAHOHREDFASNEVYVYNAKDDLDPEKNDSEPSQRIK---PVFIEDANFR----- 157  
 Db 138 KTRQGNVYKTSINPSVIITG-----PRENIIDPSTFKLTNNTFAAQEGFALSIIIS 192  
 QY 158 -----QISYQHAHVHIPTDIYEGS-----TIVLNELNWTSAIDVFK---KNRE 198  
 Db 193 ISPRFLMITYSNAT---NDVGEGRFSKSEFCMDPILILMHELN---HAMHNLGIAIPNDQ 246  
 QY 199 EDPSLLMQVFGSATGLARYYP-----ASPWVDSRTPNKIDLYDVRPPVYIOGAASPKD 253  
 Db 247 TISSVTSNIEFVSQVNVKLEYAEIYAFGGPTID--LIPKSARKYFEKALDYRSIAKRLN 304  
 QY 254 MLILVDVSG---SVSGTLKLIR-----TSVSEMLTSLDDDFVNVASNSNAQDVSCF 304  
 Db 305 SITTANPSPFNKYGKQKLRKIRYFVPSSEGEV---TVNRKFKVEL---YNELTQIFTEF 360  
 QY 305 QHLVQANVRNKKV-LKDAVNNTAK-----GTDYKKGFSFAFQI---LNNVSR----- 351  
 Db 361 NYAKIYVQNRKIYLSNVYTPVTANILDDNVYDQNGFNIPKSNLNLVFMGNLSRNPAL 420  
 QY 352 --ANCKNIIMLFT-----DGGEERAQEIENK-----YNKD-----KKRVYR 386  
 Db 421 RKVPENMLYLFKFKHKAIDG-----RSLYNTKTLDCRELLVKVNTDLFFIGDISDKTDI 475  
 QY 387 FSVGOHNVGRPIQWACENKNGYVEIPIPSIGAIRI--NTQEV--LDVL----- 430  
 Db 476 FLRKDINETEVI-----YYPDNVSDVOVLISKNTSEHGDLDLVPSIDSEILP 526  
 QY 431 GRPMVLADGKAKOVQWNT--VYDLALELGLVITGLTPVFNITGQFENKTN----- 478  
 Db 527 GENQFYDNRTQNDYLSNYLLESQKL-----SDNVEDFTFRSIEEALDSAKYVITYPP 582  
 QY 479 -LKNOLLILGVMG-----VDVSLIEDIKRLTPRFLCPNGYFPAIDPNGYVLLHPNLOPK 530  
 Db 583 TLANKVNAVQVGGFLMWANDVVEFTTNILRKDTLKDSDVSAIIP-----YIGPALNIS 638  
 QY 531 NPKSOEPTVLDL-----DLAELENDI-----KVEIRNKWIDGESSEKTFRTL 572  
 Db 639 NSVRGNFTAEFAVGTGVTILLFAPEFTTPALGAFVIYSKVQERNELI-----KTDNC 692  
 QY 573 VRSQDERYDKGNRTYTW-----TPVNGCTYSALVLPTFYFYIYKAKLEETITQ 622  
 Db 693 LEQRIKRWKD-----SYEWMGTWLSLIITQFNINISQMYDSL-NYQAGAIAKID----- 742  
 QY 623 ARSKKMKMDSETLKP--DNFEESGYTFIAPRDYCNLDKISDNNTBELLNFNEFI----- 675  
 Db 743 LEYKKGSGSKENIKSQVENLKN-----LDVKIS-----EAMNINKFIRECSV 787  
 QY 676 -----DRKTPNPNPCNADLNLNVLDA----- 697  
 Db 788 TYLFKNMPLKVIDELNEFDRT-----KAKLIN--LIDSHNIIILVEVDKAKAVNSNF 839  
 QY 698 -----GFTN-----ELVQVYW-----SKQNIKGVKARFVVTGGITRVYPKPAGE 738  
 Db 840 QNTIPFNIFSYTNNSLLKDIINEYFNININDSKILSLQNRKNTLVDTSG-----YNAEYSE 894

SEQUENCE FROM N.A.  
 MEDLINE-90370487; PubMed-2204031;  
 RA Hauser D., Erlund M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,  
 RA Boquet P., Popoff M.R.;  
 RT "Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";  
 RL Nucleic Acids Res. 18:4924-4924(1990).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-TYPE C STOCKHOLM / C-ST;  
 RC MEDLINE-91024998; PubMed-2222445;  
 RA Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,  
 RA Yokosawa N., Takeshi K., Syuto B., Oguma K.;  
 RT "The complete nucleotide sequence of the gene coding for botulinum  
 RT type C1 toxin in the C-ST phage genome.";  
 RL Biochem. Biophys. Res. Commun. 171:1304-1311(1990).  
 RN [3]  
 RN SEQUENCE OF 2-25.  
 RC STRAIN-TYPE C STOCKHOLM / C-ST;  
 RC MEDLINE-88153072; PubMed-2450068;  
 RA Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,  
 RA Oguma K.;  
 RT "Establishment of a monoclonal antibody recognizing an antigenic site  
 RT common to Clostridium botulinum type B, Cl, D, and E toxins and  
 RT tetanus toxin.";  
 RL Infect. Immun. 56:898-902(1988).  
 RN [4]  
 RN IDENTIFICATION OF SUBSTRATE.  
 RP MEDLINE-94038966; PubMed-7901002;  
 RA Blas J., Chapman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;  
 RT "Botulinum neurotoxin C1 blocks neurotransmitter release by means of  
 RT cleaving HPC-1/syntaxin.";  
 RL EMBO J. 12:4821-4828(1993).  
 CC -1- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER  
 CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED  
 CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD  
 CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT  
 CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC  
 CC ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.  
 CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A  
 CC HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,  
 CC WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL  
 CC FORMATION AND TOXIN BINDING, RESPECTIVELY.  
 CC -1- SUBCELLULAR LOCATION: SECRETED.  
 CC -1- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF  
 CC BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.  
 CC -1- MISCELLANEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C  
 CC STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE  
 CC BACTERIOPHAGE.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC  
 CC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN  
 CC SUBFAMILY.  
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 CC  
 CC EMBL; X66433; CAA47060.1;  
 CC EMBL; X72793; CAA51313.1;  
 CC EMBL; X53751; CAA37780.1;  
 CC EMBL; D90210; BAA14235.1;  
 CC EMBL; X62389; CAA44263.1;  
 CC PIR; S11291; S11291.  
 CC PIR; A35396; A35396.  
 CC PIR; A43503; A43503.  
 CC MEROPS; M27.002;  
 CC InterPro; IPR000130;  
 CC InterPro; IPR000395;  
 CC Pfam; PF01742; Peptidase\_M27; 1.  
 CC PRINTS; PR00760; BONTOTOXILYSIN.



QY 739 --NWQENPETYEDSFYKRSNDNDNYVFTAPYENKSGPGAYESSIMVSKAVEIYIOGKLK 796  
DB 895 EGDVQLNP-----IF--PFDKLGSSGDEGRKVIIVTQENINVNSMTE 935  
QY 797 PAVVGKIDVNSWNIENFTKTSIRDCAGPVCCKRNSDVMDCVILDDGGFLIMANH-- 853  
DB 936 SFSISPIRWINKWSNLPCTIID-----SVKNNSGWSIGIISNLFVTLKQNEDESEQ 988  
QY 854 -----DYNQIGR-----PFGEIDPSLRHLNWSIYAFNKSVDYQSVCE 893  
DB 989 SINFSYDISNAPGYNKWFVTVNNMG-----NMKIYINGKLIDTIKVKRE 1035

RESULT 14  
Y103\_SINY3  
ID Y103\_SINY3 STANDARD; PRT; 420 AA.  
AC Q55874;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HYPOTHETICAL 45.8 KDA PROTEIN SLL0103.  
GN SLL0103.  
OS Synecocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96127529; PubMed=8590279;  
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
RA Sugita M., Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
RT region from map positions 64 to 92% of the genome."  
RL DNA Res. 2:153-166(1995).  
CC -1- SIMILARITY: TO E.COLI YFBC.  
CC -----  
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CC -----  
DR EMBL; D64004; BAA10635.1; -  
DR InterPro; IPR002035; -  
DR Pfam; PF00092; vwa; 1.  
DR PROSITE; PS0234; VWFA\_DOMAIN; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 420 AA; 45849 MW; E7111B51478E7AF3 CRC64;

Query Match 2.8%; Score 151.5; DB 1; Length 420;  
Best Local Similarity 20.8%; Pred. No. 0.089;  
Matches 85; Conservative 85; Mismatches 183; Indels 55; Gaps 16;  
QY 251 PKMLILVDVSGVSGTGLKLTISVSEMLETSDDDFVNVAFSNAQDVSCFHLVQA 310  
DB 41 PLNLCLVLDHSGSDGQPLETVKSAALGLDLRLEEDRLSVIAFDHRAKIV-----IENQ 95  
QY 311 NVRNKKVLKDAVNNITAKGTTDYKKGFSFAFEOILLNVNVRANCNTIMLTGDEGEAQ 370  
DB 96 QVRNGAIAKAEIKLKAEGTAGTDEGLKLIQEAAGKEDRVS---HIFLTGEGNEHGD 152  
QY 371 E----IPFNKNDKKVRFRFSVQGHNYERGPQWACENKG---YYEIPSGAIRINTQ 424  
DB 153 NDRCLKLGTVASDYKLTVHTLFGDH\*WQNDVLEAIAAQAQSLSYIENPS-EALHTFRQ 210  
QY 425 EYLDVLRPWLADGKAKQVQWNTNVIYDALELG-----LVITGLTPVNTGQENKTNLK 480  
DB 211 LF-----QRMNSNVLGNLAHL-LLEAPQAHAI--VKPVAQVSPETMDLT-VQ 254  
QY 481 NQLILGVMGVDVSLEDIKRLTPRTTLCPCNGYYPFAIDPNGVLLHPNLPKNPKSQE---- 536

DB 255 MQGATEEVRGLDMLTDQERV-----LLNLNLYLDQLLPGOHVIGQVQIRYDDPASGOTNLL 309  
QY 537 ----PVTLDLDAELENKIKVEIRNMIDGSEKGT--FRTLKKSODERYIDKGRITYW 590  
DB 310 SDPLPLTIQ-VQTQPSSTDVQVQESILTLAKYRQTQIAETKLKAGDRQGAATMLQTA 368  
QY 591 TPVNGTDSLALVLTYSFYIKALEETITQARSKGKMDSETLKP 638  
DB 369 TALQMGDKNGATILQTN-----TRLOSGEDLSEGRKTRVSKTTLQ 413

RESULT 15  
ITHA\_PIG  
ID ITHA\_PIG STANDARD; PRT; 921 AA.  
AC P79263;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY  
DE CHAIN H4) (INTER-ALPHA-TRYPsin INHIBITOR FAMILY HEAVY CHAIN-RELATED  
DE PROTEIN) (IHRP) (MAJOR ACUTE PHASE PROTEIN) (MAP).  
GN ITI4 OR IHRP.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 28-36; 595-703 AND 710-722.  
RX TISSUE=Liver;  
RX MEDLINE=96271024; PubMed=8830057;  
RA Hashimoto K., Tobe T., Sumiya J.-I., Sano Y., Choi-Miura N.-H.,  
RA Ozawa A., Yasue H., Tomita M.;  
RT "Primary structure of the pig homologue of human IHRP: inter-alpha-  
RT trypsin inhibitor family heavy chain-related protein."  
RT J. Biochem. 119:577-584(1996).  
RN [2]  
RP PRELIMINARY SEQUENCE OF 267-556 FROM N.A.  
RX TISSUE=Liver;  
RX MEDLINE=90371455; PubMed=1697703;  
RA Buchman T.G., Cabin D.E., Vickers S., Deutschman C.S., Delgado E.,  
RA Sussman M.M., Bulkley G.B.;  
RT "Molecular biology of circulatory shock. Part II. Expression of four  
RT groups of hepatic genes is enhanced after resuscitation from  
RT cardiogenic shock."  
RT Surgery 108:559-566(1990).  
RN [3]  
RP SEQUENCE OF 28-54 AND 223-240.  
RX TISSUE=Serum;  
RX MEDLINE=96013138; PubMed=7556597;  
RA Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A.,  
RA Garcia-Gil A., Lampreave F., Pineiro A.;  
RT "The major acute phase serum protein in pigs is homologous to human  
RT plasma kallikrein sensitive PK-120."  
RL FEBS Lett. 371:227-230(1995).  
CC -1- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.  
CC -1- TISSUE SPECIFICITY: LIVER-SPECIFIC.  
CC -1- INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC  
CC SHOCK.  
CC -1- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).  
CC -1- PTM: CLEAVED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA  
CC FRAGMENTS.  
CC -1- SIMILARITY: BELONGS TO THE ITI4 DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
CC -1- CAUTION: REF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER  
CC SEQUENCING ERRORS.  
CC -----  
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or send an email to license@sib-sib.ch).

CC EMBL; U43164; AAD00024.1; -  
DR EMBL; S62800; AAB46821.1; -  
DR EMBL; M29507; -; NOT\_ANNOTATED\_CDS.  
DR InterPro; IPR002035; -  
DR Pfam; PF00092; vwa; 1.  
DR PROSITE; PS0234; VWFA\_DOMAIN; 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein. 1 27 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
FT SIGNAL 28 921 H4.  
FT CHAIN 28 921  
FT DOMAIN 270 428  
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 49 50 HT -> SK (IN REF. 3).  
FT CONFLICT 703 703 D -> H (IN REF. 1; AA SEQUENCE).  
SQ SEQUENCE 921 AA; 102146 MW; E2BF95925DE8D07C CRC64;

Search completed: July 23, 2001, 07:48:25  
Job time: 586 sec

Query Match 2.8%; Score 150.5; DB 1; Length 921;  
Best Local Similarity 19.9%; Pred. No. 0.31;  
Matches 156; Conservative 100; Mismatches 264; Indels 265; Gaps 36;

QY 4 GCLLALTLTL-----FQSLIGPSSEPPPSAVTIKSWDK---MOED--- 43  
DB 10 GLLVLPPLLAQLSTAAHKNDIINIYSTVDKSSRFAHTVTSRVYKNGSAVQATFQ 69  
QY 44 -----LVTLAKTAGVNLVDIYEK--YQDLYT--VEPNNAQOLVEIAARDIEKL--- 89  
DB 70 MELPKKAFITNFMIIDGVTPGNKEKAAAEQYSAVARGESAGLVRAATGRTKTEQFVA 129  
QY 90 LSNRSKALVSLALEAEKVOAARHONREDPASNEVYVYNAKDDLDPEKNDSEPGSQRIKPVF 149  
DB 130 VSVAPAAKVTFEYELLARH-----LGYYELLKTIQPO-----QLVKHLQ 171  
QY 150 IEDANFGKQ--ISY-OHAAVHIPTDIYEGSTIVLNE---LWTSALDEVFKKNEEDPSL 203  
DB 172 MDIHIFEPQGISFLETESTFTNELAEALTISQNTKAHIREKPTLSQ--QKSPEQOEIV 230  
QY 204 L-----WQVFGSATG-----LARYYPASFWVDNSRTPNKKIDLYVRRRPWYIQG 247  
DB 231 LDGNFIVRYDVNRTVGGSIQIENGIFYVHYFAPEW----- 266  
QY 248 AASPDKMLILVDVSGSVGLTLKLINTSVSEMLETLSDDDFVNVASFNSNAQDVSCFQHL 307  
DB 267 SAIPKNVIFVIDTSGMRGKIQOTREALIKILGDLGRDQFNLSVFSGEAPR-----RRA 322  
QY 308 VQANVRNKKVLDVANNIYAKGIDYKGFSAFEGFOLLNAYNSRANCNKI-----IM 359  
DB 323 VAASAENVEEAKSYAAEIIHAQGTNTNDAMLMAVQLL-----ERANREELLPARSVTFII 377  
QY 360 LFTDG---GEERAQEIFNKYKDKVRV-----FRFSVQGHNYERGPQIOWMA 403  
DB 378 LFTDGDFTVGETNPSKI-----QKNVREAIQGHSLFCGLFGFDVPYAFLEK-----MA 426  
QY 404 CENKG-----YY-----YEIPSGAIRINTQYLDVL--GR 432  
DB 427 LENGGLARRIYEDSDALQEDFYQEVANPLRLVAPEYPS-NAVEEVTQDNFRLPFKGS 485  
QY 433 PMVLG---DKAKOVQNTVYLDALGLVITGTLPVFNITGQFENKTNLKNQLILG--- 486  
DB 486 ELVVAGKLRLDQSPDV-----LSAKYRGQLHMENVTVMESRVAEQAEFLSPKY 534  
QY 487 -----VMGVDVSLEDI--KRLTPRTFLCPNGYGFYFAIDPNGYVLLHPNL 527  
DB 535 IFHSMERLWAYLTIOQLLAQTVAESAEEKALEARALSLSLNYSFVYPLTSMVITKPEG 594  
QY 528 QPKNPKSQEPVTLDFDAELENDIKVEIRNKMIDGEGSEKTFRTLKVSQDERYIDKGNRT 587



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:47:07 ; Search time 125.88 Seconds  
(without alignments)  
1088.878 Million cell updates/sec

Title: US-09-397-548-16  
Perfect score: 5443  
Sequence: 1 MAAGCLLALTLFQSLIIG.....RLIIQAEQTSQGNPCDMVK 1036

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16:  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.unclassified:\*  
13: sp.vertebrate:\*  
14: sp.virus:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5409.5	99.4	1110	4 Q9U1U0	Q9U1U0 homo sapien
2	5380	98.8	1091	6 Q77773	Q77773 sus scrofa
3	5291	97.2	1091	11 Q9RS3	Q9RS3 rattus norv
4	5223	96.0	1103	11 Q08532	Q08532 mus musculus
5	3667	67.4	745	4 Q9UDQ3	Q9UDQ3 homo sapien
6	2948	54.2	1150	4 Q9NY47	Q9NY47 homo sapien
7	2920.5	53.7	1143	4 Q9NY48	Q9NY48 mus musculus
8	2918.5	53.6	1156	11 Q9EQG2	Q9EQG2 mus musculus
9	2907.5	53.4	1145	4 Q9Y268	Q9Y268 homo sapien
10	2886.5	53.0	1076	4 Q9UEN0	Q9UEN0 homo sapien
11	2717	49.9	975	4 Q9NSA6	Q9NSA6 homo sapien
12	1085	19.9	1091	11 Q9Z1L5	Q9Z1L5 mus musculus
13	1015	18.6	997	4 Q9NY16	Q9NY16 homo sapien
14	929.5	17.1	2190	5 Q9NK64	Q9NK64 drosophila
15	912.5	16.8	2172	5 Q9VJN0	Q9VJN0 drosophila
16	891	16.4	1191	5 Q9VJN7	Q9VJN7 drosophila
17	886	16.3	1255	5 Q9NK83	Q9NK83 drosophila
18	875	16.1	170	4 Q9UDL7	Q9UDL7 homo sapien
19	839	15.4	1022	5 Q9V6T7	Q9V6T7 drosophila

Q9ny18 homo sapien  
Q17517 caenorhabdi  
Q9ud81 homo sapien  
Q9glh1 bos taurus  
Q9ud82 homo sapien  
Q9ud5 homo sapien  
Q9ud80 homo sapien  
Q95026 homo sapien  
Q9r142 mus musculu  
Q9hcj9 homo sapien  
Q9v917 drosophila  
Q9u7p4 eufolliculi  
Q9hjo thermoplasm  
Q15870 plasmodium  
Q9gl55 oryctolagus  
Q96154 plasmodium  
Q46342 clostridium  
Q86488 staphylococ  
Q35802 rattus norv  
Q45793 bacillus th  
Q9em28 ansacta moo  
Q9n2m3 plasmodium  
Q26216 plasmodium  
Q94ly6 oryctolagus  
Q25905 helicobacte  
Q9uq54 homo sapien

## ALIGNMENTS

RESULT 1

Q9U1U0  
ID Q9U1U0 PRELIMINARY; PRT: 1110 AA.  
AC Q9U1U0;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE DIHYDROPIRIDINE RECEPTOR ALPHA 2 SUBUNIT.  
GN CACNA2D1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20005942; PubMed=10534405;  
RA Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;  
RT "Genomic structure and functional expression of a human alpha(2)/delta  
calcium channel subunit gene (CACNA2).";  
RL Genomics 61:201-209(1999).  
DR EMBL; AF083854; AAF03259.1; JOINED.  
DR EMBL; AF083817; AAF03259.1; JOINED.  
DR EMBL; AF083818; AAF03259.1; JOINED.  
DR EMBL; AF083819; AAF03259.1; JOINED.  
DR EMBL; AF083820; AAF03259.1; JOINED.  
DR EMBL; AF083821; AAF03259.1; JOINED.  
DR EMBL; AF083822; AAF03259.1; JOINED.  
DR EMBL; AF083823; AAF03259.1; JOINED.  
DR EMBL; AF083824; AAF03259.1; JOINED.  
DR EMBL; AF083825; AAF03259.1; JOINED.  
DR EMBL; AF083826; AAF03259.1; JOINED.  
DR EMBL; AF083827; AAF03259.1; JOINED.  
DR EMBL; AF083828; AAF03259.1; JOINED.  
DR EMBL; AF083829; AAF03259.1; JOINED.  
DR EMBL; AF083830; AAF03259.1; JOINED.  
DR EMBL; AF083831; AAF03259.1; JOINED.  
DR EMBL; AF083832; AAF03259.1; JOINED.  
DR EMBL; AF083833; AAF03259.1; JOINED.  
DR EMBL; AF083834; AAF03259.1; JOINED.  
DR EMBL; AF083835; AAF03259.1; JOINED.  
DR EMBL; AF083836; AAF03259.1; JOINED.  
DR EMBL; AF083837; AAF03259.1; JOINED.

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DR EMBL; AF083843; AF083259.1; JOINED.
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DR EMBL; AF083846; AF083259.1; JOINED.
DR EMBL; AF083847; AF083259.1; JOINED.
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DR EMBL; AF083850; AF083259.1; JOINED.
DR EMBL; AF083851; AF083259.1; JOINED.
DR EMBL; AF083852; AF083259.1; JOINED.
DR EMBL; AF083853; AF083259.1; JOINED.
DR InterPro; IPR000885; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
DR ProDom; PD002078; -. 1.
KW Receptor.
SQ SEQUENCE 1110 AA; 125307 MW; 8358DC6AD489C074 CRC64;

Query Match 99.48; Score 5409.5; DB 4; Length 1110;
Best Local Similarity 97.98; Pred. No. 0;
Matches 1033; Conservative 1; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGCLLALTTLTFLQSLIGPSSPEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60
DB 1 MAAGCLLALTTLTFLQSLIGPSSPEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60
QY 61 YEKYODLVTFEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
DB 61 YEKYODLVTFEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
QY 121 EVVYNNAKDDLDPEKNDSEPGSRKPKVFIEDANFGROISYQHAHVHTPTDIYEGSTIVL 180
DB 121 EVVYNNAKDDLDPEKNDSEPGSRKPKVFIEDANFGROISYQHAHVHTPTDIYEGSTIVL 180
QY 181 NELNWTSSALDEVFKKRNREDSLSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
DB 181 NELNWTSSALDEVFKKRNREDSLSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
QY 241 RPWYTOGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
DB 241 RPWYTOGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKGFSAFEQLLNYSRANCNKIIML 360
DB 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKGFSAFEQLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKYNDKKVRFVSQGHYNERGPIQWACENKGYIYIPISGAIR 420
DB 361 FTDGGEERAQEIFNKYNDKKVRFVSQGHYNERGPIQWACENKGYIYIPISGAIR 420
QY 421 INTQEYLDVLGRPMVLADKAKQVQWNTYLDALGLGLVITGTLPVFNITGQFENKTNLK 480
DB 421 INTQEYLDVLGRPMVLADKAKQVQWNTYLDALGLGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQLILGVMGVDVSLIEDIKRLTFRFLCPNGYFFADPNGYVLLHNLQPK----- 530
DB 481 NQLILGVMGVDVSLIEDIKRLTFRFLCPNGYFFADPNGYVLLHNLQPK----- 530
QY 531 -----NPKSQBPVTLDFDAELENIDIKVEIRNKMIDGESGKTFPLVKSDQERY 581
DB 541 LKRRPNIQNSQBPVTLDFDAELENIDIKVEIRNKMIDGESGKTFPLVKSDQERY 600
QY 582 DKGNRITYTTPVNGTDYSLALVLPYTSFYIYIKAKLEETITQARSKGKMKDSETLKPNDF 641
DB 601 DKGNRITYTTPVNGTDYSLALVLPYTSFYIYIKAKLEETITQARSKGKMKDSETLKPNDF 660
QY 642 EESGYTFIAPROYCNDLKISDNNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 701
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DB 661 EESGYTFIAPROYCNDLKISDNNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 720
QY 702 ELVQNTWSKOKNIKGKVARVTVTDGGITRYVYPREAGENWQENPETYEDSYKKSLDNDNY 761
DB 721 ELVQNTWSKOKNIKGKVARVTVTDGGITRYVYPREAGENWQENPETYEDSYKKSLDNDNY 780
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIKIDVNSWIENFTKTSIRDP 821
DB 781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIKIDVNSWIENFTKTSIRDP 840
QY 822 CAGPVCDCCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVYA 881
DB 841 CAGPVCDCCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVYA 900
QY 882 FNKSYDYSQVCEGPAAPKQAGAGHRSATVPSVADILQIGWATAAANWILQOFLSLTFPR 941
DB 901 FNKSYDYSQVCEGPAAPKQAGAGHRSATVPSVADILQIGWATAAANWILQOFLSLTFPR 960
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDSSKSGVLDCGNCGRIFHGEKLMNTNL 1001
DB 961 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDSSKSGVLDCGNCGRIFHGEKLMNTNL 1020
QY 1002 IFIMVESKGTCPDTRLLIQAEQTSQDGNPCDMYK_1036
DB 1021 IFIMVESKGTCPDTRLLIQAEQTSQDGNPCDMYK_1055

RESULT 2
QY 077773 PRELIMINARY; PRT; 1091 AA.
AC 077773;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2 DELTA SUBUNIT PRECURSOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel
RT subunit from porcine cerebral cortex. Expression of a soluble form of
RT the protein that retains [3H]gabapentin binding activity.";
RL J. Biol. Chem. 273:25458-25465(1998).
DR EMBL; AF077665; AAC36289.1; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
KW Signal.
FT SIGNAL 1 24
FT CHAIN 25 1091
FT SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9E560E CRC64;

Query Match 98.8%; Score 5380; DB 6; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTFLQSLIGPSSPEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60
DB 1 MAAGCLLALTTLTFLQSLIGPSSPEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60
QY 61 YEKYODLVTFEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
DB 61 YEKYODLVTFEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASN 120
QY 121 EVVYNNAKDDLDPEKNDSEPGSRKPKVFIEDANFGROISYQHAHVHTPTDIYEGSTIVL 180
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Db 121 EVVYNAKDDLDPEKNDSEPGSQRIRKPVFIDDFANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEYFKKRNREDPSLLMQVFGSATGLARYYPASPWVDSRTPNKNIDLYDVR 240  
Db 181 NELNWTSSALDEYFKKRNREDPSLLMQVFGSATGLARYYPASPWVDSRTPNKNIDLYDVR 240  
QY 241 RPWYIQAASPKDMLILVDVSGVSGSLTKLRTSVSEMLETLSDDDFFNVASFNSNAQD 300  
Db 241 RPWYIQAASPKDMLILVDVSGVSGSLTKLRTSVSEMLETLSDDDFFNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360  
QY 361 FTDGGERAQEIFNKNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPISGAIR 420  
Db 361 FTDGGERAQEIFNKNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPISGAIR 420  
QY 421 INTQEYLDVLRPMVLGAKAKQVQWNTYLDLLEGLVITGTLPVFNITGQFENKTNLK 480  
Db 421 INTQEYLDVLRPMVLGAKAKQVQWNTYLDLLEGLVITGTLPVFNITGQFENKTNLK 480  
QY 481 NQILGVMGVDVSLDDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
Db 481 NQILGVMGVDVSLDDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYISFYIYKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFTAPRDYCNLDKI 660  
Db 601 ALVLPYISFYIYKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFTAPRDYCNLDKI 660  
QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRHLNYSVYAFNKSVDYOSVCEPQAPKQ 900  
Db 841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRHLNYSVYAFNKSVDYOSVCEPQAPKQ 900  
QY 901 GAGHSAYVPSVADIIQIGWATAAASIIQOFLLSITPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSIADIIHIGWATAAASIIQOFLLSITPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTQYFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
Db 961 SCITEQTQYFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
QY 1021 QABQTSDDGPNPCDMVK 1036  
Db 1021 QABQTSDDGPNPCDMVK 1036

RESULT 3  
Q9ERS3 PRELIMINARY; PRT: 1091 AA.  
AC Q9ERS3;  
DT 01-MAR-2001 (treMBLrel. 16, Created)  
DT 01-MAR-2001 (treMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (treMBLrel. 16, Last annotation update)  
DE VOLTAGE-GATED CALCIUM CHANNEL ALPH2/Delta-1 SUBUNIT.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;  
RA Lin Y., Lipscombe D.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF286488; AAG28164.1; - GSAT -> AADR.  
FT VARIANT 209 212 S -> T.  
FT VARIANT 338 338 S -> T.  
FT VARIANT 599 600 SL -> RY.  
FT VARIANT 869 869 S -> R.  
SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;

Query Match 97.2%; Score 5291; DB 11; Length 1091;  
Best Local Similarity 96.4%; Pred. No. 0;  
Matches 999; Conservative 22; Mismatches 15; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFQSLILGSPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTLTLFQSLILGSPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQHREDFASN 120  
Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQHREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIRKPVFIDDFANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIRKPVFIDDFANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEYFKKRNREDPSLLMQVFGSATGLARYYPASPWVDSRTPNKNIDLYDVR 240  
Db 181 NELNWTSSALDEYFKKRNREDPSLLMQVFGSATGLARYYPASPWVDSRTPNKNIDLYDVR 240  
QY 241 RPWYIQAASPKDMLILVDVSGVSGSLTKLRTSVSEMLETLSDDDFFNVASFNSNAQD 300  
Db 241 RPWYIQAASPKDMLILVDVSGVSGSLTKLRTSVSEMLETLSDDDFFNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQOLLNYSRANCNKIIML 360  
QY 361 FTDGGERAQEIFNKNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPISGAIR 420  
Db 361 FTDGGERAQEIFNKNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEIPISGAIR 420  
QY 421 INTQEYLDVLRPMVLGAKAKQVQWNTYLDLLEGLVITGTLPVFNITGQFENKTNLK 480  
Db 421 INTQEYLDVLRPMVLGAKAKQVQWNTYLDLLEGLVITGTLPVFNITGQFENKTNLK 480  
QY 481 NQILGVMGVDVSLDDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
Db 481 NQILGVMGVDVSLDDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRNKMIDGESGKFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYISFYIYKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFTAPRDYCNLDKI 660  
Db 601 ALVLPYISFYIYKAKLEETITQARSKKGMKQSETLKPDPNFESGYTFTAPRDYCNLDKI 660  
QY 661 SDNTEFLNNEFIDRKTTPNPNPCNADLINRVLLDAGFTNVLQVNSKQKNIKGVKAR 720  
Db 661 SDNTEFLNNEFIDRKTTPNPNPCNADLINRVLLDAGFTNVLQVNSKQKNIKGVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCVI 840

Db 781 MYSKAVELYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDCAGPCVCDCKRNSDYMDCVI 840  
QY 841 LDGGGLMANHDDYTNQIGRFEIDPSLMRHLNYSVAFNKSYDVSQVCEPGAAPKQ 900  
Db 841 LDGGGLMANHDDYTNQIGRFEIDPSLMRHLNYSVAFNKSYDVSQVCEPGAAPKQ 900  
QY 901 GAGHRSAYVPSVADILQIGWATAAAMWSILOQFLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHRSAYVPSVADILQIGWATAAAMWSILOQFLSLTPRLLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQYFFNDNSFSGVLDGCGNCSRIFFHGEKLMNTNLFIMVESKGTGCPDTRLLI 1020  
Db 961 SCITEQYFFNDNSFSGVLDGCGNCSRIFFHGEKLMNTNLFIMVESKGTGCPDTRLLI 1020  
QY 1021 QAEQTSQDGNPCDWMK 1036  
Db 1021 QAEQTSQDGNPCDWMK 1036

RESULT 4  
O08532 PRELIMINARY; PRT: 1103 AA.  
ID O08532; O08533; O08534; O08535; O08536;  
AC 01-JUN-1998 (Tremblrel. 06, Created)  
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)  
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA  
DE SUBUNITS PRECURSOR.  
GN CACNA2D1 OR CACNA2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97113514; PubMed=8955374;  
RA Angelotti T., Hofmann F.;  
RL FEBS Lett. 397:331-337(1996).  
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
CC EXCITATION-CONTRACTION COUPLING.  
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
CC ALPHA-1, ALPHA-2, BETA AND GAMMA.  
CC -1- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-  
CC LINKED.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E,  
CC ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE  
CC SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.  
CC -1- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND  
CC AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS  
CC EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN  
CC SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE  
CC CARDIOVASCULAR SYSTEM.  
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
CC A PRECURSOR FORM  
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
DR EMBL: U73484; AAB50139.1;  
DR EMBL: U73485; AAB50140.1;  
DR EMBL: U73483; AAB50138.1;  
DR EMBL: U73486; AAB50141.1;  
DR EMBL: U73487; AAB50142.1;  
DR MGD: MGI:88295; CACNA2D1.  
DR InterPro: IPR002035; -.  
DR Pfam: PF00092; vwa; 1.  
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
KW Alternative splicing.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 957 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT.  
FT CHAIN 958 1103 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.  
FT TRANSMEM 446 469 POTENTIAL.  
FT TRANSMEM 918 942 POTENTIAL.

TRANSMEM 1079 1098  
FT MOD\_RES 501 501 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
FT MOD\_RES 845 845 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 348 348 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 475 475 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 604 604 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 675 675 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 781 781 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 824 824 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 888 888 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 895 895 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 985 985 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 998 998 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARSPLIC 531 549 MISSING (IN ISOFORMS 2B AND 2E).  
FT VARSPLIC 531 554 MISSING (IN ISOFORMS 2C AND 2D).  
FT VARSPLIC 644 644 Y -> SKKGKMKD (IN ISOFORMS 2A, 2D AND 2E).  
SQ SEQUENCE 1103 AA; 124629 MW; 103773BA735120D4 CRC64;  
Query Match 96.0%; Score 5223; DB 11; Length 1103;  
Best Local Similarity 94.1%; Pred. No. 0;  
Matches 993; Conservative 22; Mismatches 14; Indels 26; Gaps 2;  
QY 1 MAAGCLLALTTLFOSLLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTTLFOSLLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTPENNARQLYEIAARDIEKLLSNRSKALVSLAEAEKVAQAHOHWRDFASN 120  
Db 61 YEKYQDLYTPENNARQLYEIAARDIEKLLSNRSKALVSLAEAEKVAQAHOHWRDFASN 120  
QY 121 EYVYVNAKDDLPKNDSEPGSORIKPFVIEDANFQRQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 EYVYVNAKDDLPKNDSEPGSORIKPFVIEDANFQRQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNMTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
Db 181 NELNMTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
QY 241 RPYIOGAASPKDMLILVDYSGVSGTLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300  
Db 241 RPYIOGAASPKDMLILVDYSGVSGTLTKLIRTSVSEMLETSLDDDFVNVASFNSAQD 300  
QY 301 VSCFQHLVQANVRNKKVLKADAVNNITAKGTTYDKGFSFAFOLLNYSRANCKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLKADAVNNITAKGTTYDKGFSFAFOLLNYSRANCKIIML 360  
QY 361 FTDGGEERAQEIFNKYKDKKVRVFRFSYQHNRYERGPQIOWMACENKGYEIPSGAIR 420  
Db 361 FTDGGEERAQEIFNKYKDKKVRVFRFSYQHNRYERGPQIOWMACENKGYEIPSGAIR 420  
QY 421 INTQEYLDVLGRPMVLGAKAKQVQNTNVLDALELGLVTGLTPVNTITGQFENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLGAKAKQVQNTNVLDALELGLVTGLTPVNTITGQFENKTNLK 480  
QY 481 NQLILGMVGVDVSLDIKRLTPRTLCPCNGYYFAIDPNGVLLHPNLPK- 530  
Db 481 NQLILGMVGVDVSLDIKRLTPRTLCPCNGYYFAIDPNGVLLHPNLPK- 530  
QY 531 - - - - - NPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESSEKTFRTLVSQDERYI 581  
Db 531 - - - - - NPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESSEKTFRTLVSQDERYI 581  
QY 582 DKGNTYTTVPVNGTDYSALVLPYTSFYIKAKLEETITQARKSGKGMKDSITLKPDNF 641  
Db 582 DKGNTYTTVPVNGTDYSALVLPYTSFYIKAKLEETITQARKSGKGMKDSITLKPDNF 641  
QY 601 DKGNTYTTVPVNGTDYSALVLPYTSFYIKAKLEETITQARKSGKGMKDSITLKPDNF 653  
Db 601 DKGNTYTTVPVNGTDYSALVLPYTSFYIKAKLEETITQARKSGKGMKDSITLKPDNF 653



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QY 642 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 701
DB 654 EESGYTFIAPREYCNLDKPSDNNTFLLNFEFIDRKTNNPNSCNTDLINRILLDAGFTN 713
QY 702 ELVQYNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETEYDSFYKRSILDNDNY 761
DB 714 ELVQYNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETEYDSFYKRSILDNDNY 773
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP 821
DB 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP 833
QY 822 CAGPVCDCRNSDVNDYVLDGGFLLMANHDDYTNQIGRWATAAAWSILQQFLLSLTTPR 941
DB 834 CAGPVCDCRNSDVNDYVLDGGFLLMANHDDYTNQIGRWATAAAWSILQQFLLSLTTPR 953
QY 882 FNKSYDYOSVCEPGAAPQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSLTTPR 941
DB 894 FNKSYDYOSVCEPGAAPQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSLTTPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTFYFNDNDSKFSGLDCGNCRSRIFHGEKLMNTNL 1001
DB 954 LLEAVEMEDDDFTASLSKQSCITEQTFYFNDNDSKFSGLDCGNCRSRIFHGEKLMNTNL 1013
QY 1002 IFIMVESKGTCPDTRLLIQAEQTSFGPNPCDMVK 1036
DB 1014 VFIWVESKGTCPDTRLLIQAEQTSFGPNPCDMVK 1048

RESULT 5
QYUQ03 PRELIMINARY; PRT: 745 AA.
ID QYUQ03
AC QYUQ03
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE WUGSC:H.DJ0560014.1 PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Mead K., Bauer C.;
RT "The sequence of Homo sapiens PAC clone RP4-560014.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006145; AAD20938.1;
DR InterPro; IPR02035;
FT NON_TER 1
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;

Query Match 67.4%; Score 3667; DB 4; Length 745;
Best Local Similarity 99.7%; Pred. No. 3.2e-226;
Matches 688; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 347 YNVSRANCKNIIMLFTDGGEEAQAIFNKYKNDKKVRFVFSVGHQHYERGIQWACEN 406
DB 1 YNVSRANCKNIIMLFTDGGEEAQAIFNKYKNDKKVRFVFSVGHQHYERGIQWACEN 60

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QY 407 KGYIYEIPSGAIRINTOEYLDVLGRPMVLAGDKAKQVOMTVNYLDALGLVITGILPV 466
DB 61 KGYIYEIPSGAIRINTOEYLDVLGRPMVLAGDKAKQVOMTVNYLDALGLVITGILPV 120
QY 467 FNITQGFENKTNLKNQILGVMDVDSLEDIKRLTPRTFLCPNGYVPAIDPNGYVLLHPN 526
DB 121 FNITQGFENKTNLKNQILGVMDVDSLEDIKRLTPRTFLCPNGYVPAIDPNGYVLLHPN 180
QY 527 LOPKNPKSQEPVTLDFDLAELENDIKVEIRNMIDGESGEKTFRTLVSQDERYIDKGNR 586
DB 181 LOPKNPKSQEPVTLDFDLAELENDIKVEIRNMIDGESGEKTFRTLVSQDERYIDKGNR 240
QY 587 TYTWPVNGTYSIALVLPYTSFYIKAKLETITQARSKKGMKDSSETLKPDNFEESGY 646
DB 241 TYTWPVNGTYSIALVLPYTSFYIKAKLETITQARSKKGMKDSSETLKPDNFEESGY 300
QY 647 TFIAPRDYCNLDKISDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 706
DB 301 TFIAPRDYCNLDKISDNNTFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 360
QY 707 YNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETEYDSFYKRSILDNDNYVFTAP 766
DB 361 YNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETEYDSFYKRSILDNDNYVFTAP 420
QY 767 YFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP 826
DB 421 YFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDP 480
QY 827 CDCRNSDVNDYVLDGGFLLMANHDDYTNQIGRWATAAAWSILQQFLLSLTTPR 946
DB 481 CDCRNSDVNDYVLDGGFLLMANHDDYTNQIGRWATAAAWSILQQFLLSLTTPR 540
QY 887 DYOSVCEPGAAPQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSLTTPR 946
DB 541 DYOSVCEPGAAPQAGHRSAYVPSVADIIQIGWATAAAWSILQQFLLSLTTPR 600
QY 947 EMEDDDDFTASLSKQSCITEQTFYFNDNDSKFSGLDCGNCRSRIFHGEKLMNTNL 1006
DB 601 EMEDDDDFTASLSKQSCITEQTFYFNDNDSKFSGLDCGNCRSRIFHGEKLMNTNL 660
QY 1007 ESKGTCPDTRLLIQAEQTSFGPNPCDMVK 1036
DB 661 ESKGTCPDTRLLIQAEQTSFGPNPCDMVK 690

RESULT 6
QYUQ47 PRELIMINARY; PRT: 1150 AA.
ID QYUQ47
AC QYUQ47;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RC Klugbauer N.;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RC Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251368; CAB86193.1;
DR InterPro; IPR002035;

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SQ SEQUENCE 1150 AA; 129875 MW; 37B75F687AF5E73C CRC64;

Query Match 54.2%; Score 2948; DB 4; Length 1150;
Best Local Similarity 54.5%; Pred. No. 6.3e-180;
Matches 573; Conservative 168; Mismatches 281; Indels 30; Gaps 13;

QY 7 LALTTLTQSLLLIGSPSEPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDIYKYOD 66
DB 44 LWLLPLPLLAAPGASAYSPQOHTMQHWRRLQEQVDGVMRIFGGVQQLREIYKDNRN 103
QY 67 LYTVFPNNARQIVTAARDIEKLLSNRSKALVSALAEKQVAAHQWREDFASNEVYYIN 126
DB 104 LFEVQENPQKLVKVGADIESLLDRKVKQALKRLADAENQKAHRWQDNKEEDIVYVD 163
QY 127 AKDDL---DPEKNDSEPGSQ--RIKPVFIEDANFGRIQISYQHAHVHIPTDIYEGSTIVLN 181
DB 164 AKADAELDDPESEDVERGSKASTLRDLDFIEDPNFKKNKYNSYAAVQIPTDIYKGVSTVLN 223
QY 182 ELNWTLSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVRRR 241
DB 224 ELNWTLEALNFMENRRQDPTLLMQVFGSATGVTRYYPATPW---RAPKKIDLYDVRRR 279
QY 242 PWYIOGASPKDMLTLDVSGSVGLTLKRTISVSEMLETSLDSDDFVNVASFNSNAQDV 301
DB 280 PWYIOGASPRDMLTLDVSGSVGLTLKRTISVSEMLETSLDSDDFVNVASFNEKAQPV 339
QY 302 SCFOHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSAFEQQLNLYNVRANCNKIIMLF 361
DB 340 SCFTHLVQANVRNKKVLEKAVQGMVAKGTYGKAGFYAFDQLQNSNITRANCNKIMMF 399
QY 362 TDGGERAQEIENKYN-KDKKVRVRFSGVGHNYERGPQIOWMACENKGYIYETPSIGAIR 420
DB 400 TDGGERVQDVFEKYNPNRTVRVTFSGVGHNYDVTPLQWMACANKGYIFEIPSGAIR 459
QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480
DB 460 INTQEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGTLPVFNITQ--DGPGEKK 517

Query Match 53.7%; Score 2920.5; DB 4; Length 1143;
Best Local Similarity 54.3%; Pred. No. 3.6e-178;
Matches 571; Conservative 166; Mismatches 278; Indels 37; Gaps 14;

QY 7 LALTTLTQSLLLIGSPSEPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDIYKYOD 66
DB 44 LWLLPLPLLAAPGASAYSPQOHTMQHWRRLQEQVDGVMRIFGGVQQLREIYKDNRN 103
QY 67 LYTVFPNNARQIVTAARDIEKLLSNRSKALVSALAEKQVAAHQWREDFASNEVYYIN 126
DB 104 LFEVQENPQKLVKVGADIESLLDRKVKQALKRLADAENQKAHRWQDNKEEDIVYVD 163
QY 127 AKDDL---DPEKNDSEPGSQ--RIKPVFIEDANFGRIQISYQHAHVHIPTDIYEGSTIVLN 181
DB 164 AKADAELDDPESEDVERGSKASTLRDLDFIEDPNFKKNKYNSYAAVQIPTDIYKGVSTVLN 223
QY 182 ELNWTLSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVRRR 241
DB 224 ELNWTLEALNFMENRRQDPTLLMQVFGSATGVTRYYPATPW---RAPKKIDLYDVRRR 279
QY 242 PWYIOGASPKDMLTLDVSGSVGLTLKRTISVSEMLETSLDSDDFVNVASFNSNAQDV 301
DB 280 PWYIOGASPRDMLTLDVSGSVGLTLKRTISVSEMLETSLDSDDFVNVASFNEKAQPV 339
QY 302 SCFOHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSAFEQQLNLYNVRANCNKIIMLF 361
DB 340 SCFTHLVQANVRNKKVLEKAVQGMVAKGTYGKAGFYAFDQLQNSNITRANCNKIMMF 399
QY 362 TDGGERAQEIENKYN-KDKKVRVRFSGVGHNYERGPQIOWMACENKGYIYETPSIGAIR 420
DB 400 TDGGERVQDVFEKYNPNRTVRVTFSGVGHNYDVTPLQWMACANKGYIFEIPSGAIR 459
QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480
DB 460 INTQEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGTLPVFNITQ--DGPGEKK 517
```



AC Q9Y268;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE KIAA0558 PROTEIN.  
 GN KIAA0558  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRIN;  
 RA Sekido Y., Duh F.-M., Latif F., Ding J., Lin J., Mathis M.,  
 RA Minna J.D.;  
 RT "Gene 26, a new candidate human tumor suppressor gene located in the  
 RT 3p21.3 small cell lung cancer homozygous deletion region homologous to  
 RT a voltage gated calcium channel alpha 2/ delta subunit.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,  
 RA Zabarovsky E., Johnson B., Lerman M.I.;  
 RT "A new alpha 2 delta subunit of the L-type voltage gated calcium  
 RT channel resides in the lung cancer critical region on 3p21.3.";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=BRIN;  
 RC MEDLINE=98290545; PubMed=9628581;  
 RX Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 5:31-39(1998).  
 DR EMBL; AF040709; AAC70914.1; -;  
 DR EMBL; AF042792; AAB96913.1; -;  
 DR EMBL; AB011130; BAA25484.1; -;  
 DR InterPro: IPR02035; -;  
 SQ SEQUENCE 1145 AA; 129268 MW; 9ADA4807FC70971B CRC64;

Query Match 53.4%; Score 2907.5; DB 4; Length 1145;  
 Best Local Similarity 54.1%; Pred. No. 2.4e-177;  
 Matches 570; Conservative 167; Mismatches 278; Indels 39; Gaps 15;

QY 7 LAULTLTFQSLIGPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVIEKYQD 66  
 DB 44 LWLLPLLLPLLAAPGASAYSPQOQHTQHWARLEQVGVGMIFGVQQLREIYKDNRN 103  
 QY 67 LYTVEPNAROLVEIAARDTEKLLSNKALVSLALEAKVQAAHQRDEFASNEVYYN 126  
 DB 104 LFEVQNEPKLVKRVAGDIESLLDRKVALKRLADAAENFQKARHQDNKEEDIVYD 163  
 QY 127 AKDDL---DPEKNDSEPSQ--RIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVLN 181  
 DB 164 AKADAELODPESEDVERGSKASTLRDFIEDPNPKNVNYSYAAVQIPTDIYKGSTIVLN 223  
 QY 182 ELNWTSLALDEYFKNREDEPSLLHQVGSATGLARYYPASPWVDNSRTPNKIDLYDVR 241  
 DB 224 ELNWTALENVFMNRQDPTLLQVFGSATGVTRYYPATPW----RAPKKIDLYDVR 279  
 QY 242 PWYIOGAASPKDMLIVDVSGVSGGLTKLRTSVSEMLETSLDDEDFVNVASFNSAQDV 301  
 DB 280 PWYIOGAASPKDMLIVDVSGVSGGLTKLRTSVSEMLETSLDDEDFVNVASFNEKAQV 339  
 QY 302 SCFOHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNYNVSRANCKIIMLF 361  
 DB 340 SCFTHLVQANVRNKKVLEKAVQGVKAGTTCYKAGFYAFDQLQNSITRANCKNIMMF 399  
 QY 362 TDGGERAQELFNKN--KDKVVRFRSVGQHNHYERGPQIOMACENKGYEIEPSIGAIR 420

DB 400 TDGGERVQDVFEKYNWPNRTYRVFTFSVGQHNHYDVTPLQWMACANKGYEIEPSIGAIR 459  
 QY 421 INTQEYDLVGRPMVLADGAKAQVQWNTNYLDALGLGLVITGTLPVFNITGOFENKTNLK 480  
 DB 460 INTQEYDLVGRPMVLADGAKAQVQWNTNYLDALGLGLVITGTLPVFNITG--DGPGEKK 517  
 QY 481 NCLILGVMGVDVSLIEDIKRLTPREFLCPNGYFAIDPNGYVLLHPNLOPKNKSOEPVTL 540  
 DB 518 NCLILGVMGIDVALNDIKRLTPNTYLGANGYFAIDNLNGYVLLHPNLOPKNTNFREPVL 577  
 QY 541 DFLDAELENDIKVEIRNKMIDGESKEFTLVKSDERYIDKGNRTYTWTPVNGDYSL 600  
 DB 578 DFLDAELENDIKVEIRNKMIDGESKEFTLVKSDERYIDVTRNYTWTPVIRSTNYSL 637  
 QY 601 ALVLPYSYIYKALEETITQARSKKGMKSETLKPONFESGYTFIAPRDYCNLDLKI 660  
 DB 638 GLVLPYSYIYKALEETITQARSKKGMKSETLKPONFESGYTFIAPREYCKDLNA 690  
 QY 661 SONNTEFLNENEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNVSKOK--NIKGVKA 719  
 DB 691 SONNTEFLNENEFTDRKTPNPNPCNADLINRVLLDAGFTNELVQNVSKOK--NIKGVKA 750  
 QY 720 RFVVTGGITRVYKPEAGENWOENPETYEDSFYKSLDNDNYVFTAPYFNK--SGPGAYES 778  
 DB 751 VFAATDGGITRVYKPEAGENWOENPETYEDSFYKSLDNDNYVFTAPYFNK--SGPGAYES 810  
 QY 779 ---GIMYSKAVEIYIOGKLLKPAVGIKIDVNSWINEF-----TKTISIRDP--CAGP--- 825  
 DB 811 DTVGILVSTAVELSLGRTRLRPAVGVKLDLEAWAEKFKVLASNRTHQPOQKOC--GPNSH 869  
 QY 826 -VCDCKRNSDVMDCVILDGSGFLMANHDDYTNQIGREFGEIDPSLMRHLVNI SVYAFNK 884  
 DB 870 CEMDCVNEEDLVCVLIDGGLVLSNQHQWQVGRFFSEVDANLMLALYNNSTYTRKE 929  
 QY 885 SYDYQVSCVPGAPKOGAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSLTFPRLLE 944  
 DB 930 SYDYQVSCVPGAPKOGAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSLTFPRLLE 989  
 QY 945 AVEMEDDDDTASLUSKOSCITEQTYFFDNDKSKFSGLVDCGNCGRIFHGEKLNNTLIFI 1004  
 DB 990 ADPAEAEG--SPETRESSCVMKQTYTFGSVNASYNAIIDCGNCSRLFAORLTNTLLFV 1048  
 QY 1005 MVESKCTCCDTRLLIQAEQ--TSDGPNPCDMVK 1036  
 DB 1049 VAEKPLCSOCEAGRLLQKQTHCPADGPEQCELVQ 1082

RESULT 10  
 Q9UEW0 PRELIMINARY; PRT; 1076 AA.  
 AC Q9UEW0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE ALPHA 2 DELTA CALCIUM CHANNEL SUBUNIT ISOFORM II.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,  
 RA Zabarovsky E., Johnson B., Lerman M.I.;  
 RT "A new alpha 2 delta subunit of the L-type voltage gated calcium  
 RT channel resides in the lung cancer critical region on 3p21.3.";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF042793; AAB96914.1; -;  
 DR InterPro: IPR02035; -;  
 SQ SEQUENCE 1076 AA; 122116 MW; EEC474836B7EDA05 CRC64;

Query Match 53.0%; Score 2886.5; DB 4; Length 1076;  
 Best Local Similarity 54.6%; Pred. No. 4.8e-176;

Matches 561; Conservative 166; Mismatches 262; Indels 39; Gaps 15;

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QY 33 IKSWVDKQEDLVTLAKTASGVNOLVDYIKYQDLYTVEPNARQLVEIAARDIEKLISN 92
Db 1 MQHWRLEQEVGVGMIFGVQVQLREIYKDNRLNFVEQNEPKLVKVEKAGDIESLLDR 60
QY 93 RSKALVSLAEAEKQVAHQWREDFASNVVYNAKDL---DPEKNDSEPGSQ--RIKP 147
Db 61 KVQALKKLADAAEFQAHWRQDNKEEDIVYDADAEALDDPSESDVERGSKASTLRL 120
QY 148 VFIEDANFGQISYQHOAAVHPTDIYEGSTIVLNELNWTSLADYFKKNEEDPSLLQV 207
Db 121 DFTEDPNFKKNVSYAAVQIPDIYKGSVILNENWTALENVFNENRQDPTLLQV 180
QY 208 FGSATGLARYPASPWWNSRTNPKIDLYVRRRPWYIOGAASPKDMLILDVSGSVSGL 267
Db 181 FGSATGVTRYYPATPW---RAPKKIDLYVRRRPWYIOGASSPKDMLILDVSGSVSGL 236
QY 268 TLKLI RTSVSEMLETSLDDDFVNVASNSNAQDVSCFQHLVQANVRNKKVLKDAVNITA 327
Db 237 TLKLMKTSVCEMLDTSDDDYVNVASFNERKAQPVSCFTHLVQANVRNKKVFEKAVQGMVA 296
QY 328 KGITDYKKGFSFAFEOQLNVTNVRANCKTIIMLTGDEGEERAQEIFNKYN-KKKVVRER 386
Db 297 KGTGYKAGFEYAFDQNSNITRANCNKIMMFTDGEDRVQDVFEKYNWPNRTVRFT 356
QY 387 FSVGQHNRYERGP IQWMAKENGKYYEIPSGAINTQYEDLVLRPMVLGAKAKOVQW 446
Db 357 FSVGQHNRYDVTPLQWMAKENGKYYEIPSGAINTQYEDLVLRPMVLGAKAKOVQW 416
QY 447 TNYVLDALGLVITGTPLVFNITGOFENKTNKQILGVMGVDSLEDIKRLTPRFTL 506
Db 417 TNYVEDALGLVITGTPLVFNLTQ--DGPGEKKQILGVMGIDVALNDIKRLTPNYTL 474
QY 507 CPNGYFAIDPNCYVLLHNPQLQPNKSPQRPVTLDFDALENDIKVIEIRNKMIDGESGE 566
Db 475 GANGYFAIDNLGNYVLLHNPQLQPNKSPQRPVTLDFDALENDIKVIEIRNKMIDGNKGH 534
QY 567 KTFRTLVKSODERYIDKGNRTYTWTPVNGDYDSLALVLPYISFYIKAKLEETITQARSK 626
Db 535 KQIRTLVKSLDERYIDEVTNYTWTPVIRSNYSGLVLPYISFYIQANLSDQILQ---- 590
QY 627 KGKMKDSETLKPNFEESGTYTPIADRYCNDLKISDNNTFLLNFNEFIDRKTNPNSCN 686
Db 591 ---VKYFEFLPSSFESEGHVFIAPREYKDLNASDNNTFLLNFNEFIDRKTNPNSQCN 647
QY 687 ADLINRVLLDAGTNELVQYNSKQK-NIKGVYARFVVTGGITRYVPKBAENQWENPE 745
Db 648 NFLHLNILDGTQQLVERWRDQDLNTYSLAVFAATDGGITRYVPKBAEDWTENPE 707
QY 746 TYEDSFYKRSLDNDYVFTAPYFNK-SGPGAYES---GIMVSKAVETIYIOGKLLKPAVVG 801
Db 708 PFNASYRSLDNHGYVFPHPHODALLRPLENDVTGLVSTAVELSGRRTLRFAVVG 767
QY 802 IKIDVNSWIENF-----TKTSIRDP--CAGP-----VCDCKRNSDVMDCVILDDGGELLMA 850
Db 768 VKLDLEAWAEKFKVYLASNRTHQDQPKC-GPNSHCEMDCEVNNEDLLCVILDDGGFLVLS 826
QY 851 NHDDYINQIGRPFGEIDPSLMRLHVNISYAFNKSVDYQSVCEPGAAPKOGAGHRSAYVP 910
Db 827 NONHODVQGRFSEVDANLMLALYNSFTRKESYDYQAACAPQPPGNGALAPRGVFPV 886
QY 911 SVADILQIGWATAAAWSILQFLLSLTTPRLLEAVEMEDDDFTASLSKSCITEQTOYF 970
Db 887 TVADFNLNLTWTSAAWSLQFLLGLYLSHWFQADPAEAG-SPETRESSCVNMQTOY 945
QY 971 FDNDSKSGVLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTCTPCDTRLLTQABQ--TSDG 1028
Db 946 FGSVNASYNALIDCGNCSRLFHAQRLTNTNLLFVVAEKLPLCSQCEAGRLLQKETHCPADG 1005
QY 1029 PNPCDMVK 1036
Db 1006 PEQCELVQ 1013
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RESULT 11

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Q9NSA6 PRELIMINARY; PRT; 975 AA.
AC Q9NSA6;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE LUAC11.1 (CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 2D SUBUNIT
DE (KIAA0558)) (FRAGMENT).
GN LUAC11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z84492; CAB41767.2; -
DR InterPro; IPR002035; -
FT NON_TER 1
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;
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Query Match 49.9%; Score 2717; DB 4; Length 975;  
Best Local Similarity 56.8%; Pred. No. 2.9e-165;  
Matches 526; Conservative 139; Mismatches 225; Indels 36; Gaps 14;

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QY 132 DPEKNDSEPGSQ--RIKPVFIEDANFGQISYQHOAAVHPTDIYEGSTIVLNELNWTSL 189
Db 2 DPESEDVERGSKASTLRLDFIEDPNFKKNVSYAAVQIPDIYKGSVILNENWTEAL 61
QY 190 DEYFKKNEEDPSLLQVFGSAGLARYYPASPWWNSRTPNPKIDLYVRRRPWYIOGAA 249
Db 62 ENYFMENRRQDPTLLMQVFGSATGVTRYYPATPW---RAPKKIDLYVRRRPWYIOGAS 117
QY 250 SPKDMLLIVDVSGSVGLTKLI RTSVSEMLETSLDDDFVNVASNSNAQDVSCFQHLVQ 309
Db 118 SPKDMLLIVDVSGSVGLTKLMKTSVCEMLDTSDDDYVNVASFNERKAQPVSCFTHLVQ 177
QY 310 ANVRNKKVLKDAVNNTAKGITYKGFSAFQOLLNVTNVRANCKNIIIMLTGDEGEERA 369
Db 178 ANVRNKKVFEAYQGVAKCTGYKAGFEYAFDQNSNITRANCNKIMMFTDGEDRV 237
QY 370 QEIFNKYN-KDKKVRPFRPSVGHNYERGP IQWMAKENGKYYEIPSGAINTQYSLD 428
Db 238 QDVFKEYNWPNTVRVFTFSVGHNYDVTPLQWMAKENGKYYEIPSGAINTQYSLD 297
QY 429 VLGRPMVLAGKAKOVQWNTNYVLDALGLVITGTPLVFNITGOFENKTNKQILGVM 488
Db 298 VLGRPMVLAGKAKOVQWNTNYVEDALGLVITGTPLVFNLTQ--DGPGEKKQILGVM 355
QY 489 GVDVSLIEDIKRLTPRETCLCPNGYFFAIDPNGYVLLHNPQLQPNKSPQRPVTLDFDALE 548
Db 356 GIDVALNDIKRLTPNYTLGANGYFAIDNLGNYVLLHNPQLQPNKSPQRPVTLDFDALE 415
QY 549 NDKVIEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTYSALVLPYIS 608
Db 416 DENKESTIRSMIDGNKGHKQIRTLVKSLDERYIDEVTNYTWTPVIRSNYSGLVLPYIS 475
QY 609 FYIYKAKLEETITQARSKKMKDSETLKPDNEEESGTYTPIADRYCNDLKISDNNTFEL 668
Db 476 TFYQLANLSDQILQ-----VKYFEFLPSSFESEGHVFIAPREYKDLNASDNNTFEL 528
QY 669 LNFNEFIDRKTNPNSCNADLINRVLLDAGTNELVQYNSKQK-NIKGVYARFVVTGG 727
Db 529 KNFIELMEKVTYPSKQCNFNFLHNLILDGTQQLVERWRDQDLNTYSLAVFAATDGG 588
QY 728 ITRVYPKBAENQWENPEYEDSFYKRSLDNDYVFTAPYFNK-SGPGAYES---GIMVS 783
Db 589 ITRVFPKAAEDWTENPEPNASFYRRSLDNHGYVFPHPHODALLRPLENDVTGLVLS 648
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QY 784 KAVEIYIOGKLLPAPVGVKIDVNSWIEP-----TKTSDRP--CAGP-----VDCCKRN 832
DB 649 TAVELSGRRTRLPAPVGVKIDVNSWIEP-----TKTSDRP--CAGP-----VDCCKRN 707
QY 833 SDVMDCVILDDGGFLMANHDDYTNQIGRFGFETDPSLMRHLVNIISYAFNKSVDYQSV 892
DB 708 NEDLLCVILDDGGFLVLSNQHNDQVGRFSEVDANMLALNNSEYTRKESDYQVQAC 767
QY 893 EPGAAPKOGAGHSAYVPSVADILQIGWATAAANSTLOQLFLSLFPRLLEAVEMEDDD 952
DB 768 APQPPGNLGAAPRGVFPVTVADFLNLAAMWTSAANSLFQOLLYGLIYHSFQADPAEAG 827
QY 953 FTASLSKQSCITEOTQYFFDNDKSGFVLDGNCGRIFHGEKLMNTNLIIFINVESKGT 1012
DB 828 -SPETRESSCMKQTYFSGVNSYNAIIDGNCGRSLFHAQRLTNTNLLFVVAERPLCS 886
QY 1013 PCDRLLIQAEQ--TSDGPNPCDVK 1036
DB 887 QCEAGRLLQKETHCPADGPEOCELQ 912

RESULT 12
Q921L5 PRELIMINARY; PRT; 1091 AA.
AC Q921L5
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CALCIUM CHANNEL ALPHA-2-DELTA-C SUBUNIT.
GN CACNA2D3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=9098955; PubMed=9880589;
RA Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).
DR EMBL: AJ010949; CAA09423.1;
DR MGD: MGI:1338890; CACNA2D3.
DR InterPro: IPR002035; -.
DR SEQUENCE 1091 AA; 122777 MW; 7ABEE2BDA10077A0A CRC64;

Query Match 19.98; Score 1085; DB 11; Length 1091;
Best Local Similarity 28.78; Pred. No. 8.3e-61;
Matches 309; Conservative 222; Mismatches 416; Indels 128; Gaps 40;

QY 3 AGCLLALTTLFOSLLIGSPSEPPSAVTIKSVWDMQEDLVTAKTAGVNLVDIYE 62
DB 14 ASALLA-TALLYAALGDVVRSEEQIPLSV-VKLWASAFGEIKSIAKYSQSLQKKYK 71
QY 63 KYQDLYTEPNNAOLVIAARDIEKILSNRKSALVLSLALEAEKVAQAAHQRDEFASNEV 122
DB 72 EYKDVATEEIDGLQVLKALKINEEMPHKSEAVRRLVEAAEEAHLKHEFDADL--QY 128
QY 123 VYNNAK--DDLDPEKNDSEPGSQIKPVFIEDANFR--QISYQHAAVHIPDIYEGSTIV 179
DB 129 EYFNAVLINERDKGNFLELGEFT--LAPNDHFNLPNLSISLSDVQVPTMYNKDPAI 185
QY 180 LNELNMTSALDEVEKKEEDPSLLWVFGSATGLARYPASVWDSNRTNPKIDLVDVR 239
DB 186 VNGVWSSSLNKFVNDPDRPSLIWQYFGSAKGFYRPGIKWEPDE--NGVIAPDCR 242
QY 240 RPWTYIOGAASPDKMLIILVDYSGVSGVLTLLKRTSSEMLETSLDDDFVNVASFNSNAQ 299
DB 243 NRKWIQAOTSPKDVILVDYSGVMKGLRLTAKOTVSSILDTLGDGDFNLIYNEELH 302
QY 300 DVS-CFQ-HLVQANVRNKKVLKDAVNNTAKGIDTYKKGFSAFEQLLNINVRAN--CN 355
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DB 303 YVEPCLNGTLVQADRTNKEHREHLKLFKAGIGMLDIALNEAFNILSDFNHTGQGSICS 362
QY 356 KIIMLTDDGGEBAQAFIFKNYN-KDKKRVFRFSVGOHNYTERGPIQWACENKGYIYEIP 414
DB 363 QAIMLTDDGAVDITDIFAKYNNPDRKVRIFTYLIIGREAAAFADNLKWMACANKGFFQIS 422
QY 415 SIGAIRINTOEYLDVLGRPMVLADKAKOVQWNTNVYL-----ALELGLVI--TGT 463
DB 423 TLADVENWMEYLHLSRPKVI--DQEHVVTWEAYIDSTLPOAKLADDOGLVMTVA 480
QY 464 LPVFNITGPFENKTNLKNQILGVMGVDSLEDIKRTPRTFTCPNGYIFAIDPNGVLL 523
DB 481 MPVES---KONETRSKG-ILLGVVGTDVPVKELLTKPKYKLGIGHYAFAITNNGYILT 535
QY 524 HPNLQP---KNPKSQEP--VTDFLDAELENDIKVEIRNMIDGSECEKFTFRLVKQODE 578
DB 536 HPELRPLYEEGKKRRKPNYSVDLSEVEDRDDV-LRNAMVNRKTKG--FSMEVK---- 586
QY 579 RYIDKGNRT-----YTWTPVNGTDYSALVLPY-YSFYIKAKLEETITQARSKKGMK 631
DB 589 KTVDKGRVLWNTDYITDIKGTFFSLGVALSGHCKGYF-----RGNTV 634
QY 632 DSETLKPDNFEESGYTFIAPRDYCN-DLKISDNNTEFLNNEFIDRKTPNPNNSCNADLI 690
DB 635 IEELG--HDLEHPDVSADWESYCNLDLHPEHRHLSOLEAIKLYLKGEK-LLQCDKELI 691
QY 691 NRVLDAAGFTNELVQNTWS-----KKNIKGVKARFVTDGGITRVYP----- 733
DB 692 QEVLFDA-VVSAPIEAYWTSALNKSNSDKGVEAFVLTGTRSLRNLNLFVGAQDLNQD 750
QY 734 -KAGENQWENPETEYDSFYKRSLDN--DNKYFTAPY---FNKSGPGAYESGLWMSKAV 786
DB 751 FLKAGDKENIFNADHFLNTRRAEQTAGSFVYIPSTGTVNS-----NVYATSTSI 804
QY 787 EYIQGKLLKPAVVGKIDVNSWIEPNTKTSIRDPAGVPCDKRNSDMVDMCVILDDGGF 846
DB 805 QLLDERKSPVVAAGVQMKLEFFORKEFTWASROCASLDGKCSISCDDETVCYLIDNNGF 864
QY 847 LLMANHDDYTNQIGRFGFETDPSLMRHLVNIISYAFNKSVDYQSVCEPGAAPKOGAGHS 906
DB 865 ILVS--EDYT--QTGDFFEVEGAVNMKLLTMGSEKRTLDYDQAMCR---ANKESSDSAH 918
QY 907 AYVPSVADILQIGWATAAANSTLOQLFLSLTFPRLLEAVEMEDDDFTASLSK-----QS 961
DB 919 GLLDPYKAFI-----SAAKWIMTELVLFLVEF---NLCSWHSDMTAKAKLQKLEP 968
QY 962 CITEQTYFFDNDKSGFVLDGNCGRIFHGEKLMNTNLIIFINVESKGTCPDPT 1016
DB 969 CDTEYPAFVSERTIKETGNTACEDCSKSFVIQIOPSSNLFMVVDS--SCLCES 1021

RESULT 13
Q9NY16 PRELIMINARY; PRT; 997 AA.
AC Q9NY16
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CALCIUM CHANNEL ALPHA2-DELTA3 SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Buger P., Hanke S., Chudek J., Kovacs G.;
RT "Analysis of a putative tumor suppressor gene region of 100 kb at chromosome 3p21.1 in conventional renal cell carcinoma.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ272268; CAB5962.1;
DR InterPro: IPR002035; -.

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[illegible]



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Db 305 ENIEVFNOQIEQLDDPEGYANLTLAYETAFLRLRYKYSRHCVTNSTCNOQIMLVTDGVA 364
Qy 367 ERAOEIENKYN-----KDKKVRVFRFSVGOHNERGPIQWACENKNGYIPIPSIGA 418
Db 365 GNTVEVOKYNGNGENGTQMDRFRVLYLLGKVEYKVRLEQWACLNRGYSHVQILDE 424
Qy 419 IRIHQEYLDVLGRPMVLGAKAKQVQWTVNYLDAL-----ELGLVTIGLPLVFN 469
Db 425 VHEEVLKVDVIATPLVLQNEQHPPT-WTHAFTDKTYDPKTSNEKRPLMTISVGPFAFDR 483
Qy 470 TGOPEKTNLKNOLLGVMGVDSLEDKRLTPFTLPCNGYFAIDPBGVYLLHPNLOP 529
Db 484 FYRANSTNPRAR-LGVAGDVDPVEDIDKLTLPYKGVNGYSFVSNNGVYLLHPDURP 542
Qy 530 -----KNPKSQEPVTFDLDAE-LENDIK-----VEIRNKWIDGESGE-KTFFTLV 573
Db 543 IGTGKNMPNPNY---SIDFTEVHELFEDQSPREGESILHINRAWVRHEANFEKSISVKE 599
Qy 574 KSQDERYIDKGNRTYWTVPVNGTYSIALVLPT-YSFYIKAKLEETITQARSKKGKMD 632
Db 600 HYDKMRRYSEKQDYFFAPLEPTFTLGIWMPSEYGTWIKVGEVD-----KNKHKMINI 655
Qy 633 SETLKPDPNFE-----SGYTFIAP-----RDVC-----NDLKISDNNTEFLNEN 672
Db 656 SDFFIGENKWKHPDWYCKYHYLEGHEKTEPEALREFLAKQNDKWSEYADESDWD 715
Qy 673 EFID-----RKTNPNS--CNADLINRVLDDAGFTNELQNTW-----SKQNKIGVKA-- 719
Db 716 DKDDLNCGRKTLGDDAYYCNKELNLLIFDAKVTNS-SYGVWRPFESDEERQLIERFRADL 774
Qy 720 RPYVTDGITRVYKPEAGENQ-----ENPTEVDSFYKSL-----D 757
Db 775 RFVATMSGLTR-----WQIFGEVEVDTRFEGDHTTAIDETWYKSAILOHEDR 825
Qy 758 NDNYVFTAPYENKSPGAYESGINYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTS 817
Db 826 AESFYVSKYID-----DPMEDSE 844
Qy 818 IRDPCAGPVCCKRNSVDMCVILDDGFLMANHDDVTNIGRFFGIDPSLMRHLVNI 877
Db 845 VKCNHCLPIC-----TDDVDVCVINDNAYIVIGQN---INTTGRFEGFHGDVMTAMVER 897
Qy 878 SVYAFNKSYDQSVQ--EPGAPKOGAGHRSAVPSVAD-ILQIGWATAAASWLQOFL 934
Db 898 GIFLSIEYIDYQEOCKEPEKAVME-----YTDEIEDEVAVGDGKSSA-----941
Qy 935 LSLTPRLLEAVEMEDDDFTASLQ-----QSCITEQTOYFFDNDSKFSFGLDC--G 985
Db 942 -----SKPKDSDDENAMFEDEPEPDIYKACDKRSTLYAL--QPSALVGINDFVEA 990
Qy 986 NCSRIFHGEKLMNTNLIFIMV 1006
Db 991 PSTRPFLVKKIPNSNLVLVV 1011
RESULT 15
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AC QVJMO
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CG12455 PROTEIN.
BG:DS07473.1 OR CG12455.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
KC STRAIN=BERKELEY;
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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova K., Bouchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Folsler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-F., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "the genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003650; AAF53505.1; -.
DR FlyBase; FBgn028859; BG:DS07473.1.
DR InterPro; IPR002035; -.
SQ SEQUENCE 2172 AA; 247574 MW; 39AA7BCB470DIA39 CRC64;
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Query Match 16.8%; Score 912.5; DB 5; Length 2172;

Best Local Similarity 25.1%; Pred. No. 2.7e-49;

Matches 275; Conservative 207; Mismatches 383; Indels 229; Gaps 42;

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Qy 29 SAVTIKSWDKMQEDLVTLAKTAGVNLVDIYKYQDLYTEPNARQLVEIARDIEK 88
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Qy 89 LLSNRKALVSLALEAEKVAQAAHQWREDA--SNEVYVYINAKDDLDPKNDSEPG----S 142
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Qy 143 QRIKPVFTEDANF-GRQISYQAAHVHPTDIYEGSTIVNELNWTSDALDEFFKKREEDP 201
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Qy 202 SLLQVFGSATGLARYYPASPWNDSRTPNKLIDLVRRRPWYIQGAASPKDMLILVDVS 261
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Qy 320 DAVNNI-TAKGITDYKKGFSFAFOLLNYSVR-----ANCKIIMLTGDGEERAQEIF 373
Db 294 QQIEQLDDPEGYANLTLAYETAFLRLRYKYSRHCVTNSTCNOQIMLVTDGVAAGTTEVF 353
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Mon Jul 23 08:36:32 2001

us-09-397-548-16.rspt

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| | | | | : : : : : | | | | | : : : : :  
Db 354 QKYNWNGENGTSQMDTRVFTLLGKEVTKVREIQWACLNRCGYSHVQTLDEVHEEVK 413  
QY 426 YLDVLCRPVVLADGKAKQVQWTVNYLDAL-----ELGLVITGTLVPFNITGOFENK 476  
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Db 414 YVDVIATPLVLQNEQHPPT-WTFAFTDKYDPTKSNEKRPRLMISVGPAPAFDRFYRHANS 472  
QY 477 TNLKNOLIILGVMGVDSLEDIKRLTFRFTLCPNGYFYFAIDPNGYVLLHLPNLP-----K 530  
| | | | | : : : : : | | | | | : : : : :  
Db 473 TNPRL-LGVAGTDPVEDIDKLTLPYKLGVNGYFVVSNNNGYVLLHLPDLRPIGTNGKM 531  
QY 531 NPKSQBPVTLDFLDAE-LENDIK-----VEIRKMDGESGE-KTFTLVKSQDERY 580  
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Db 532 NPNN-----SIDTEVEHLEFQSPREFGESILHIRNAMVRHEANEFKSISVKFHYDKMRR 588  
QY 581 IDGNRTYTWTPYNGIDYSLALVLT-YSFYIKAKLEETITQARSKKGKMKDSETLKPD 639  
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Db 589 VSEKODYFAPLNPFTPLTGIWMPSEYKGTWIKVGEVD-----KNHKMINISDFIGE 644  
QY 640 NFEE-----SGYTFIAP-----RDYC-----NDLKISDNTEFLNFNEFID--- 676  
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QY 677 -RKTNNPS--CNADLINRVLLDAGFTNELVQNVW-----SKOKNIKVKA--RFVYTDG 726  
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Db 705 GRKTLGDADAYCNKELVLLIFDAKVNS-SYGVWRFESDEEROLIERFRADLRFVATMS 763  
QY 727 GTRVYYPEKAGENWQ-----ENPETYEDSFYKRSL-----DNDNYVFT 764  
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Db 815 VKYD-----DPMEDSEVKCNHCL 833  
QY 825 PVCCKRNSVMDCVILDDGGFLLMANHDDYNOIGRPFGEIDPSLMRHLVNSVYAFNK 884  
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Db 834 PIC-----TDDVDVCWIDNNAYIVIGN--INTTGRFFGEFGDVMVTAMVERGIFLSIE 886  
QY 885 SYDYQSV--EPGAAPKOGAGRSAYVPSVAD-TLOIGWATAAAWSILOQFLLSLTFPR 941  
| | | | | : : : : : | | | | | : : : : :  
Db 887 VDYQEQQCKEPPKAVME-----YTDEIEDEYVAVDGGKSSA----- 923  
QY 942 LLEAVEMEDDDFTASLSK-----QSCITEQTOYFFDNDKSFSGVLDC--GNCSRIFF 992  
| | | | | : : : : : | | | | | : : : : :  
Db 924 --SKPKDSDDENAMFEPEPDPYKACDKRSTLYAL--QPSALVGINDFVEAPSTREFL 979  
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| | | | | : : : : : | | | | | : : : : :  
Db 980 VKKIPNSNLVLVV 993

Search completed: July 23, 2001, 07:47:28  
Job time: 614 sec

GenCore version 4.5  
Copyright (C) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 07:36:44 ; Search time 92.97 Seconds  
(without alignments)  
693.162 Million cell updates/sec

Title: US-09-397-548-17  
Perfect score: 5599  
Sequence: 1 MAACLLALITLFSLLIG.....PDVCFDNNVLEDTDCGGVS 1063

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries:

Database : A\_Geneseq\_0601.\*  
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2: /cgnl\_9/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5599	100.0	1091 19	AA1981
3	5599	100.0	1091 21	AA1982
4	5599	99.9	1091 19	AA1983
5	5593	99.9	1091 14	AA1984
6	5579.5	99.7	1110 19	AA1985
7	5559.5	99.3	1086 16	AA1986
8	5559.5	99.3	1086 21	AA1987
9	5559.5	99.3	1086 19	AA1988
10	5542.5	99.0	1084 16	AA1989
11	5542.5	99.0	1084 19	AA1990

12	5542.5	99.0	1084 21	AA1991
13	5523	98.6	1103 16	AA1992
14	5523	98.6	1103 19	AA1993
15	5523	98.6	1103 21	AA1994
16	5503	98.3	1079 19	AA1995
17	5503	98.3	1079 21	AA1996
18	5497	98.2	1079 16	AA1997
19	5385.5	96.2	1106 18	AA1998
20	5385.5	96.2	1106 18	AA1999
21	5385.5	96.2	1106 21	AA2000
22	5364.5	95.8	1106 16	AA2001
23	5257.5	93.9	1100 10	AA2002
24	5257.5	93.9	1100 10	AA2003
25	5257.5	93.9	1100 10	AA2004
26	5257.5	93.9	1100 10	AA2005
27	5257.5	93.9	1100 10	AA2006
28	5257.5	93.9	1100 10	AA2007
29	5257.5	93.9	1100 10	AA2008
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32	5257.5	93.9	1100 10	AA2011
33	5257.5	93.9	1100 10	AA2012
34	5257.5	93.9	1100 10	AA2013
35	5257.5	93.9	1100 10	AA2014
36	5257.5	93.9	1100 10	AA2015
37	5257.5	93.9	1100 10	AA2016
38	5257.5	93.9	1100 10	AA2017
39	5257.5	93.9	1100 10	AA2018
40	5257.5	93.9	1100 10	AA2019
41	5257.5	93.9	1100 10	AA2020
42	5257.5	93.9	1100 10	AA2021
43	5257.5	93.9	1100 10	AA2022
44	5257.5	93.9	1100 10	AA2023
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ALIGNMENTS

RESULT 1  
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ID AA1980 standard; Protein; 1091 AA.  
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AC AA1980;  
XX  
DT 01-DEC-1995 (first entry)  
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DE Human neuronal calcium channel subunit alpha 2b.  
XX  
KW Calcium channel subunit; antagonist; agonist; diagnosis;  
KW Lambert Eaton Syndrome.  
XX  
OS Homo sapiens.  
XX  
PN W09504822-A.  
XX  
PD 16-FEB-1995.  
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PF 11-AUG-1994; 94WO-US09230.  
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PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
PI Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;  
XX  
XX WPI; 1995-090900/12.  
XX  
DR N-PSDB; AAQ84664.  
XX  
PT DNA encoding human calcium channel sub-unit(s) - used for  
PT developing prods. for studying calcium channels, e.g. for  
PT obtaining agonists and antagonists



CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
CC that allow controlled entry of calcium ions into cells. This leads  
CC to depolarisation events required for muscle contraction. The recombinant  
CC subunit, when expressed with nucleic acids encoding the complete calcium  
CC channel, can be used in assays for the detection and characterisation of  
CC compounds that modulate the channel. The DNA encoding the subunits can  
CC be alternatively spliced when transcribed, giving more than one form of  
CC the protein from the same transcript, each having slightly different  
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
CC molecules from the serum of an individual with Lambert Eaton Syndrome  
CC (LES) can be used as a diagnostic for the disease.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5599; DB 19; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 EYVYNAKDDLPEDKNDSPGSGRIKPVFIEDANFGRQISYHAAVHPIDYIEGSTIVL 180  
DB 121 evyynakddlpedkndspgsgrikpvfiedanfrqisqhaavhiptdiyegstivi 180  
QY 181 NELNWSALDEVFKKNEEDPSLLQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
DB 181 nelnwsaldevfkneedpsllqvfgsatglaryypaspvwdnsrtpnkidlydvr 240  
QY 241 RPWYIGASPKDMLIIVDVGSGVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
DB 241 rpwyigaspkdmliivdvgsgvsgltklirtsvsemlletlsdddfvnvasfnasnaqd 300  
QY 301 VSCFQHLVQANVRNKKVLDAVNNTAKGITYDKKGFSAFEOQLLNVNVRANCKIIML 360  
DB 301 vscfqlvqanvrnkvkldavnnitakgitydkkgsfafedllnvnvrancnkiml 360  
QY 361 FTDGGERAQEIPKYNKKKVRFRFSQGHNYERGIQWACENKGYIYEIPSGAIR 420  
DB 361 ftdggeeraqeipkynkkkvrfrfsvqghnyergiqwacenkgyiyeipsigair 420  
QY 421 INTQEVLDVLRPMVLGDKAKQVQNTVYLDALGLVITGTLPVFNTGQFENKTNLK 480  
DB 421 intqevldvlgprpmvlgdkakqvqntvnyldaleglvitgtlpvnitgqfenktnlk 480  
QY 481 NQILGVMGVDVSLDIDKRLTRFTLCPNGIYFPAIDPNGVLLHPNLOPKNPKSQBPVTL 540  
DB 481 nqilgvmgvdsledidkrltrftlcpngiyyfpaidpngvllhpnlopnkpsqbpvtl 540  
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QY 601 ALVLPYISFYIKAKLEETITQARSKGKMKDSEITLKPONFESGYTFTIAPRDYCNLDKI 660  
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QY 661 SDNTEFLNFEFIDRKTPNPNPCNADLNRYLLDAGFTNELVQWNSKOKIKGVKAR 720  
DB 661 sdntefllnfefidrktpnpnpncnadlnrylldagftnelvqwsokikgvkar 720  
QY 721 FVVTGGITRVYPKAENQENPETEYDFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780  
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RESULT 3  
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ID AAB10576 standard; Protein; 1091 AA.  
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AC AAB10576;  
XX  
DT 22-DEC-2000 (first entry)  
XX  
DE Human calcium channel alpha-2 subunit protein.  
XX  
KW Human; calcium channel; calcium channel subunit; diagnosis;  
KW Lambert Eaton Syndrome; calcium channel subunit alpha-2.  
XX  
OS Homo sapiens.  
XX  
PN US6096514-A.  
XX  
PD 01-AUG-2000.  
XX  
PF 25-MAY-1995; 95US-0450562.  
XX  
PR 04-APR-1988; 88US-0176899.  
PR 02-FEB-1990; 90US-0482384.  
PR 08-NOV-1990; 90US-0603751.  
PR 30-NOV-1990; 90US-0620250.  
PR 15-AUG-1991; 91US-0745206.  
PR 10-APR-1992; 92US-0868354.  
PR 13-JUL-1992; 92US-0914231.  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
PR 07-FEB-1994; 94US-0193078.  
PR 04-APR-1994; 94US-0223305.  
PR 11-AUG-1994; 94US-0290012.  
PR 23-SEP-1994; 94US-0311363.  
PR 28-SEP-1994; 94US-0314083.  
PR 07-NOV-1994; 94US-0336257.  
PR 13-MAR-1995; 95US-0404950.  
XX  
PA (SIBI-) SIBIA NEUROSCIENCES INC.  
XX  
PI Ellis SB, Williams ME, McCue AF, Harpold MM;  
XX  
DR WPI; 2000-548230/50.  
XX  
DR N-PSDB; AAA71707.  
XX  
PT Human calcium channel beta subunit polynucleotides, useful for  
PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
XX Syndrome  
XX  
PS Example IV; Column 135-144; 153pp; English.  
XX  
CC This invention describes a novel isolated DNA molecule (I) comprising a  
CC sequence encoding a beta3-1 subunit of a human calcium channel.  
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of

CC beta\_3 subunit encoding DNA are useful for isolation and cloning of  
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 CC express heterologous calcium channel are useful for identifying compounds  
 CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit of eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2 subunit which is  
 CC described in the method of the invention.

XX Sequence 1091 AA;

Query Match 100.00; Score 5599; DB 21; Length 1091;  
 Best Local Similarity 100.00; Pred. No. 0;  
 Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFOSLLIGPSEPPFSAVTVIKSWDKMQEDLVTLAKTAGVNLQVLDI 60  
 Db 1 maagcllaltlfigsligpseepfssavtikswdkmqedlvltaktagvnlqldi 60  
 QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQWRDPASN 120  
 Db 61 yekyqdltyvepnnaqqlveiaardieklkllnsrkalslaleaeqvaaahqwrdfasn 120  
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYSQHAHVHTPTDIYEGSTIVL 180  
 Db 121 evvyynakddldpekndsepgsqrikpvfiedanfgroisqhaahvhtptdiyegstivl 180  
 QY 181 NELNWTSAIDVEFKKNEEDPSLLQWFGSATGLARYYPASPVWDSNTPNKIDLYDVR 240  
 Db 181 nelnwtalsaidvefkknreedpsllqwfgsatglaryypaspvwdsnrtpnkidyvrr 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSGTLKLIQTSVEMLETLSDDDFVNVASNSNAQD 300  
 Db 241 rpwyioqaaspkdmlilvdvsgvsgtlklirtsvemletlsdddfvnvasnsnaqd 300  
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGSFAFEQLNLNVSRANCKLIIML 360  
 Db 301 vscfqlhqvqanvrnkvlkdavnntakgitdykkgsfafeqllnlvnsrancnkliiml 360  
 QY 361 FTDGGEERAQEIFNKYKDKKVRFRSVQGHNYERGIOMACENKGYIYEIPSGAIR 420  
 Db 361 ftdggeeeraqeifnkynkdkkvrfrsvqghnyerqpiqmacenkgyyeipsigair 420  
 QY 421 INTQEYLDVLGRPMVLAKGAKOVQNTVYLDALGLVITGTLVPFNITGQFENKTNLK 480  
 Db 421 intqeyldvlgrpmvlakgakovntvylldaleglvitgtlvpfnitgqfenktnlk 480  
 QY 481 NQLILGVMGVDSLEDIKRLTPRTFLCPNGYYFAIDPNGVYLLHPNLQPKNSQEPVIL 540  
 Db 481 nqlilgvmgvdsledikrltprtflcpngyyfaidpngvyllhpnlpknpsqepvtil 540  
 QY 541 DFLDAELENDIKVEIRNKMIIDGSGSEKTRTLVKSDERYIDKGNRTYTPTVNGDYSL 600  
 Db 541 dfldaelendikveirnkmiidgsgsekttrtlvksderyidkgnrtytptvngdyisl 600  
 QY 601 ALVLPYSFYIKAKLEETITQARSKGKMKUSETLKPDPNFESGVTFIAPRDYCNLDKI 660  
 Db 601 alvlpysfyyikaleetitqarskgkkmkusetlkdpnfnesgvtfiaprdycondki 660  
 QY 661 SDNTEFLNFEIDRKPNNPNSCNADLINRVLLDAGFTNELVQYNSKQNKIGVKAR 720  
 Db 661 sdnteflnfneidrpkpnnpscnadlinrvlldagftnelvqynskqknigvkarr 720  
 QY 721 FVVTGGITRVTPKEAGENWQENPETEDSFYKRSIDNDNYFTTAPYFNKSGPGAYESGI 780  
 Db 721 fvvtggitrvtvtpkeagenwqenpetedsfykrsldndnyfttapyfnksgpgayesgi 780  
 QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPACGVPDCKRNSDVMDCVI 840  
 Db 781 mvskevayioyggkllkpaavgkldvnswieenftktsirdpcagvpdckrnsdvmdcvi 840

QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNISYAFNKSYDYQSVCEPGAAPKQ 900  
 Db 841 lddggfllmanhddytngigrffgeidpslmrhlvnisyaafnksydyqsvcepgaapkq 900  
 QY 901 GAGHSAYVPSVADILQIGWATAAASILQOFLSLTPFLLEAVEMEDDDFTASLSKQ 960  
 Db 901 gaghsayvpsvadilqigwataaawsilqflsltpflleavemedddftaslskq 960  
 QY 961 SCITETOTVFFPNDKSFSGVLDGNCNCSIFHGEKLMNTNLIFIMVESKGTCPDPTLLI 1020  
 Db 961 sciteqtotvffndksfsgvldcncnscrifhgeklmntnlifimveskgtpcdptlll 1020  
 QY 1021 QAEQTSQDGNPCDMVKQPRYRKGPVDFCNVLEDTDCGGVS 1063  
 Db 1021 qaeqtsdgnpcdmvkpryrkgpdcvdfannvledytdcgvgvs 1063

#### RESULT 4

AAW37879

ID AAW37879 standard; Protein; 1091 AA.

XX AAW37879;

AC AC  
 DT 28-AUG-1998 (first entry)

XX Human calcium channel a2d subunit.

DE Calcium channel; human; central nervous system disorder;  
 XX Lambert-Eaton syndrome; diagnosis; therapy.

OS Homo sapiens.

XX WO9811131-A2.

PD 19-MAR-1998.

XX 11-SEP-1997; 97WO-US16146.

XX 16-SEP-1996; 96US-0713118.

XX (AMHP ) AMERICAN HOME PROD CORP.

XX Chen ARS, Franco R, Shuey DJ;

XX WPI; 1998-207325/18.

XX N-PSDB; AAV29060.

PT DNA encoding human neuronal calcium channel subunit(s) - useful for  
 PT diagnosis of and treatment of central nervous system disorders, e.g.  
 PT Lambert-Eaton syndrome

XX Disclosure; Fig 2; 89pp; English.

CC This polypeptide comprises the a2d subunit of the human neuronal  
 CC calcium channel. cDNA clones (see AAV29059-61) encoding the a1b  
 CC subunit (see AAW37879), the a2d subunit and a b3 subunit (see AAW37880)  
 CC have been isolated. These have been inserted into expression  
 CC vectors and are stably expressed in transformed cell lines. The  
 CC transformed cells show omega-conotoxin GVIA binding activity.  
 CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated  
 CC calcium uptake, indicating that the proteins expressed by the  
 CC clones are capable of forming a functioning calcium channel.  
 CC Nucleic acids encoding the 3 subunits, as well as vectors, host  
 CC cells and methods of isolating nucleic acids encoding related  
 CC calcium channels are disclosed. Fusion proteins incorporating the  
 CC subunit proteins, antibodies, and assays for identifying agents  
 CC that modulate calcium channel activity are also provided. Such  
 CC agents can be used to treat certain central nervous system  
 CC disorders by altering calcium channel activity. Methods of  
 CC diagnosing diseases associated with particular calcium channels,  
 CC such as Lambert-Eaton syndrome, are disclosed.

XX Sequence 1091 AA;

XX SQ

Query Match 99.9%; Score 5595; DB 19; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTLFQSLILGPSSEEPFPAVITKSWDKMOEDLVTLAKTASGVNOLVDI 60  
DB 1 maagcllatl tlfqslilgpsseepfpaavitkswdkmqedlv tlaktasgvnqlvdi 60

QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120  
DB 61 yekyqdl ytevpe nna rqlveiaardie kllsnrskalvslaleaekvqaahq wredfasn 120

QY 121 EVVYNAKDDLPEKNDSPGSGORIKPVFIEDANFORQISYQHAHVHPDIYEGSTIVL 180  
DB 121 evvynakddl pekndspgsgorikpvfi edanforqis yqhaahv hptdi yegstivl 180

QY 181 NELNWTSADEVFKKNEEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKKIDLDYVR 240  
DB 181 nelnwt s adevf kkn eedpsllwqvf gsa tglaryyp asp wvdns rtpnkkid ldyvr 240

QY 241 RPWYIQGAASPKDMLILVDSGVSGLTLKLRITSVSEMLETSLDDDFNVASFNSNAOD 300  
DB 241 rpwyiqgaaspk dmlilvds gvs gltlklritsvse mletsl dddf nvasfnsnaod 300

QY 301 VSCFQHLVQANVRNKKVLKDAVNNIPAKGIDYKGFSAFEQLLNYNVRANCNKIIML 360  
DB 301 vscfqlvqanvrnkkvlkdavn nipa kgid yk gfsa f e qllny nvrancnkiiml 360

QY 361 FTDGGERAQEINFKYKDKYVRFPSVGOHNYERGPTQWACENKGYIYEIPSGAIR 420  
DB 361 ftdgge raqe in fkykdk yvrfps vgo hny ergpt qwac enkgyi yeipsgair 420

QY 421 INTQEYLDVLGRPMVLGAKQOVQNTVYLDALGLVITGTPLENTGQFENKTNLK 480  
DB 421 intqeyl dvlgrpmvlgakqvntv yldal glvitgt pletn t gqfenktnlk 480

QY 481 NQILGVMGVDSLEDKRLTRFTLCPNGYVFAIDPNGYVLLHPLNLPKNPKSQBPVTL 540  
DB 481 nqilgvmgvdsle dkr ltrftlcpngy vfa idp ng yvll hplnlpkn pksqbpv tl 540

QY 541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600  
DB 541 dfldaelndi kveirnk midges gktrtlv ksdery idkgnrt ytwtpvngtdysl 600

QY 601 ALVLPYSFYVYIKAKLEETITQARSKGKMDSETLKPDNFEESGYTFAPRDYCNDLKI 660  
DB 601 alvlpysfyy ika leet itqar skgkmd setl kpdnfeesgy t faprdy cndlki 660

QY 661 SDNTEFLNFEFIDRKTPNPNSCADLINRVLLDAGFTNELVQYWSQKNIKGVKAR 720  
DB 661 sdnteflnfe fidrkt pnpnscadlinrvll dagftnelvqywsqknikgvkar 720

QY 721 FVYTDGIRVYVYKAGEWQENPEYEFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
DB 721 fvytdg irvyv ykagewqenpe yefy krsldndnyftapyfnksgpgayesgi 780

QY 781 MYSKAVEIYIQGLKLPVAVGVIKIDVNSNIENFTKTSIRDPACGPVCDCKRNSDVMDCVI 840  
DB 781 myskaveiyiqglklp vavvgvikidvnsni enftktsir dpcagpvcdckrnsdvm dcvl 840

QY 841 LDGCGFLMANHDDYVNIQIRFFGEIDPRLMRHLNVNISYAFNKSXYDOSVCEPGAAPKQ 900  
DB 841 ldggcflmanhdd yvniqirffge idp rlmrhl nvnisyafnksxydosvcepgaapkq 900

QY 901 GAGHRSAYVPSVADIIQIGWATAAASWILQOFLSLTFRLLLEAVEMEDDDFTASLSKQ 960  
DB 901 gaghrs ayvpsvadi iqigwataaasw ilqoflsl tfrllleav emedddftaslskq 960

QY 961 SCTTEQYVFFDNDKSFSGVLDCGNCRIHFGEKLMNTNLIFIMVESKGTCTCPDRLLI 1020  
DB 961 sctteqy vffdn dksfsgvl dcncri hfgek lmn tnlifimveskgtctcpdrll i 1020

QY 1021 QABQTSQDGNPCDMVKQPRYRKGPVCFDNNVLEDYTDGGSV 1063  
DB 1021 qaetsdgnp cdmvkqpryrk gpdvcfdnnvledy tdcgsvs 1063

RESULT 5  
AAR33553  
ID AAR33553 standard; Protein; 1091 AA.  
XX  
AC AAR33553;  
XX  
DT 30-JUN-1993 (first entry)  
XX  
DE Sequence of the alpha 2 human calcium channel subunit.  
XX  
KW Human calcium channel subunit; diagnosis; agonist; antagonist;  
KW Lambert Eaton syndrome.  
XX  
OS Homo sapiens.  
XX  
PN W09304083-A.  
XX  
PD 04-MAR-1993.  
XX  
PF 14-AUG-1992; 92WO-US06903.  
XX  
PR 15-AUG-1991; 91US-0745206.  
PR 10-APR-1992; 92US-0868354.  
XX  
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
PI Williams ME;  
XX  
WPI: 1993-093936/11.  
DR N-PSDB; AAQ37821.  
XX  
PT DNA encoding specific human calcium channel sub-units - used for  
PT identifying calcium channel agonists and antagonists and  
PT diagnosing Lambert Eaton syndrome  
XX  
PS Disclosure; Page 134-138; 150pp; English.  
XX  
CC DNA encoding a human neuronal calcium channel alpha 2 subunit was  
CC isolated from a human genomic DNA library probed under low and high  
CC stringency conditions with a fragment of DNA encoding the rabbit  
CC skeletal muscle calcium channel alpha 2 subunit. The fragment  
CC included nucleotides having a sequence corresponding to the  
CC nucleotide sequence between nucleotides 43 and 272 inclusive of  
CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.  
CC PCR analysis identified splice variants of the human calcium alpha  
CC 2 subunit transcript. In particularly preferred embodiments, the  
CC DNA encoding the alpha 2 subunit is produced by alternative  
CC processing of a primary transcript that includes DNA encoding the  
CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted  
CC between nucleotides 1624 and 1625 of AAQ37821.  
XX  
SQ Sequence 1091 AA;

Query Match 99.9%; Score 5593; DB 14; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTLFQSLILGPSSEEPFPAVITKSWDKMOEDLVTLAKTASGVNOLVDI 60  
DB 1 maagcllatl tlfqslilgpsseepfpaavitkswdkmqedlv tlaktasgvnqlvdi 60

QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120  
DB 61 yekyqdl ytevpe nna rqlveiaardie kllsnrskalvslaleaekvqaahq wredfasn 120



QY 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 evvynakddldpekndsepsqrikpvfiedanfgroisqhaavhiptdiyegstivl 180  
QY 181 NELNWTSSALDEVFKKREEDPSLLQVFGSATGLARYPPASPDWNGRTNPKIDLYDVR 240  
Db 181 nelnwtssaldevfkkreedsllqvfgsatglaryppaspdwnrtpnkidydvrr 240  
QY 241 RPWTQGAASPKDMLILVDSGSGVTLKIRTSVSEMLETLSDDDFVNVASFNQAQD 300  
Db 241 rpwtqgaaspkdmlilvdsdsgvstlklrtsvsemletlsdddfvnvasfnnaqd 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTIDYKKGSEFAPEQLLNNVSRANCKIIML 360  
Db 301 vscfqhlvqanvrnkvlkavnnitakgtidykkgsefafeqlnnvsvrancnkliiml 360  
QY 361 FTGGERAEQIEFNKYNKKVRFVRSVQGHNYERGPIQWACENKGYEYIEPSTGAIR 420  
Db 361 ftdggeraeqiefnkynkkvrvfsvqghnyergpiqwmacenkgyyeiepstgaair 420  
QY 421 INTQEYLDVLGRPMVLGADKAKQVQWNTNVLDALEGLVITGLPVFNITQGFENKTNLK 480  
Db 421 intqeyldvlgrpmvlgadkakqvqwnvnyldaleglvitgltpvfnitqgfentnlik 480  
QY 481 NQILGVMGVDSLEDIKRLTPRTCLPCNGYFPAIDPNGVYLLHPNLQPKNKSQEPVTL 540  
Db 481 nqilgvmgvdsleedikrltpftclpncgyfpaidpngvylhpnlpknksqepvtl 540  
QY 541 DFLDAELENDIKVEIRNKNMIDGESGKFTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 dfldaeelndikveirnkndmidesgkftlvksoderyidkgnrtytwtvpvngtdysl 600  
QY 601 ALVLPYSPYITAKLEETITQARSKKGNKSETLKPNFEESGYTFIAPRDYCNLDKI 660  
Db 601 alvlpyspyitakleetitqarskkgnksetlkdpnfeesgytftiaprdocndlki 660  
QY 661 SDNTEFLNFEIDRTPNPNPCNADLINRVLLDAGTNELVQNYWSKQNKIKGVAR 720  
Db 661 sdntefllnfeidrtktpnpsncadlinrvlldagtneelvqnywskgnkikgvark 720  
QY 721 FVVTGGITRVYPKAGENQENPTYEDSFYKSLDNDNVYFTAPYFNKSGPGAYESGI 780  
Db 721 fvtvtdggitrvypkagenqenptyedsfykrsldndnvftapyfnkspggaysesi 780  
QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFYKTSIRDCAGPVCCKRNSVMDCVI 840  
Db 781 mvskaveiyiogkllkpaavgkldvnswnienfyktsirdcagpvcckrnsdvmdevi 840  
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPMSLRHLVNIISVYAFNKSXYQSCVCEGAPKQ 900  
Db 841 lddggflmanhddytngirffgeidpmslrhlvniisvyafnksxyqscvcegapkq 900  
QY 901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLSLTFFRLLLEAVEMEDDDFTASLSKQ 960  
Db 901 gaghrsayvpsvadilqigwataaansilqflsltffrllleavemedddftaslskq 960  
QY 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFPHGKLNWNLIFIMVSKGTCPDCTRLI 1020  
Db 961 sciteqtyffndksfsgvldgcgnsrifphgklnwnlifimvskgtcpdctrlli 1020  
QY 1021 QAEQTSQGNPCDMVKQPRYKKGPDVCFDNNVLEDYDTCGGVS 1063  
Db 1021 qaeqtsqgnpcdmvkprykgpdvcfdnnvledydcggvs 1063

RESULT 6  
AAW63148  
ID AAW63148 standard; Protein; 1110 AA.  
XX  
AC AAW63148;  
XX  
DF 12-OCT-1998 (first entry)  
XX

DE Human calcium channel alpha-2 subunit.  
XX  
KW Alpha-2 subunit; human; calcium channel; assay; detection;  
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN US5792846-A.  
PD 11-AUG-1998.  
PF 31-MAY-1995; 95US-0455543.  
PR 04-APR-1994; 94US-0223305.  
PR 04-APR-1988; 88US-0176899.  
PR 04-APR-1989; 89US-0603751.  
PR 04-APR-1989; 89WO-US01408.  
PR 20-FEB-1990; 90US-0482384.  
PR 30-NOV-1990; 90US-0620250.  
PR 15-AUG-1991; 91US-0745206.  
PR 31-MAY-1995; 95US-0455543.  
XX (SIBI-) SIBIA NEUROSCIENCES INC.  
PA Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
PI Williams WE;  
XX  
DR WPI; 1998-456192/39.  
DR N-PSDB; AAV42694.  
XX  
PT DNA encoding human calcium channel alpha 1B subunit protein -  
PT useful for recombinant production of the channel for screening of  
PT its modulators, and diagnosis of Lambert Eaton Syndrome  
XX  
PS Disclosure: Columns 131-138; 166pp; English.  
XX  
CC The present sequence represents the alpha-2 subunit of a human calcium  
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
CC that allow controlled entry of calcium ions into cells. This leads  
CC to depolarisation events required for muscle contraction. The recombinant  
CC subunit, when expressed with nucleic acids encoding the complete calcium  
CC channel, can be used in assays for the detection and characterisation of  
CC compounds that modulate the channel. The DNA encoding the subunits can  
CC be alternatively spliced when transcribed, giving more than one form of  
CC the protein from the same transcript, each having slightly different  
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
CC molecules from the serum of an individual with Lambert Eaton Syndrome  
CC (LES) can be used as a diagnostic for the disease.  
XX  
SQ Sequence 1110 AA;

Query Match 99.7%; Score 5579.5; DB 19; Length 1110;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 19; Gaps 1;  
QY 1 MAAGCLLALTTLTLPQSLLIGPSSSEPPPSAVTTSWYDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 maagcllalttltfqslilgppsseepfsvatikswvdkmqedlvtlaktasgvnqlvdi 60  
QY 61 YEKYQDLYTVEPNNAQOLVEIAARDTEKLLSNRSKALVSLAEAKVQAAHQWREDFASN 120  
Db 61 yekyqdytvepnnarqlveiaardteklslsnrskalvslaeakvqaahqwrdfasn 120  
QY 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 evvynakddldpekndsepsqrikpvfiedanfgroisqhaavhiptdiyegstivl 180  
QY 181 NELNWTSSALDEVFKKREEDPSLLQVFGSATGLARYPPASPDWNGRTNPKIDLYDVR 240  
Db 181 nelnwtssaldevfkkreedsllqvfgsatglaryppaspdwnrtpnkidydvrr 240  
QY 241 RPWTQGAASPKDMLILVDSGSGVTLKIRTSVSEMLETLSDDDFVNVASFNQAQD 300  
Db 241 rpwtqgaaspkdmlilvdsdsgvstlklrtsvsemletlsdddfvnvasfnnaqd 300

|||||  
Db 241 rpyiqgaaspkamllilvdvsgsvgltklirtsvaeletlsdddfnvvaafnsnaq 300  
QY 301 VSCFQHLVQANVRNKKVLDKADANNITAKGIDYKGFSAFQOLLNYSRANCNKIIML 360  
Db 301 vscfqlvqanvrnkkvldkadvnnitakgitykgsfafeqllnynvrancnkilml 360  
QY 361 FTGGGERAQEIEFNKYNKDKKVRFRFSVGOHNYERGPTQMACENKGYEYIEPSTCAIR 420  
Db 361 ftdgggeerqaeiefnkynkdkkvrfrfsvgohnyergptqmacenkgyeypsiga 420  
QY 421 INTQEDLDVLRPMVLGAKAKOVQNTNVDALGLVITGTPVFNITGQFENKTNLK 480  
Db 421 intqeyldvlgprmvlagkakqvntnvyldalelgvltgtpvfnitgqfentn 480  
QY 481 NQILGVMGVDVSLDLEIKRLTPFTICPNGYFAIDPNGVYLHLPNLQPK----- 530  
Db 481 nqilgvmgvdsledikrltpfticpngyyfaidpnpvylhlpnlqpkpivgip 540  
QY 531 -----NPKSQEPVTLDFDAELNDKVEIRKMDGESGKTFRTLVKSQDERYI 581  
Db 541 lrkrrpnlgpksqepvtldfdaelndkveirkmidgesgektfirtlvksqder 600  
QY 582 DKGNRYYTTPVNGTDSLALVLTPTSFYIYKAKLEETITQARSKGKMDSETLKPDNF 641  
Db 601 dkgnrtytvpngtdyslalvltptsfyiykakleetitqarskgkmdsetl 660  
QY 642 EESGYTFIAPRDYCNLDKISDNTEFLNPFIDRKTPNPNPCNADLINRVLLDAGFTN 701  
Db 661 eesgytfiaprdycndlkisdnteflnpfidrktpnpscnadlinrvlldagft 720  
QY 702 ELVONYWSKQNKIKGVKARFVVTGCTRVYKPEAGENQENPETYEDSFYKESLNDNY 761  
Db 721 elvqnywsqknkigvkarfvvtgctrvypkeagenqenpetyedsfykrsldnd 780  
QY 762 VETAPFNKSGGAYESGIMSKAVIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRD 821  
Db 781 vftapyfnskaggayesgimskaveiyqgkllkpaavgikidvnswiefnfkt 840  
QY 822 CAGPVCDCRNSDMVCVLDGGFLLMANHDDYTNOIGRFFGDEIDPSLMRHLVNSVYA 881  
Db 841 cagpvcdcrnsdmvcvldggfllmanhddytngirffgdeidpslmrhlvns 900  
QY 882 FNKSYDQVSCPEGAAPKAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFPR 941  
Db 901 fnksydyqsvcepgaapkgaghrsayvpsvadilqigwataaasilqgfls 960  
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTYBFNDKSKFSGLDCGNGSRIFPHGKLMNTNL 1001  
Db 961 lleavemedddftaslskqsciteqtyffndskfsfgldcngscrifhgekl 1020  
QY 1002 IFIMVESKTCPCDTRLLLOAQSOTSGPNPCDMVKOPRYKRGPDVCFDNNVLEDYDCGG 1061  
Db 1021 ifimveskgtcpcdtrlllqaetsgpnpcdmvknprykgpdvcfdnnvledy 1080  
QY 1062 VS 1063  
Db 1081 VS 1082

RESULT 7  
AAR71013  
ID AAR71013 standard; Protein; 1086 AA.  
XX  
AC AAR71013;  
XX  
DT 01-DEC-1995 (first entry)  
XX  
DE Human neuronal calcium channel subunit alpha 2c.  
XX  
KW Calcium channel subunit; antagonist; agonist; diagnosis;  
KW Lambert Eaton Syndrome.  
XX

OS Homo sapiens.  
XX  
PN W09504822-A.  
XX  
PD 16-FEB-1995.  
XX  
PF 11-AUG-1994; 94WO-US09230.  
XX  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
XX  
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
PI Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;  
XX  
DR WPI; 1995-090900/12.  
XX  
PT DNA encoding human calcium channel sub-unit(s) - used for  
PT developing prods. for studying calcium channels, e.g. for  
PT obtaining agonists and antagonists  
XX  
PS Disclosure; Page 237-242; 285pp; English.  
XX  
CC Human neuronal alpha 2 coding sequence (AA084664) transcript is  
CC differentially processed in skeletal muscle, aorta, and CNS in  
CC the region corresp. to nt 1595-1942 of AA084664 in each of the  
CC tissues. Five alternatively spliced variant transcripts that differ  
CC in the presence or absence or one to three different portions of  
CC this region. There are three sequences involved (see AA084664 FT  
CC and AA084665 FT), sequence 1, sequence 2 and sequence 3. The five  
CC alpha 2 encoding transcripts from the different tissues include  
CC different combinations of the three sequences, except for one of  
CC the alpha 2 transcripts expressed in aorta which lacks all three  
CC sequences. The five alpha 2 forms identified are (1) a form that  
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
CC expressed in aorta and (5) one that lacks sequences 1 and 3  
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
CC are set forth in AA084666-Q84669 and AAR71012-R71015 respectively.  
XX  
SQ Sequence 1086 AA;

Query Match 99.3%; Score 5559.5; DB 16; Length 1086;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
QY 1 MAAGCILLALTTLTFLQSLLLIGPSSSEPPSPAVTTKSWVDKMQEDLVTLAKTAGVGNQLVDI 60  
Db 1 maagcillaltltlftqslilligpsseepfpavttkswvdkmqedlvtlaktasvgnqlvdi 60  
QY 61 YEKYQDLYTVEPNARQLVEIAARDTEKLSNRSKALVSLALEAEKVQAAHQRNEDFASN 120  
Db 61 yekyqdytvepumarqlveiaardteklslnrskalvslaleaeqvaaqhqrnfasn 120  
QY 121 EYVYNKADDLDPKNDSEPGSQRIKPVFTEDANFRQISQYHAAVHIPTDIYEGSTIVL 180  
Db 121 evvynakaddldpekndsepgsqrikpvftedanfrqisqyhaavhiptdiyegstivl 180  
QY 181 NELNWTALDEVEFKKREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKKIDLDVRR 240  
Db 181 nelnwtalsaldevefknreedpsllwqvfgsatglaryypaspwvdnsrtpnkdldyvrr 240  
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFNVVASFNSNAQD 300  
Db 241 rpwyiogaaspkdmlilvdvsgsvgltklirtsvsemletisdddfnvvaafnsnaqd 300  
QY 301 VSCFQHLVQANVRNKKVLDKADANNITAKGIDYKGFSAFQOLLNYSRANCNKIIML 360  
Db 301 vscfqlvqanvrnkkvldkadvnnitakgitykgsfafeqllnynvrancnkilml 360

QY 361 FTDGGEERAQELFNKYNKDKKVRVERESVGOHNYERGIQWACENKGYEIPISGAIR 420  
 Db 361 ftdggeeeraqelfnkynkdkkvrveresvgohnyergiqwacenkgyeipisgaair 420  
 QY 421 INTQEYLDVLRGPMVLGADKAKQVQWNTVYLDALGLVITGTLVPVFNITGQFENKTNLK 480  
 Db 421 intqeyldvlgprpmvlgadkakqvwntvyl DaleGLVITGTLVPVFNITGQFENKTNLK 480  
 QY 481 NQILGVNGVDVSLIEDIKRLTPRITLCPNGYFAIDPNGYVLLHPNLPKNKSOEPTVL 540  
 Db 481 nqilgvngvdvsliedikrltpritlcpngyfaidpngyvllhpnlpknksoeptvl 540  
 QY 541 DFLDAELNDIKVEIRNMIDEGSEGTFTLKSQDERYIDKGNRTYTWTPVNGTDSL 600  
 Db 541 dfldaelndikveirnmidsegstftlksqderydkggnrtytwtvpngtdysl 600  
 QY 601 ALVLPYTFYIYAKLETTQARSKGKMDSETLKPDPNFESGYTFIAPRVCNDLKI 660  
 Db 601 alvlpptyfyiyakleTTQARSKGKMDSETLKPDPNFESGYTFIAPRVCNDLKI 660  
 QY 661 SDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQWNSKQNKIGVKAR 720  
 Db 661 sdnTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQWNSKQNKIGVKAR 720  
 QY 721 FVVDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNYVETAPYFNKSGPGAYESGI 780  
 Db 721 fvvtdggitrvyKPEAGENWQENPETYEDSFYKRSLDNDNYVETAPYFNKSGPGAYESGI 780  
 QY 781 MYSKAVEIYQGLKPAVVGKIDVNSWIENTFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
 Db 781 mvsKAVEIYQGLKPAVVGKIDVNSWIENTFTKTSIRDPCAGPVCDCRNSDVMDCVI 840  
 QY 841 LDGSGFLMANHDDYNTQIGRFGEDTSLMRHLVNSIYAFNKSVDYQSGVCEPAAAPKQ 900  
 Db 841 ldgsgflmanhddyntqigrfgedtSLMRHLVNSIYAFNKSVDYQSGVCEPAAAPKQ 900  
 QY 901 GAGHSAYVPSVADIIQIGWATAAASWTLQOFLSLAPRLLLEAVEMDDFTASLSKQ 960  
 Db 901 gaghsayvpsvadIIQIGWATAAASWTLQOFLSLAPRLLLEAVEMDDFTASLSKQ 960  
 QY 961 SCITQOTQFFNDKSGSVGLDCGNCRIHGEKLMNTNLIFFINVESKGTCPDTRILLI 1020  
 Db 961 scitqotqffndksgsvglDCGNCRIHGEKLMNTNLIFFINVESKGTCPDTRILLI 1020  
 QY 1021 QAEQTSQDPNCDMVKQRYKGPDPVCFDNNVLEDYTDGCGVS 1063  
 Db 1021 qaeqtsqdpncdmvkqrykgpdpvcfdnnvledytdcgvs 1063

RESULT 8  
 AAW63153  
 ID AAW63153 standard; Protein; 1086 AA.  
 AC AAW63153;  
 DT 12-OCT-1998 (first entry)  
 DE Human calcium channel alpha-2c subunit.  
 DE Alpha-2 subunit; human; calcium channel; assay; detection;  
 KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 KW Homo sapiens.  
 OS US5792846-A.  
 PN 11-AUG-1998.  
 PD 31-MAY-1995; 95US-0455543.  
 PF 04-APR-1994; 94US-0223305.  
 PR 04-APR-1988; 88US-0176899.

PR 04-APR-1989; 89US-0603751.  
 PR 04-APR-1989; 89WO-US01408.  
 PR 20-FEB-1990; 90US-0482384.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 31-MAY-1995; 95US-0455543.  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 PI Williams ME;  
 FI WPI; 1998-456192/39.  
 DR N-PSDB; AAV42702.  
 XX DNA encoding human calcium channel alpha 1B subunit protein -  
 useful for recombinant production of the channel for screening of  
 its modulators, and diagnosis of Lambert Eaton Syndrome  
 Claim 3; Columns 293-300; 166pp; English.  
 CC The present sequence represents the alpha-2c subunit of a human calcium  
 channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 that allow controlled entry of calcium ions into cells. This leads  
 to depolarisation events required for muscle contraction. The recombinant  
 subunit, when expressed with nucleic acids encoding the complete calcium  
 channel, can be used in assays for the detection and characterisation of  
 compounds that modulate the channel. The DNA encoding the subunits can  
 be alternatively spliced when transcribed, giving more than one form of  
 the protein from the same transcript, each having slightly different  
 properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 molecules from the serum of an individual with Lambert Eaton Syndrome  
 (LES) can be used as a diagnostic for the disease.  
 XX Sequence 1086 AA;  
 SQ

Query Match 99.3%; Score 5559.5; DB 19; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
 QY 1 MAAGCLLALTTLFOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60  
 Db 1 maagcllalttlfosl ligpsspeppsa vti kswdkmqedlv tlaktasgvnqlvdi 60  
 QY 61 YEKYQDLYTVEPNNAQLVEIARDIEKLLSNRKSALVSLAEKVKQAAHOWREDFASN 120  
 Db 61 yekyqdlytvepnnarqlveiaardiekl lsnrksalvslaeakvqaahqwredfasn 120  
 QY 121 EVVYNNAKDDLDPKNDSEPGSQRIKPVFIEDANFGROIYQHAHVHPTDIYEGSTIVL 180  
 Db 121 evvynnakddl dpekn dsepgsqrikpvfi edanfgroi yqhaavhiptdi yegstivl 180  
 QY 181 NELNWTALDEVFKKNEEDPSLLQVFGSATGLARYPPASPVVDNRTPNKIDLYDVR 240  
 Db 181 nelnwtaldevfkkneedpsllq vfgsatglaryppaspvvdnrt pknidlydvr 240  
 QY 241 RPWYIGAAAPKMDLILVDYSGVSLTLKIRTSVSEMLETISDDDFNVASFNSNAQD 300  
 Db 241 rpwyigaaapkdmlilvdysgsvgtlklir tsvseml etisdddfnv asfnsnaqd 300  
 QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGIDYKKGFSAFEQLLNNVSRANCKIIML 360  
 Db 301 vscfhlvqanvrnkkvldvannitakgid ykkgf safeql lnnv srancnk iiml 360  
 QY 361 FTDGGEERAQELFNKYNKDKKVRVERESVGOHNYERGIQWACENKGYEIPISGAIR 420  
 Db 361 ftdggeeeraqelfnkynkdkkvrveresvgo hnyergiqwacenkgyeipisgaair 420  
 QY 421 INTQEYLDVLRGPMVLGADKAKQVQWNTVYLDALGLVITGTLVPVFNITGQFENKTNLK 480  
 Db 421 intqeyldvlgprpmvlgadkakqvwntvyl DaleGLVITGTLVPVFNITGQFENKTNLK 480

QY 481 NOLILGVMGVDSLEDIKRLTPRETCNPGYFAIDPNGYVLLHPNLQPNKPSQSEPVTL 540  
 DB 481 nqlllgvmgvdsleedikrltpretpcnpgyfaidpngyvlhpnlpqk-----epvtl 535  
 QY 541 DFLDAELENDIKVEIRNKNMIDGESGEKTRTLVKQSODERYIDKGNRTYTWTPVNGTDYSL 600  
 DB 536 dfldaelendikveirnkmidgesgektftrlvksqderidkgnrtwtvpngtdysl 595  
 QY 601 ALVLTPTSYIYKAKLEETITQARSKKGMKDSITLKPONFESGYTFAPRDYCNLDLKI 660  
 DB 596 alvltptsyiykaleetitqarskkgmkdsetlkipdnfeesgytfiaprdydcndlki 655  
 QY 661 SDNNTFELNFEFIDRKPNNPNCNADLINRVLLDAGFTNELVQYWSKOKNIKGVKAR 720  
 DB 656 sdnteflnfnefidrktppnpscnadlinrvlldagftnelvqnywskknkigvkar 715  
 QY 721 FVVTGGITRVYPKRAGENQWNPETIEDSFYKRSRDNDNYFTAPYFNKSGPGAYESGI 780  
 DB 716 fvtvggitrvypkeagenwqenpetyedsfykrsldndnyftapyfnksgpgayesgi 775  
 QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTSIRDPGAGPVCDCKRNSDVMDCVI 840  
 DB 776 mvskaveiyigkllkpvavgikidvnswnientftksirdpcagpvcdckrnsdvmdevi 835  
 QY 841 LDGGFLLMANHDDYTNQIGRFFGETDPSLMRLHLYNISVYAFNKSVDYOSVCEPGAAPQ 900  
 DB 836 ldggfllmanhddytngqirffgetdpslmrlhlynisvafnksydyosvcepgaaq 895  
 QY 901 GAGHRSAYVPSVADILQIGWATAAASWILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960  
 DB 896 gaghrsayvpsvadilqigwataaaswllqflsltprrlleavemedddftaslskq 955  
 QY 961 SCITEQTOYFFDNDKSFSGVLDCGNCSEIRFHEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
 DB 956 sciteqtqyffndksfsgvlcdgncsrfhgeklmntnlifimveskgtcpdtrlli 1015  
 QY 1021 QAEQTSDDGNPCDMVKQPYRKGPDVCFNNVLEDTDCGGVS 1063  
 DB 1016 qaeqtsdgnpcdmvkqpyrkgpdvcfnnvledtcdggvs 1058  
 RESULT 9  
 AAB10587  
 ID AAB10587 standard; Protein; 1086 AA.  
 AC AAB10587;  
 XX  
 XX  
 DT 22-DEC-2000 (first entry)  
 DE Human calcium channel alpha-2c subunit protein.  
 KW Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2c.  
 XX Homo sapiens.  
 XX  
 XX US6096514-A.  
 XX  
 XX 01-AUG-2000.  
 XX  
 XX 25-MAY-1995; 95US-0450562.  
 XX  
 PR 04-APR-1988; 88US-0176899.  
 PR 02-FEB-1990; 90US-0482384.  
 PR 08-NOV-1990; 90US-0603751.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 10-APR-1992; 92US-0868354.  
 PR 13-JUL-1992; 92US-0914231.  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 PR 07-FEB-1994; 94US-0193078.  
 PR 04-APR-1994; 94US-0223305.

PR 11-AUG-1994; 94US-0290012.  
 PR 23-SEP-1994; 94US-0311363.  
 PR 28-SEP-1994; 94US-0314083.  
 PR 07-NOV-1994; 94US-0336257.  
 PR 13-MAR-1995; 95US-0404950.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX  
 PI Ellis SB, Williams ME, McCue AF, Harpold MM;  
 XX  
 XX WPI; 2000-548230/50.  
 DR N-PSDB; AAA71725.  
 XX  
 PT Human calcium channel beta subunit polynucleotides, useful for  
 PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
 PT Syndrome -  
 XX  
 XX Disclosure; Column 237-244; 153pp; English.  
 XX  
 CC This invention describes a novel isolated DNA molecule (I) comprising a  
 CC sequence encoding a beta3-1 subunit of a human calcium channel.  
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
 CC beta3 subunit encoding DNA are useful for isolation and cloning of  
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 CC express heterologous calcium channel are useful for identifying compounds  
 CC that modulate calcium channel activity and in assays for identifying  
 CC agonists and antagonists of calcium channel activity in humans. Human  
 CC calcium channel subunit or eukaryotic cells expressing the channel are  
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 CC sequence represents the human calcium channel alpha-2c subunit which is  
 CC described in the method of the invention.  
 XX  
 SQ Sequence 1086 AA;  
 Query Match 99.3%; Score 5559.5; DB 21; Length 1086;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1058; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
 QY 1 MAAGCCLALTLTLFQSLILGSPSEEPFPPSAVTIKSWVDKMQEDLVTLAKTAGVQNLVDI 60  
 DB 1 maagcclaltltlfsqslilgspseepfppsaavtikswvdkmqedlvtlaktasgvnqlvdi 60  
 QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQHREDFASN 120  
 DB 61 yekyqdlytvepnnaqlveiaardieklksnrskalvslaleaeqvaaahqhvredfasn 120  
 QY 121 EVVYVNAKODLDPKNDSEPGSORIKPVFTEDANFGROISYQHAHVHPTDIYEGSTIVL 180  
 DB 121 evvyynakodldpkndsepgsorkpvtftedanfgroisyqhahvhpdiyegstivl 180  
 QY 181 NELNWTSAALDEVEFKNREDEPSSLWQVFGSATGLARYYPASPVWVNSRTPNKIDLYDVR 240  
 DB 181 nelnwtasaldevfknredepsllwqvfgsatglaryypaspvwdnsrtpnkidlydvrr 240  
 QY 241 RPWYIOGAASPKNMLILVDVSGSVGLTKLIRTSVSEMLETSLSDDDFVNVASFNSAQD 300  
 DB 241 rpwyiggaaspkdmllilvdvsgsvgltklirtsvemletssdddfvnvasfnsnaqd 300  
 QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEOLLNYSRANCNKIIML 360  
 DB 301 vscfhlvqanvrnkklvkdavnnitakgtdykgkfsfafefqllnysrancnkiml 360  
 QY 361 FTDCGEERAQEIFNKYKNDKRVFRFVSQGHNYERGIQWACENKGYIYEIPSGAIR 420  
 DB 361 ftdggeeraqeifnknkndkrrvfrfvsqghnyerpiqwacenkgyiyeipsigair 420  
 QY 421 INTQEYLDVLGRPMVLGADKAKQVQWTVNVLDALEGLGVITGTLVPFNITGQENKTNLK 480  
 DB 421 intqeyldvlgrpmvlagkakqvqwtvnvldalelgvltgtlvpfnitgqenknknlk 480  
 QY 481 NOLILGVMGVDSLEDIKRLTPRETCNPGYFAIDPNGYVLLHPNLQPNKPSQSEPVTL 540



QY 661 SDNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQNKIGVKAR 720  
 DB 654 sdntefllnfeidrktpnpnpscnadlinrvlldagftnelvqnywsqknigvkqr 713  
 QY 721 FVVTGGITRVYPKEAGENWQENPEYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 714 fvtvtdggitrvyypkeagenwqenpeteyedsfyrksidndnyvftapyfnkspggayesgi 773  
 QY 781 MYSKAVEIYIQGLKLPAYVIGIKIDVNSWIENTFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840  
 DB 774 mvskaiveiyiqglklpavvgikidvnswnientftktsirdpcagpvcddckrnsdvmdcvi 833  
 QY 841 LDGGFLLMANHDDYTNQIGRWATAAASWILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960  
 DB 834 lddggfllmanhddytngqirgfwataaawslqgflsltprrlleavemedddftaslskq 893  
 QY 901 GAGHRSAYPSVADILQIGRWATAAASWILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960  
 DB 894 gaghrsaypsvadilqigrwataaawslqgflsltprrlleavemedddftaslskq 953  
 QY 961 SCITEQTYFFDNDKSFSGVLDGCGNCSRIFFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
 DB 954 sciteqtgyffndksfsgvldcgncsriffhgeklmntnlifimveskgtpcdtrlli 1013  
 QY 1021 QAEQTSQGNPCDMVKQPRYRGDPVCFDNNVLEDTYDCGGVS 1063  
 DB 1014 qaeqtsqgnpcdmvkqpryrkgdpvcfdnnvledtydcggvs 1056

RESULT 11  
 ID AAW63155 standard; Protein; 1084 AA.  
 AC AAW63155;  
 DT 12-OCT-1998 (first entry)  
 XX Human calcium channel alpha-2e subunit.  
 KW Alpha-2 subunit; human; calcium channel; assay; detection;  
 KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
 OS Homo sapiens.  
 XX US5792846-A.  
 XX 11-AUG-1998.  
 XX 31-MAY-1995; 95US-0455543.  
 XX 04-APR-1994; 94US-0223305.  
 XX 04-APR-1988; 88US-0176899.  
 XX 04-APR-1985; 89US-0603751.  
 XX 04-APR-1985; 89WO-US01408.  
 XX 20-FEB-1990; 90US-0482384.  
 XX 30-NOV-1990; 90US-0620250.  
 XX 15-AUG-1991; 91US-0745206.  
 XX 31-MAY-1995; 95US-0455543.  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
 XX Williams ME;  
 XX WPI: 1998-456192/39.  
 XX N-PSDB; AAW42704.  
 XX DNA encoding human calcium channel alpha 1B subunit protein -  
 PT useful for recombinant production of the channel for screening of  
 PT its modulators, and diagnosis of Lambert Eaton Syndrome  
 XX Claim 3; Columns 305-310; 166pp; English.  
 XX

CC The present sequence represents the alpha-2e subunit of a human calcium  
 CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
 CC that allow controlled entry of calcium ions into cells. This leads  
 CC to depolarisation events required for muscle contraction. The recombinant  
 CC subunit, when expressed with nucleic acids encoding the complete calcium  
 CC channel, can be used in assays for the detection and characterisation of  
 CC compounds that modulate the channel. The DNA encoding the subunits can  
 CC be alternatively spliced when transcribed, giving more than one form of  
 CC the protein from the same transcript, each having slightly different  
 CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
 CC molecules from the serum of an individual with Lambert Eaton Syndrome  
 CC (LES) can be used as a diagnostic for the disease.  
 XX Sequence 1084 AA;  
 SQ

Query Match 99.0%; Score 5542.5; DB 19; Length 1084;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCCLALTTLFQSLIGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTAGVGNOLVDI 60  
 DB 1 maagcclalttlfqslligpsseepfpsavtikswdkmqedlvltlaktasgvnqlvdi 60  
 QY 61 YEKYQDLYTVEPNNAQOLVEIARDEKLLSNRSKALVSLALEAEKVAQAHOHREFASN 120  
 DB 61 yekyqdytvepnnarqlveiaardiekllsnrskalvslaleaeekvqaahqvfrefasn 120  
 QY 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVFTEDANFGRQISYQAAHVHPDIDYEGSPVL 180  
 DB 121 evvyvynakddldpekndsepgsqrikpvfiedanfgrqisyqaaahvipdidiyegstivl 180  
 QY 181 NELNWTSAIDVEFKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
 DB 181 nelnwtaldevfkknreedpsllwqvfgsatglaryypaspwvdnsrtpnkidlydvrr 240  
 QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTTLKIRTSVSEMLETSLDDDFVNVASFNSAQD 300  
 DB 241 rpwyiogaaspkdmllldvsvsgvsgltlklirtsvsemlletisdddfvnvasfnasqd 300  
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDKGFSFAFEOALLNYSRANCNKIIML 360  
 DB 301 vscfqlvqanvrnkvldkavnnitakgitydkgfsfafedqllnysrancnkiml 360  
 QY 361 FTDGGEERAQEIFENKYNKDKKRVFRFVSQGHNYERGPIQMACENKGYIYEIPSGAIR 420  
 DB 361 ftdggeeraqefenknkdkkrrvfrfvsqghnyergpiqmacenkgyyiyeipsigair 420  
 QY 421 INTQEYLDVLGRPMVLADKAKOVQNTNLYDLALEGLVITGLTPVFNITGQENKTNLK 480  
 DB 421 intqeyldvlgrpmvlagdkakovqntnlydlaleglvitgltpvfnitgqenktnlk 480  
 QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYIYFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540  
 DB 481 nqlilgvmgvdsledikrltpfrftlcpngyiyfaidpngyvvllhpnlpknpskqepvtl 540  
 QY 541 DFLDAELNDIKVEIRNKMIDGESGEKFTFLVKSQDERYIDKGNRTYTPVNGTDYSL 600  
 DB 541 dfldaelndikveirnkmidgesgektftrlvksqderydkgnrtytvpvngtdysl 600  
 QY 601 ALVLPYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPROYCNDLKI 660  
 DB 601 alvlpysfyiykakleetitqary-----setlkdndfreesgytfiaproycndalki 653  
 QY 661 SDNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQNKIGVKAR 720  
 DB 654 sdntefllnfeidrktpnpnpscnadlinrvlldagftnelvqnywsqknigvkqr 713  
 QY 721 FVVTGGITRVYPKEAGENWQENPEYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
 DB 714 fvtvtdggitrvyypkeagenwqenpeteyedsfyrksidndnyvftapyfnkspggayesgi 773  
 QY 781 MYSKAVEIYIQGLKLPAYVIGIKIDVNSWIENTFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840

Db 774 mvskavelyigkllkpvavvgikldvswlenfktksirtpcagpvcckrnsdmdcvl 833  
 Qy 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLNLSVYAFNKSVDYQSVCEPGAAPKQ 900  
 Db 834 lddggflmanhddytqgrffgeidpslmrhlvnlsvyafnksydyqsvcepgaapq 893  
 Qy 901 GAGHRSAYVSVADILQIGWATAAASILQOFLLSLTFFPRLLLEAVEMEDDDFTASLSKQ 960  
 Db 894 gaghrrsayvsvadilqigwataaawslilqqlfllstfprllleavemeddftaslskq 953  
 Qy 961 SCITEQYQYFFDNDKSFSGVLDCGNCSTRIFPHGCKLMTNLIIFIMVESKGTCTPCDTRLII 1020  
 Db 954 sciteqyqyffndksfsgvlcdgncsrifhgeklmntnlifimveskgtcptcdtrlll 1013  
 Qy 1021 QAEQTSQPNPCDMVQPRYKGPVDFCVFNNVLEDTDCGGVS 1063  
 Db 1014 qaeqtsdgnpcdmvqprykgpdcvfdnnvledydcggvs 1056

## RESULT 12

AAB10589  
 ID AAB10589 standard; Protein; 1084 AA.

AC AAB10589;  
 XX

DT 22-DEC-2000 (first entry)

DE Human calcium channel alpha-2e subunit protein.

KW Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2e.

XX Homo sapiens.

XX US6096514-A.

XX 01-AUG-2000.

XX 25-MAY-1995; 95US-0450562.

XX 04-APR-1988; 88US-0176899.

XX 02-FEB-1990; 90US-0482384.

XX 08-NOV-1990; 90US-0603751.

XX 30-NOV-1990; 90US-0620250.

XX 13-APR-1991; 91US-0745206.

XX 10-APR-1992; 92US-0868354.

XX 13-JUL-1992; 92US-0914231.

XX 11-AUG-1993; 93US-0105536.

XX 05-NOV-1993; 93US-0149097.

XX 07-FEB-1994; 94US-0193078.

XX 04-APR-1994; 94US-0223305.

XX 11-AUG-1994; 94US-0290012.

XX 23-SEP-1994; 94US-0311363.

XX 28-SEP-1994; 94US-0314083.

XX 07-NOV-1994; 94US-0336257.

XX 13-MAR-1995; 95US-0404950.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Ellis SB, Williams ME, McCue AF, Harpold MM;

XX WPI; 2000-548230/50.

XX N-PSDB; AAA71727.

CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
 beta.3 subunit encoding DNA are useful for isolation and cloning of  
 calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
 express heterologous calcium channel are useful for identifying compounds  
 that modulate calcium channel activity and in assays for identifying  
 agonists and antagonists of calcium channel activity in humans. Human  
 calcium channel subunit or eukaryotic cells expressing the channel are  
 useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
 sequence represents the human calcium channel alpha-2e subunit which is  
 described in the method of the invention.

XX Sequence 1084 AA;

Query Match 99.0%; Score 5542.5; DB 21; Length 1084;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

Qy 1 MAAGCLLALTTLFQSLITGPSSEPPFSAVTIKSWDKMQEDVTLAKTASGVNQLVDI 60  
 Db 1 maagcillaaltltlfgslitgpsseepfseavtikswdkmqedvltlaktasgvnqlvdi 60  
 Qy 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
 Db 61 yekyqdytvepnnarqlveiaardieklslsnrskalvslaleaeqvaaqhrdfasn 120  
 Qy 121 EVYYNAKDDLPEKNDSEPGSQRKPKVFIEDANFGROISQHOAAVHIPTDIYEGSTIVL 180  
 Db 121 evyyinakddlpeknndsepgsqrikpvpfiedanfgroisqhoavhiptdiyegstivl 180  
 Qy 181 NELNWTSALEDEVFKKREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKKIDLYDVR 240  
 Db 181 nelnwtasaldevfkknreedpsllwqvfgeatglaryypaspwvdnsrtpnkidlydvr 240  
 Qy 241 RPWYIQGAASPKDMLILVDVSGSVSGTLKLIRTSVSEMLETLSDDDFVNVASFNSNAOD 300  
 Db 241 rpwyiggaaspkdmllilvdvsgsvsgtlklirtsvseemletlstdddfvnvafnsnaod 300  
 Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKGSFAFEQLLNINVSANCKNITML 360  
 Db 301 vscfqlhvqanvrnkvlkdavnnitakgitdykgsfafelqllnynvarancnkli 360  
 Qy 361 FTDCGERAQEIFNKNKRRVFRFVSQGHYERGPQIOWMACENKGYEYEPSIGAIR 420  
 Db 361 ftdggeeraqeifnknkrrvfrfvsqghyergpqiowmacenkgyeyepsigair 420  
 Qy 421 INTQEYLDVLGRPMVLGADKAKQVQMTNLYLDALEGLVITGLTPVFNITGFQENKTNLK 480  
 Db 421 intqeyldvlgrpmvlagdkakqvqmtnlyldaleglvitgltpvfnitgfenktnlk 480  
 Qy 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPLNLPKNKSOBPTVL 540  
 Db 481 nqlilgvmgvdsledikrltpftlcpngyyfaldpngyvlhplnlpknksoqbpvtl 540  
 Qy 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSDERYIDKNRTYTWTPVNGDYSL 600  
 Db 541 dfldaelendikveirnkmidgesgktrtlvksderyidknrtytwtvpvngdysl 600  
 Qy 601 ALVLTPTSYFYIKALEETITQARSKKGMKMDSETLKPDNFEESGYTFTAPRDCNDLKI 660  
 Db 601 alvltptsyfyyikaleetitqary-----setlkdndfeesgytftaprdydcndlki 653  
 Qy 661 SDNNTFELLNFEFTDRKTPNPNPCNADLINLVLLDAGFTNELVQNSKQNKIKGVKAR 720  
 Db 654 sdnnfcllnfnefldrtpnnpncnadlinvllldagftnelvqnsqknkikgvkar 713  
 Qy 721 FVVDGGITRVYPKEAGENWQENPETYEDSFVKRSLDNDNYFTTAPYFNKSGPGAYESGI 780  
 Db 714 fvvtdggitrvykpeagenwnqenpetyedsfvykrsldndnyfttapyfnksgpgayesgi 773  
 Qy 781 MVSKAVEYIIQGLKLKPAVVGIKIDVNSWIENFTKTSIRDPACGVCCKRNSDVMDCVI 840  
 Db 774 mvskaveiyigkllkpvavvgikidvnswienvfkttsirdpcagvcdckrnsdvmdcvi 833



QY 841 LDGGFLMANHDDYTNQIGRFFGEIDPSLMRLHVNISYAFNKSYDYOSVCEPGAAPKQ 900  
Db 834 ldggflmanhddytngirffgeidpslmrlhvnlsyafnkxydyosvcepgaapq 893  
QY 901 GAGHSAYPSVADILQIGWATAAAWSILOQFLSLTFRLLLEAVEMEDDFTASLSKQ 960  
Db 894 gaghsaypsvadilqigwataaawsllqqflsltprileavevmedddftaslskq 953  
QY 961 SCITEQTOFFONDKSFSGVLDCGNCSTRIFHGEKLMNTNLFIMVESGTCPCDTRLLI 1020  
Db 954 sciteqtqyffndkshsfsgvldcncstrifhgeklmntnlfimveskgtpcdtrlll 1013  
QY 1021 QAEQTSNGNPNCDMVKQPKRYKGPVCFNNVLEDTYDCGGVS 1063  
Db 1014 qaeqtsdgnpcdmvkqpyrykpgdvcfndnnvledydcggvs 1056

RESULT 13  
AAR71012  
ID AAR71012 standard; Protein; 1103 AA.  
AC AAR71012;  
XX  
DT 01-DEC-1995 (first entry)  
XX  
DE Human neuronal calcium channel subunit alpha 2a.  
XX  
KW Calcium channel subunit; antagonist; agonist; diagnosis;  
KW Lambert Eaton Syndrome.  
XX  
OS Homo sapiens.  
XX  
PN W09504822-A.  
XX  
PD 16-FEB-1995.  
XX  
PF 11-AUG-1994; 94WU-0509230.  
XX  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
XX  
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
PI Ellis SB, Gillespie A, Harpold MW, Mccue AF, Williams ME;  
XX WPI: 1995-090900/12.  
XX N-PSDB; AAQ84666.  
XX  
PT DNA encoding human calcium channel sub-unit(s) - used for  
PT developing prods. for studying calcium channels, e.g. for  
PT obtaining agonists and antagonists  
XX  
PS Disclosure; Page 231-236; 285pp; English.  
XX  
CC Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
CC differentially processed in skeletal muscle, aorta, and CNS in  
CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
CC tissues. Five alternatively spliced variant transcripts that differ  
CC in the presence or absence of one to three different portions of  
CC this region. There are three sequences involved (see AAQ84664 FT  
CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
CC alpha 2 encoding transcripts from the different tissues include  
CC different combinations of the three sequences, except for one of  
CC the alpha 2 transcripts expressed in aorta which lacks all three  
CC sequences. The five alpha 2 forms identified are (1) a form that  
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
CC expressed in aorta and (5) one that lacks sequences 1 and 3  
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
CC are set forth in AAQ84666-084669 and AAR71012-R71015 respectively.

XX SQ Sequence 1103 AA;  
Query Match 98.6%; Score 5523; DB 16; Length 1103;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1055; Conservative 0; Mismatches 1; Indels 26; Gaps 2;  
QY 1 MAAGCILLATLTTFQSLILGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 maagcillaltltlfsllgspseepfpsavtikswdkmqedlvtlaktasgvnqlvdi 60  
QY 61 YEKYQDLYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQHREFASN 120  
Db 61 yekyqdytvepnnaqolveiaardiekllsnrskalvslaeaeqvqaahqrefasn 120  
QY 121 EYVYVNAKDDLDPKNDSPGSIQKPVFIEDANFQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 evvyynakddldekndspgsiqkpvfiedanfgrqisyqhaahvhiptcdiyegstivl 180  
QY 181 NELNMTSALDEVEFKNREEDPSLLQWFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
Db 181 nelnwtlsaldevfkknreedpsllwqvfsgatglaryypaspwvdnsrtpnkiidlydvr 240  
QY 241 RPWYIOGAASPDKMLILVDVSGVSGILTLKIRTSVSEMLETLSSDDDFVNVASFNSNAQ 300  
Db 241 rpwyiggaaspdkmlilvdvsgsvsgiltklirtsvsemletlssdddfvnvasfnsnaq 300  
QY 301 VSCFOHLVQANVNNKKVLDAVNNITAKGITDYKKGFSFAFOLLNVNVRANCNKIIML 360  
Db 301 vscfghlvqanvnnkkvlkdvnnitakgitdykkgfsfafellnvnvrancnkliml 360  
QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQGHNYERGPQWACENKGYIYEIPSGAIR 420  
Db 361 ftdggeeraqeifnknynkdkkvrfrfsvqghnyergpqwacenkgyiyeipsigair 420  
QY 421 INTQEYLDVLGRPMVLGADKAKOVQNTNVLDALELGLVITGTPVFNITGQENKTNLK 480  
Db 421 intqeyldvlgrpmvlgadakqvntnvldalelglvitgtlvpfnitgqenknlnk 480  
QY 481 NQLILGVMGVDVSLIEDIKRLTPRTICPNGYIFAIDPNGVYLLHPNLQPK----- 530  
Db 481 nqlilgvmgvdvsledikrltprticpngyyfaidpngyvllhpnalqpkpvgigiptin 540  
QY 531 -----NPKSOEPVTLDFDAELENDIKVEIRNMKMDGESGEKTFRLVKSQDERYI 581  
Db 541 lrrrrpnigpnksqepvtidfaelendikveirnmkmdgesgektftrlvksqderyi 600  
QY 582 DKGNRRTYTPVNGTDYSLALVLPYTSFYIYKAKLEETITQARSKGKMKDSTLKPDNF 641  
Db 601 dkgnrtytvpngtdyslalvlpysfyiykakleetitqary-----setlkipdnf 653  
QY 642 EESGYTFIAPRDXCNDLKISDNNTPELLNNEPFIIDKTPNPNPCNADLNRVLLDAGFTN 701  
Db 654 eesgytfiaprdycndlkisdntellnnepfidktpnpsncadlnrvlldagftn 713  
QY 702 ELVONVWSKQNKIKGVKARFVVTGGITRVYPKEAGENWOENPETVEDSFYKRSLDNDNY 761  
Db 714 elvqnyskqknikgvkarfvvtddgitrvypkeagenwoenpetvedsfykrslndndy 773  
QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDP 821  
Db 774 vftapyfnksgpgayesgimvskaveiyioqkllkpavvgikidvnswieenftktsirdp 833  
QY 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRLHVNISVYA 881  
Db 834 cagpvcdcrnsvmdcvilddggfllmanhddytngirffgeidpslmrlhvnlsvya 893  
QY 882 FNKSYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLSLTFR 941  
Db 894 fnksydyqsvcepgaapkgaghrsayvpsvadilqigwataaawsllqqflsltfr 953  
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDKSFSGVLDCGNCSTRIFHGEKLMNTN 1001

Db 954 lleaveedddftaslsksciteqtgyffandsksfsgvldcncsrifhgeklmtnl 1013  
Qy 1002 IFIMVESKGTCPDTRLLIOAEQSDGPNCDVMYKQPRYKGPDPVCDNNVLEDYTDGCG 1061  
Db 1014 ifimveskgtcpdtrlliaeqsdgpnpcdmvkgprykgpdcvcdnnvledytdcgg 1073  
Qy 1062 VS 1063  
Db 1074 vs 1075  
RESULT 14  
AAW63151  
ID AAW63151 standard; Protein; 1103 AA.  
XX AC AAW63151;  
XX AC  
XX 12-OCT-1998 (first entry)  
XX Human calcium channel alpha-2a subunit.  
DE Alpha-2 subunit; human; calcium channel; assay; detection;  
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
XX Homo sapiens.  
OS  
XX US5792846-A.  
XX PN  
XX PD 11-AUG-1998.  
XX PF 31-MAY-1995; 95US-0455543.  
XX PR 04-APR-1994; 94US-0223305.  
XX PR 04-APR-1988; 88US-0176889.  
XX PR 04-APR-1989; 89US-0603751.  
XX PR 04-APR-1989; 89MO-US01408.  
XX PR 20-FEB-1990; 90US-0482384.  
XX PR 30-NOV-1990; 90US-0620250.  
XX PR 15-AUG-1991; 91US-0745206.  
XX PR 31-MAY-1995; 95US-0455543.  
XX (SIBI-) SIBIA NEUROSCIENCES INC.  
XX PA  
XX PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
PI Williams ME;  
XX WPI; 1998-456192/39.  
XX N-PSDB; AAV42700.  
XX DNA encoding human calcium channel alpha 1B subunit protein -  
XX useful for recombinant production of the channel for screening of  
XX its modulators, and diagnosis of Lambert Eaton Syndrome  
XX Claim 3; Columns 287-294; 166pp; English.  
XX The present sequence represents the alpha-2a subunit of a human calcium  
XX channel. Calcium channels are membrane-spanning, multi-subunit proteins  
XX that allow controlled entry of calcium ions into cells. This leads  
XX to depolarisation events required for muscle contraction. The recombinant  
XX subunit, when expressed with nucleic acids encoding the complete calcium  
XX channel, can be used in assays for the detection and characterisation of  
XX compounds that modulate the channel. The DNA encoding the subunits can  
XX be alternatively spliced when transcribed, giving more than one form of  
XX the protein from the same transcript, each having slightly different  
XX properties. In addition, the reactivity of the alpha 1 subunit with IgG  
XX molecules from the serum of an individual with Lambert Eaton Syndrome  
XX (LES) can be used as a diagnostic for the disease.  
XX Sequence 1103 AA;  
Query Match 98.6%; Score 5523; DB 19; Length 1103;

Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1055; Conservative 0; Mismatches 1; Indels 26; Gaps 2;  
Qy 1 MAAGCLLATLTIFQSLIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
Db 1 maagcllatltifqsligpseepfppsaavtkswdkmqedlvtlaktasgvnqlvdi 60  
Qy 61 YEKYQDLYTVEPNNAQOLVEIARDEKLLSNRKSALVLALEAEKVQAHHOWREDFASN 120  
Db 61 yekyqdlytvepnnaqlveiaardieklksnrksalvslaleaekvqaahqwredfasn 120  
Qy 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROIYSQHAAVHIPTDIYEGSTIVL 180  
Db 121 evvynakddldpeknsepgsgrlkpvfiedanfgroisqhaaahiptdiyegstivl 180  
Qy 181 NELNWTSAIDDEVFKNREDEPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVER 240  
Db 181 nelnwtalsaldevfknreedspsllmqvfgsatglaryypaspwvdnsrtpnkidlydver 240  
Qy 241 RPWYIOGAASPKDMLILYDVSGSVSGLIKLIRTSVSEMLETSLDDDFNVNASFNSAQD 300  
Db 241 rpwyiogaaspkdmlilvdvsgsvsgltklirtsvsemletlsdddfnvvasfnsaqd 300  
Qy 301 VSCFOHLYQANVRNKKVLKDAVNNTAKGITDYKGFSAFEQLLNINVRANCNKIIML 360  
Db 301 vscfghlvqanvrnkvlkdavnnitakgitdykgsfafaqellnynvrancnkiiiml 360  
Qy 361 FTDGGERAQEIFNKYNKDKKVRFRFSVGQHYNERGPIOMACENKGYIYEISIGAIR 420  
Db 361 ftdggeeraqeifnkynkdkkvrfrfsvgqhynerpiqmacenkgyiyeisigair 420  
Qy 421 INTOEYLDVLGRPMVLADGKAKQVQWTVNYLDALDELGLVITGTLPVFNITQOFENKTNLK 480  
Db 421 intoeyldvlgrpmvlagdkakqvqwtvnyldalelglvigtltlpvfnitqofenknlnk 480  
Qy 481 NQLILGYMGVDVSLIEDIKRLTPRETLCPNGYIFAIDPNGVYLLHPNLQPK----- 530  
Db 481 nqlilgvmgvdvsliedikrltpretlcpngyifaidpnyvllhpnlnqpk----- 530  
Qy 531 -----NPKSQBPVTLDLDALENDIKVEIRKNKIDGESGEKTFRTLVSQDRIY 581  
Db 541 lrkrpniqpksegepvtldflaelendikveirknkmidgesgektfrtlvsqderiy 600  
Qy 582 DKNRRTYTTPVNGTDYSLALVLPYTFYIYKAKLEETITQARSKGKMDSETLKPDNF 641  
Db 601 dkgnrtytvtpvngtdyslaivlptysfyyikakleetitqary-----setlkpdnf 653  
Qy 642 EESGYTFIAPRDYCNLDKISDNNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTN 701  
Db 654 eesgytfiaprdycndkisdnteflnfnefidrktppnpscnadlinrvlldagftn 713  
Qy 702 ELVQNYWSKQNKIKGVKARFVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDVY 761  
Db 714 elvqnywskgnikgvkarfvvtggitrvyvpkeagenqenpetyedsfyrksldndy 773  
Qy 762 VFTAPYENKSGPAGESGIMVSKAVEIYIOGKLLPAPVVGIIKIDVNSWIENFTKTSIRD 821  
Db 774 vftapyfnksgpgayesgimvskaveiyioqkllpavvgiikidvnswieftktsirdp 833  
Qy 822 CAGPYCDCRNSDVMDCVLDGDFLLMANHDDYTNQIGRPFGEIDPSLMRLHVNISVYA 881  
Db 834 cagpycdcrrnsdvmcdvlddggfllmanhddytnqigrpfgeidpslmrlhvnisyva 893  
Qy 882 FNKSYDYSVCEPGAAPKOGAHRSAVPSVADILQIGWATAAAWSILOQFLLSLTTPR 941  
Db 894 fnksydydsvcepgaapkgaghrsayvpsvadilqigwataaawsilqfllsttpr 953  
Qy 942 LLEAVEMEDDDFTASLSKQSCITQOTQYFFDNDKSKFSVGLDCGNCRIFHGEKLMNTNL 1001  
Db 954 lleavedddftaslskqsciteqtgyffndsksfsgvldcncsrifhgeklmtnl 1013  
Qy 1002 IFIMVESKGTCPDTRLLIOAEQSDGPNCDVMYKQPRYKGPDPVCDNNVLEDYTDGCG 1061

Db 1014 ifimveskgtcpdtrlllqaeqtsdgnpcdmvkgprykrpdpvcfdnnvledytdcgg 1073

QY 1062 VS 1063

Db 1074 vs 1075

RESULT 15

ID AAB10586 standard; Protein; 1103 AA.

XX AAB10586;

XX 22-DEC-2000 (first entry)

XX Human calcium channel alpha-2a subunit protein.

XX Human; calcium channel; calcium channel subunit; diagnosis;

XX Lambert Eaton Syndrome; calcium channel subunit alpha-2a.

XX Homo sapiens.

XX US6096514-A.

XX 01-AUG-2000.

XX 25-MAY-1995; 95US-0450562.

XX 04-APR-1988; 88US-0176899.

XX 02-FEB-1990; 90US-0482384.

XX 08-NOV-1990; 90US-0603751.

XX 30-NOV-1990; 90US-0620250.

XX 15-AUG-1991; 91US-0745206.

XX 10-APR-1992; 92US-0868354.

XX 13-JUL-1992; 92US-0914231.

XX 11-AUG-1993; 93US-0105536.

XX 05-NOV-1993; 93US-0149097.

XX 07-FEB-1994; 94US-0193078.

XX 04-APR-1994; 94US-0223305.

XX 11-AUG-1994; 94US-0290012.

XX 23-SEP-1994; 94US-0311363.

XX 28-SEP-1994; 94US-0314083.

XX 07-NOV-1994; 94US-0336257.

XX 13-MAR-1995; 95US-0404950.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Ellis SB, Williams ME, McCue AF, Harpold MM;

XX WPI; 2000-548230/50.

XX N-PSDB; AAA71724.

XX Human calcium channel beta subunit polynucleotides, useful for producing recombinant eukaryotic cells and for diagnosing Lambert Eaton Syndrome

XX Disclosure; Column 229-236; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a sequence encoding a beta3-1 subunit of a human calcium channel. Nucleic acid probes comprising 14-30 contiguous nucleotides of beta3 subunit encoding DNA are useful for isolation and cloning of calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that express heterologous calcium channel are useful for identifying compounds that modulate calcium channel activity and in assays for identifying agonists and antagonists of calcium channel activity in humans. Human calcium channel subunit or eukaryotic cells expressing the channel are useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This sequence represents the human calcium channel alpha-2a subunit which is described in the method of the invention.

SQ Sequence 1103 AA;

Query Match		98.6%;	Score 5523;	DB 21;	Length 1103;			
Best Local Similarity		97.5%;	Pred. No. 0;					
Matches 1055;		Conservative 0;	Mismatches 1;	Indels 26;	Gaps 2;			
QY	1	MAAGCILLATLT	LFOSLLIGPSSSEPPPSAVTI	TKSWDKMQEDLVT	LAKTASGVNQLVDI 60			
Db	1	maagcillatlt	lfgsligpsseepfpavtlk	swdkmqedlv	tlaktasgvnqlvdi 60			
QY	61	YEKYQDLYTVE	PNNARQLEIAARDIEKLL	SNRSKALVSLALEAEK	VQAAHQWREDFASN 120			
Db	61	yekyqdltyve	pnnarqlveiaardiekl	lsnrskalvslaleae	kvaahqwrdfasn 120			
QY	121	EVVYNAKDDL	DPEKNDSEPGSORIKPV	FIEDANFGQOISYQ	HAHVIPDITYEGSTIVL 180			
Db	121	evvynakddl	dpekndsepgsgrikpv	fiedanfgqisqy	haavhiptdiyegstivl 180			
QY	181	NELNWT	SALDEVFKKREEDPSLL	WVFGSATGLIARY	PASPVDNSRTNKIDLYDVR 240			
Db	181	nelnwt	saldevfkknreedsll	wvfgsatglary	ypaspwvdsrtnkidydvrr 240			
QY	241	RPWYIOGA	SPKDMILLVDVSGV	SGLTGLKIRTSVSE	MLETSDDDFVNVSFNSAQD 300			
Db	241	rpwyidga	aspkdmillivdsvgs	sltklirtsvseml	etisdddfvnvasfnsaqd 300			
QY	301	VSCFQHLV	QAVNRNKKVILKDA	VNNITAKGITDYK	KGSPAFEQLLNYSRANCNKIIML 360			
Db	301	vscfqlh	vanvrnkkvilkdavn	nitakgitdyk	kgfsafeqllnysrancnkiml 360			
QY	361	FTDGEERA	QOEIFNKYNKDKK	RVFRFESVGOHNY	VERPIOWMACENKGYGYEIPSIGAIR 420			
Db	361	ftdgeera	qoiefnknkdkkvr	frfsvgghnyer	piqwmacenkgygyeipsigair 420			
QY	421	INTQEYLD	VLGRPMVL	AGDKAKQVQWNT	NVYLDALDELGLVIT	GLTPVPFNITQGFENKTNLK 480		
Db	421	intqeyld	vlgrpmvlagkak	qvwnvnyldale	lglvitgltpvfnitqgf	enknktnlk 480		
QY	481	NQLILG	VMGVDSLEDIKRL	TPFTLCPNGY	YFAIDPNGYVLLHPNLOPK----- 530			
Db	481	nqilgvm	gvdsledikrltp	ftlcpngyfaid	pnyvllhpnlpkpgipvgiptin 540			
QY	531	-----	NPKQEPVTL	DLDAELENDIK	VEIRNMIDGESGEKTRTLVKQSDERYI 581			
Db	541	lrkrrpn	iqpkqepvcl	dlaelendikve	lrnmidgesgektfrtlvksqeryi 600			
QY	582	DKGNRTY	TWTFVNGTDY	SLALVLTYSFY	YIKAKLEETITQARS	KKGMKMDSETLKPDNF 641		
Db	601	dkgnrty	twtpvngtdysl	alvltysfyik	akleetitqary-----	setlkpdnf 653		
QY	642	EESGYT	FIAPRDYCN	DLKISDNNT	FEFLNFEFIDRT	TPNPNPCNADLINRVLLDAGFTN 701		
Db	654	eesgyt	fiaprdycnd	lkisdntefl	lnfnefidrt	pnpnpscnadlinrvlldagftn 713		
QY	702	ELYQNY	WSKOKNTK	GVKARFVTDG	GITRVVPKEAG	ENMOENPETYEDSFYKRSLDNDNY 761		
Db	714	elyqny	wsqknk	gkavrfvtdgg	itrvyk	eaenwqenpetyedsfykrsldndny 773		
QY	762	VFTAPY	FNKSGP	GAYESGIMV	SRAVEIYIQ	KLKPAVVGIKIDVNSWIENFTKTSIRD 821		
Db	774	vftapy	fnksgpayesg	lmvksavely	iqgkllkpvav	gikidvnsvienftktsirdp 833		
QY	822	CAGP	VDCKRNS	QVMDCV	ILDDGGFLL	MANHDDYTNOIGRFFG	EIDPSLRHLVNISVYA 881	
Db	834	cagp	vdckrnsqvm	dcvildggfll	manhddytng	igrffg	eidpslrhlvnisvya 893	
QY	882	FNKSYD	YQSVCE	GAAPKQ	GAHRSAY	VPVSADIT	LOIGWATAAAWITLOQFLLSLFPPR 941	
Db	894	fnksyd	yqsvcegaap	kgahrsay	vpvsadil	qgwataaa	wilqfllslfppr 953	
QY	942	LLPA	VEDDDDF	FASLSK	QSCITEQ	TQTYFFD	NDNSKFSFVLDGNC	SRIFHGEKIMTNL 1001
Db	954	llea	veddddf	faslsk	qsciteq	tyffdn	ndsksfsgvldc	gncsrifhgekimtnl 1013

QY 1002 IFIMVESKGTCPDTRLIIQAEQTSQGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGG 1061  
Db 1014 ifimveskgtcpdtrlllqaeqtsdgnpcdmvkgprykgpdpvcfdnnvledytdcgg 1073  
QY 1062 VS 1063  
Db 1074 VS 1075

Search completed: July 23, 2001, 07:37:05  
Job time: 506 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:39:05 ; Search time 37.55 seconds  
(without alignments)  
570.273 Million cell updates/sec

Title: US-09-397-548-17  
Perfect score: 5599  
Sequence: 1 MAAGCLLALTFLFOSLLIG.....PDVCFDNNVLEDYDCGGVS 1063

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgnl\_7/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgnl\_7/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgnl\_7/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgnl\_7/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgnl\_7/ptodata/1/1aa/PTUS.COMB.pep.\*  
6: /cgnl\_7/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5599	100.0	1091	1	US-07-745-206A-25
2	5599	100.0	1091	1	US-08-455-543A-52
3	5599	100.0	1091	2	US-08-223-305C-52
4	5599	100.0	1091	2	US-08-311-363-25
5	5595	99.9	1091	3	US-08-713-118-4
6	5595	99.9	1091	4	US-09-452-007-4
7	5539.5	99.3	1086	1	US-08-455-543A-54
8	5539.5	99.3	1086	2	US-08-223-305C-54
9	5542.5	99.0	1084	1	US-08-455-543A-56
10	5542.5	99.0	1084	2	US-08-223-305C-56
11	5523	98.6	1103	1	US-08-455-543A-53
12	5523	98.6	1103	2	US-08-223-305C-53
13	5503	98.3	1079	1	US-08-455-543A-55
14	5503	98.3	1079	2	US-08-223-305C-55
15	5385.5	96.2	1106	1	US-08-435-675B-5
16	5367.5	95.9	1106	1	US-08-435-675B-5
17	5134.5	91.7	1086	6	US-08-336-257A-8
18	2581.5	46.1	508	1	US-08-435-675B-6
19	182	3.3	885	3	US-09-074-579-5
20	182	3.3	885	4	US-09-388-774-5
21	159.5	2.8	946	3	US-09-074-579-3
22	159.5	2.8	946	4	US-09-388-774-3
23	154	2.8	903	1	US-08-021-601-12
24	154	2.8	903	1	US-08-082-849B-12
25	154	2.8	903	5	PCT-US94-01624-12
26	152.5	2.7	789	1	US-08-471-033-32
27	152.5	2.7	789	2	US-08-471-044-32

28 152.5 2.7 789 2 US-08-463-483A-32 Sequence 32, Appl  
29 152.5 2.7 789 2 US-08-471-046A-32 Sequence 32, Appl  
30 152.5 2.7 789 2 US-08-470-566B-32 Sequence 32, Appl  
31 152.5 2.7 789 2 US-08-838-219B-4 Sequence 4, Appl  
32 152.5 2.7 789 2 US-08-469-334-32 Sequence 32, Appl  
33 152.5 2.7 789 3 US-09-300-529-32 Sequence 32, Appl  
34 152.5 2.7 789 3 US-09-233-336A-4 Sequence 4, Appl  
35 152.5 2.7 789 4 US-09-233-752A-4 Sequence 4, Appl  
36 150.5 2.7 789 4 US-08-960-780-6 Sequence 6, Appl  
37 150.5 2.7 789 4 US-09-073-898-6 Sequence 6, Appl  
38 148.5 2.7 790 4 US-08-960-780-4 Sequence 4, Appl  
39 148.5 2.7 790 4 US-09-073-898-4 Sequence 4, Appl  
40 147.5 2.6 746 2 US-08-838-219B-6 Sequence 6, Appl  
41 147.5 2.6 746 3 US-09-233-336A-6 Sequence 6, Appl  
42 147.5 2.6 746 4 US-09-233-752A-6 Sequence 6, Appl  
43 145.5 2.6 790 4 US-08-960-780-8 Sequence 8, Appl  
44 145.5 2.6 790 4 US-09-073-898-8 Sequence 8, Appl  
45 141.5 2.5 789 1 US-08-471-033-29 Sequence 29, Appl

## ALIGNMENTS

RESULT 1  
US-07-745-206A-25  
; Sequence 25, Application US/07745206A  
; Patent No. 5429921  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: McCue, Ann  
; APPLICANT: Feldman, Daniel  
; TITLE OF INVENTION: Human Calcium Channel Compositions and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fitch, Even, Tabin & Flannery  
; STREET: 135 S. LaSalle  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07745.206A  
; FILING DATE: 19910815  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Feder, Scott B  
; REFERENCE/DOCKET NUMBER: 51504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-372-7842  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-745-206A-25

Query Match 100.0%; Score 5599; DB 1; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTFLFOSLLIGPSSEPPFSAVTKSWVDKMQEDVTLAKTASGVNQLVDI 60  
|||||  
DB 1 MAAGCLLALTFLFOSLLIGPSSEPPFSAVTKSWVDKMQEDVTLAKTASGVNQLVDI 60  
|||||

QY 61 YEKYQDLTYVEPNARQVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQHREDFASN 120  
DB 61 YEKYQDLTYVEPNARQVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQHREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFRQISYQAAHVIPTDIYEGSTIVL 180  
DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFRQISYQAAHVIPTDIYEGSTIVL 180  
QY 181 NELNWTSALEDEVEKKNEEDPSLLQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
DB 181 NELNWTSALEDEVEKKNEEDPSLLQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKLTYSVSEMLETSLDDDFVNVASFNSNAOD 300  
DB 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKLTYSVSEMLETSLDDDFVNVASFNSNAOD 300  
QY 301 VSCFQHLVQANVRKVKLVDAVNNTAKITDYKGFSEAFQOLLNYSRANCNKIIML 360  
DB 301 VSCFQHLVQANVRKVKLVDAVNNTAKITDYKGFSEAFQOLLNYSRANCNKIIML 360  
QY 361 FTDGGERAEQELFNKYNDKKVRFVRFSGVQHYERGPIONMACENKGYEIPISGAIR 420  
DB 361 FTDGGERAEQELFNKYNDKKVRFVRFSGVQHYERGPIONMACENKGYEIPISGAIR 420  
QY 421 INTQEVLDVLRPMVLGAKAKOVQNTVYLDALGLVITGLTPVFNITGOFENKTNLK 480  
DB 421 INTQEVLDVLRPMVLGAKAKOVQNTVYLDALGLVITGLTPVFNITGOFENKTNLK 480  
QY 481 NGLILGVMDVSLDIEDIKRLTPREFLCPNGYFYAIDPNGYVLLHLPNLPKPKSOEPTVL 540  
DB 481 NGLILGVMDVSLDIEDIKRLTPREFLCPNGYFYAIDPNGYVLLHLPNLPKPKSOEPTVL 540  
QY 541 DFLDAELENIDKVEIRNKMIDGSEKERTFLVKSQDERYIDKGNRTYTWTVPNGTDSL 600  
DB 541 DFLDAELENIDKVEIRNKMIDGSEKERTFLVKSQDERYIDKGNRTYTWTVPNGTDSL 600  
QY 601 ALVLPYTFYIKAKLEETIQARSKKMKDSEFLKPDNFEESYTIAPRDYCNLDKI 660  
DB 601 ALVLPYTFYIKAKLEETIQARSKKMKDSEFLKPDNFEESYTIAPRDYCNLDKI 660  
QY 661 SDNTEFLNFEIDRKTNNPCSNADLINRVLLDAGFTNELVQYWSKOKNKGKVAR 720  
DB 661 SDNTEFLNFEIDRKTNNPCSNADLINRVLLDAGFTNELVQYWSKOKNKGKVAR 720  
QY 721 FVWTDGGITRYVPKEAGENWQENETEDSYFKRSLDNNDNVFTAPYFNKSGPGAYESGI 780  
DB 721 FVWTDGGITRYVPKEAGENWQENETEDSYFKRSLDNNDNVFTAPYFNKSGPGAYESGI 780  
QY 781 MVSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSTRDPCAGVCDCKRNSDVMDCVI 840  
DB 781 MVSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSTRDPCAGVCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
DB 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHRSAYVPSVADILQGWATAAANSILQOFLSLTFFRLLEAVEMEDDDFTASLSKQ 960  
DB 901 GAGHRSAYVPSVADILQGWATAAANSILQOFLSLTFFRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKTCPCDTRLLI 1020  
DB 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKTCPCDTRLLI 1020  
QY 1021 QAEQTSDPNPNCDMWKQPRYKRGPDVCFDNNVLEDYDCGGVS 1063  
DB 1021 QAEQTSDPNPNCDMWKQPRYKRGPDVCFDNNVLEDYDCGGVS 1063

RESULT 2

US-08-455-543A-52

; Sequence 52, Application US/08455543A

Query Match 100.0%; Score 5599; DB 1; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLALTLTLFQSLILGPSSEEPFSAVTIKSWDKMQEDLVTLAKTAGSVNOLVDI 60

; Patent No. 5792846

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller &amp; McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,543A

; FILING DATE: May 31, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/223,305

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/176,899

; FILING DATE: 04-APR-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 6362-52517

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)238-0999

; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1091 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-455-543A-52

Db 1 MAAGCLLATLTLFQSLLLGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVPNNARQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
Db 61 YEKYQDLYTVPNNARQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
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Db 121 EVVYVNAKDDLPKNDSPGSGQRKPVIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180  
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Db 181 NELNWTLSALDEYFKKNREDPSLLQVFGSATGLARYYPASVWDNSRTPNKIDLYDVR 240  
QY 241 RPWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
QY 301 VSCFOHLVQANRNKVKLDVANNITAKGITDYKKGFSFAFQOLLNYSRANCNKIIML 360  
Db 301 VSCFOHLVQANRNKVKLDVANNITAKGITDYKKGFSFAFQOLLNYSRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKYKDKKVRFRFSYGOHNYERGPIONMACENKGYIYEIPSIGAIR 420  
Db 361 FTDGGEERAQEIFNKYKDKKVRFRFSYGOHNYERGPIONMACENKGYIYEIPSIGAIR 420  
QY 421 INTQBYDLVGRPMVLGAKAKOVQNTVYLDALGLVITGLPVNTITGQFENKTNLK 480  
Db 421 INTQBYDLVGRPMVLGAKAKOVQNTVYLDALGLVITGLPVNTITGQFENKTNLK 480  
QY 481 NOLILGVAGVDVSLIEDIKLITRFLPCPNGYFAIDPNGYVLLHNPQKNKSPQEPVL 540  
Db 481 NOLILGVAGVDVSLIEDIKLITRFLPCPNGYFAIDPNGYVLLHNPQKNKSPQEPVL 540  
QY 541 DFLDAELENDIIVEIRNKMIDGESKEKFTLVKSODERYIDKGNRTYTWTVPNGTDYSL 600  
Db 541 DFLDAELENDIIVEIRNKMIDGESKEKFTLVKSODERYIDKGNRTYTWTVPNGTDYSL 600  
QY 601 ALVLPYTFYIYKALEETITQARSKKGMKDSKTLKPDNFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIYKALEETITQARSKKGMKDSKTLKPDNFEESGYTFIAPRDYCNLDKI 660  
QY 661 SONTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNVLQVYNSKQKNIGVKAR 720  
Db 661 SONTEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNVLQVYNSKQKNIGVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRLDNDNYYFTAPYFNKSGPGAYESGI 780  
Db 721 FVYTDGGITRVYPKEAGENWQENPETYEDSFYKRLDNDNYYFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIQGLLKPAPVIGIKIDVNSWIENTFTSIRDPKAGPVCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIQGLLKPAPVIGIKIDVNSWIENTFTSIRDPKAGPVCDCKRNSDVMDCVI 840  
QY 841 LDGGLFLMANHDDYTNOIGRFFGEIDSLMRHLNYSIYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDGGLFLMANHDDYTNOIGRFFGEIDSLMRHLNYSIYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAASWTLQOFLSLFPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAASWTLQOFLSLFPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTYFFDNDKSFSGVLDGNCNRSIFHGEKLMNTNLIFIMVESKGTCPCTRLLI 1020  
Db 961 SCITEQTYFFDNDKSFSGVLDGNCNRSIFHGEKLMNTNLIFIMVESKGTCPCTRLLI 1020  
QY 1021 QAEQSDGNPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063  
Db 1021 QAEQSDGNPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063

RESULT 3

US-08-223-305C-52  
; Sequence 52, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Fast-Seq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-223-305C-52

Query Match 100.0%; Score 5599; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTLFQSLLLGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
|||||



Db 1 MAAGCLLALTLTLFQSLIGPSEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNAROLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120  
Db 61 YEKYQDLYTVEPNAROLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIISYQAAHVIPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIISYQAAHVIPTDIYEGSTIVL 180  
QY 181 NELNWTALDEVPKKNREEDPSLLWQVFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240  
Db 181 NELNWTALDEVPKKNREEDPSLLWQVFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240  
QY 241 RPWTIOGAASPDKMLILVDVSGVSGGLTKLIRTSVSEMLETSDDDFVNVASFNSNAQD 300  
Db 241 RPWTIOGAASPDKMLILVDVSGVSGGLTKLIRTSVSEMLETSDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360  
QY 361 FTGGEERAQEIENKYNKDKKRVRFVSGQHNYERGIOWMACENKGYIYEIPSGAIR 420  
Db 361 FTGGEERAQEIENKYNKDKKRVRFVSGQHNYERGIOWMACENKGYIYEIPSGAIR 420  
QY 421 INTQEYLDVLRPMVLAGDKAKOVQWNTVYLDALGLVITGLPVENITGQENKTNLK 480  
Db 421 INTQEYLDVLRPMVLAGDKAKOVQWNTVYLDALGLVITGLPVENITGQENKTNLK 480  
QY 481 NQLILGVMGVDSLEDIKRLTPTFTLCPNGYIYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
Db 481 NQLILGVMGVDSLEDIKRLTPTFTLCPNGYIYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540  
QY 541 DFLDAELENKIVKIRNKMIDGSGEFTFTLVKSQDERYIDKGNRTYTTVPVNGTDYSL 600  
Db 541 DFLDAELENKIVKIRNKMIDGSGEFTFTLVKSQDERYIDKGNRTYTTVPVNGTDYSL 600  
QY 601 ALVLPYTSFYIIRAKLETITQARSKKGMKDSKTLKPDNFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTSFYIIRAKLETITQARSKKGMKDSKTLKPDNFEESGYTFIAPRDYCNLDKI 660  
QY 661 SDNTEFLNNEFIDRKTNNPNSCNADLNRLVLLDAGFTNQLVQYWSKQKNIKGVKAR 720  
Db 661 SDNTEFLNNEFIDRKTNNPNSCNADLNRLVLLDAGFTNQLVQYWSKQKNIKGVKAR 720  
QY 721 FVVTDDGITTIVYKPEAGENMOENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
Db 721 FVVTDDGITTIVYKPEAGENMOENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840  
QY 841 LDDGFFILMANHDDYTQIGRFFGEIDPILMRHLVNTSVYAFNKSVDYQSVCEPBGAPKQ 900  
Db 841 LDDGFFILMANHDDYTQIGRFFGEIDPILMRHLVNTSVYAFNKSVDYQSVCEPBGAPKQ 900  
QY 901 GAGHRSAYPSVADILQIGWATAAASIIQQFLLSLTFPPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHRSAYPSVADILQIGWATAAASIIQQFLLSLTFPPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTYFFDNDKDSFSGVLDCGNCNRSRIFHGEKLMNTNLIFIMVESKGTCTPCDTRLLI 1020  
Db 961 SCITEQTYFFDNDKDSFSGVLDCGNCNRSRIFHGEKLMNTNLIFIMVESKGTCTPCDTRLLI 1020  
QY 1021 QAEOTSDGPNPCDMVKOPRYRKGPVDCFDNNVLEDYTDCCGVS 1063  
Db 1021 QAEOTSDGPNPCDMVKOPRYRKGPVDCFDNNVLEDYTDCCGVS 1063

RESULT 4

US-08-311-363-25

Sequence 25, Application US/08311363  
Patent No. 5876958  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: Human Calcium Channel Compositions and  
TITLE OF INVENTION: Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,363  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-51506  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-311-363-25

Query Match 100.0%; Score 5599; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTLFQSLIGPSEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTLTLFQSLIGPSEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNAROLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120  
Db 61 YEKYQDLYTVEPNAROLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHOREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIISYQAAHVIPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIISYQAAHVIPTDIYEGSTIVL 180  
QY 181 NELNWTALDEVPKKNREEDPSLLWQVFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240  
Db 181 NELNWTALDEVPKKNREEDPSLLWQVFGSATGLARYYPASPPWVDNSRTPNKIDLYDVR 240  
QY 241 RPWTIOGAASPDKMLILVDVSGVSGGLTKLIRTSVSEMLETSDDDFVNVASFNSNAQD 300  
Db 241 RPWTIOGAASPDKMLILVDVSGVSGGLTKLIRTSVSEMLETSDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCNKIIML 360

RESULT 5  
 : Sequence 4, Application US/08713118  
 : Patent No. 6040436  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Franco, Rodrigo  
 : APPLICANT: Sun Chen, Ai Ru  
 : APPLICANT: Suey, David J.  
 : TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
 : TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
 :  
 : NUMBER OF SEQUENCES: 6  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 : STREET: Two Militia Drive  
 : CITY: Lexington  
 : STATE: MA  
 :  
 : COUNTRY: USA  
 : ZIP: 02173-4799  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 :  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.30

Query Match	99.9%	Score	5595;	DB 3;	Length	1091;		
Best Local Similarity	99.9%;	Pred. No. 0;						
Matches 1062;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
1	MAAGCLLALTLTLFQSLILGPSEEPFPPSAVTKSWDKWQEDLVTLAKTAGVNLQYDI	60						
1	MAAGCLLALTLTLFQSLILGPSEEPFPPSAVTKSWDKWQEDLVTLAKTAGVNLQYDI	60						
61	YEXQDLYTVEPNARQOLVEIARDTEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN	120						
61	YEXQDLYTVEPNARQOLVEIARDTEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN	120						
121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAAVHIPTDIYEGSTIVL	180						
121	EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAAVHIPTDIYEGSTIVL	180						
181	NELNWTLSALDEVFKKNREEDPSLLQWVFGSATGLARIYPASPWVDSNRPNKIDLYDVR	240						
181	NELNWTLSALDEVFKKNREEDPSLLQWVFGSATGLARIYPASPWVDSNRPNKIDLYDVR	240						
241	RPWYIOGAASPDKMLILVDVSGVSGTLTKLIRTSVSEMLETSDDDFVNVAFSNSNAQD	300						
241	RPWYIOGAASPDKMLILVDVSGVSGTLTKLIRTSVSEMLETSDDDFVNVAFSNSNAQD	300						
301	VSCFQHLVQANVRNKKVLKDAVNNTAKGTDYDKKGFSAFEQLLNVYSRANCNKIIML	360						
301	VSCFQHLVQANVRNKKVLKDAVNNTAKGTDYDKKGFSAFEQLLNVYSRANCNKIIML	360						
361	FTDGEERAQEIFNKYKDKKVRFRFSVGOHNYRERGPIQWACENKGYIYETPSGAIR	420						
361	FTDGEERAQEIFNKYKDKKVRFRFSVGOHNYRERGPIQWACENKGYIYETPSGAIR	420						
421	INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALLEGVLVTGILPVENITGQFENKTNLK	480						
421	INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALLEGVLVTGILPVENITGQFENKTNLK	480						
481	NQLILGVNGVDVSLIEDIKRLTPRTLCPNGYFYAIDPNGVYLLHPNLQPNKPSQEPVTL	540						
481	NQLILGVNGVDVSLIEDIKRLTPRTLCPNGYFYAIDPNGVYLLHPNLQPNKPSQEPVTL	540						
541	DFDLDAELNDIKVEIRNKKWDIGSEKTRFLVKSQDERYIDKGNRYITWTVPVNGTDYSL	600						
541	DFDLDAELNDIKVEIRNKKWDIGSEKTRFLVKSQDERYIDKGNRYITWTVPVNGTDYSL	600						
601	ALVLPYTFYIYKALEETITQARSKKMKDSETLKPNDNEESGYTTFIAPRDYCNLDKI	660						
601	ALVLPYTFYIYKALEETITQARSKKMKDSETLKPNDNEESGYTTFIAPRDYCNLDKI	660						
661	SDNNTFEFLNNEFIDRKTNNPNSCNADLINVRLDAGFTNELLVQNTWSKOKNKGVKAR	720						
661	SDNNTFEFLNNEFIDRKTNNPNSCNADLINVRLDAGFTNELLVQNTWSKOKNKGVKAR	720						
721	FVVTDDGGITRVYPKZAGENWQENPTYEDSFYKRSLDNDNVYFTAPFNKSGPGAYESGI	780						

Db 721 FVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNVFTAPYENKSGPGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLLMANHDDYTNOIGRFFGIDPSLRHLNIVSVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDDGGFLLMANHDDYTNOIGRFFGIDPSLRHLNIVSVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLFPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLFPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTOYFFDNDKSKSPGVLDCGNCRIHFGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
Db 961 SCITEQTOYFFDNDKSKSPGVLDCGNCRIHFGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
QY 1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063  
Db 1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063

## RESULT 6

US-09-452-007-4  
; Sequence 4, Application US/09452007  
; Patent No. 6140485  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suey, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118  
; FILING DATE: 16-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-452-007-4

Query Match 99.9%; Score 5595; DB 4; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1062; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLTQSLLLIGPSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60  
Db 1 MAAGCLLALTTLTQSLLLIGPSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60  
QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALYSLEAEKVQAAHQRWEDFASN 120  
Db 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALYSLEAEKVQAAHQRWEDFASN 120  
QY 121 EVVYNNAKDDLDPKENDSEPSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYNNAKDDLDPKENDSEPSQRIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSALEDVFEKKNREEDPSLLWQVFSATGLARYYPASFWVDNSRTPNKIDLYDVR 240  
Db 181 NELNWTSALEDVFEKKNREEDPSLLWQVFSATGLARYYPASFWVDNSRTPNKIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGSYSGLTFLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPWYIQGAASPKDMLILVDVSGSYSGLTFLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGITDYKGFSAFEQLLNLYNVRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGITDYKGFSAFEQLLNLYNVRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKYKDKVRVFRFSVGOHNTYERGPQIWMACENKGYEYIPEISGAIR 420  
Db 361 FTDGGEERAQEIFNKYKDKVRVFRFSVGOHNTYERGPQIWMACENKGYEYIPEISGAIR 420  
QY 421 INTQEYLDVLGRPMVLGADKAKQVQWNTNLYDLAELGLVITGTLPVFNITGOFENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLGADKAKQVQWNTNLYDLAELGLVITGTLPVFNITGOFENKTNLK 480  
QY 481 NQLILGVNGVDVSLIEDIKRLTPRETLCPNGYFAFDNGYVLLHNPLOPKPKSOEPTVL 540  
Db 481 NQLILGVNGVDVSLIEDIKRLTPRETLCPNGYFAFDNGYVLLHNPLOPKPKSOEPTVL 540  
QY 541 DFLDAELNDIKVEIRNKMIDGESSEKTRFLVKSQDERYIDKGNRTYTWTVPVNGTDSL 600  
Db 541 DFLDAELNDIKVEIRNKMIDGESSEKTRFLVKSQDERYIDKGNRTYTWTVPVNGTDSL 600  
QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKMDSEYTKPDNFEESGYTFIAPDYCNDLKI 660  
Db 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKMDSEYTKPDNFEESGYTFIAPDYCNDLKI 660  
QY 661 SDNTEFLLNNEFTDRKTPNNPCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVKAR 720  
Db 661 SDNTEFLLNNEFTDRKTPNNPCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVKAR 720  
QY 721 FVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNVFTAPYENKSGPGAYESGI 780  
Db 721 FVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNVFTAPYENKSGPGAYESGI 780  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLLMANHDDYTNOIGRFFGIDPSLRHLNIVSVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDDGGFLLMANHDDYTNOIGRFFGIDPSLRHLNIVSVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLFPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLFPRLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTOYFFDNDKSKSPGVLDCGNCRIHFGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
Db 961 SCITEQTOYFFDNDKSKSPGVLDCGNCRIHFGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
QY 1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063  
Db 1021 QAEQTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063

Mon Jul 23 08:36:36 2001

RESULT

US-08-455-543A-54  
Sequence 54, Application US/0845543A  
Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 20-FEB-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 04-APR-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1086 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal

US-08-455-543A-54

Query Match

99.3%; Score 5559.5; DB 1; Length 1086;

		Best Local Similarity	99.5%;	Pred. No. 0;	Mismatches	0;	Indels	5;	Gaps	1;
		Matches 1058; Conservative								
QY	1	MAAGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWDKMQEDIVTLAKTASGVNQLVDI	60							
DB	1	MAAGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWDKMQEDIVTLAKTASGVNQLVDI	60							
QY	61	YEKYQDLTYVEPNNAARQLVEIAARDIEKLLSNRSKALVSALAEAKVQAAHQRDFASN	120							
DB	61	YEKYQDLTYVEPNNAARQLVEIAARDIEKLLSNRSKALVSALAEAKVQAAHQRDFASN	120							
QY	121	EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFQRQISYQAAVHIPTDIYEGSTIVL	180							
DB	121	EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFQRQISYQAAVHIPTDIYEGSTIVL	180							
QY	181	NELNWTSALDEVEFKKNEEDPSLLQVFGSATGLARYYPASPWVDNSRTNKIDLYDVR	240							
DB	181	NELNWTSALDEVEFKKNEEDPSLLQVFGSATGLARYYPASPWVDNSRTNKIDLYDVR	240							
QY	241	RPWYIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFVNVASFNSNAQD	300							
DB	241	RPWYIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFVNVASFNSNAQD	300							
QY	301	VSCFHLVQANVRNKKVYLKDAVNNTAKGITDYKKGFSFAFEQLLNTNVSRANCKIIML	360							
DB	301	VSCFHLVQANVRNKKVYLKDAVNNTAKGITDYKKGFSFAFEQLLNTNVSRANCKIIML	360							
QY	361	FTDGEERAQEIFNKNYKDKKRVFRFVSGQHNTGPIQWACENKGYEIPISGAIR	420							
DB	361	FTDGEERAQEIFNKNYKDKKRVFRFVSGQHNTGPIQWACENKGYEIPISGAIR	420							
QY	421	INTQYLDVLGRPMVLADKAKQVQWNTVLDALGLVITGLTFVFNITGOFENKTNLK	480							
DB	421	INTQYLDVLGRPMVLADKAKQVQWNTVLDALGLVITGLTFVFNITGOFENKTNLK	480							
QY	481	NQLILGVMGVDVSLDIKRLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKPKSQEPVTL	540							
DB	481	NQLILGVMGVDVSLDIKRLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKPKSQEPVTL	540							
QY	541	DFLDAELNDIKVEIRNKMIDGESGKFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL	600							
DB	541	DFLDAELNDIKVEIRNKMIDGESGKFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL	600							
QY	596	ALVLPYISFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNDLKI	655							
DB	596	ALVLPYISFYIIKAKLEETITQARSKGKMKDSETLKPDNFEESGYTFIAPRDYCNDLKI	655							
QY	661	SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR	720							
DB	661	SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR	720							
QY	721	FVVTGGITRVYPKEAGENMOENPETYEDSYKRSNDNDNYVFTAPYFNKSGPGAYESGI	780							
DB	721	FVVTGGITRVYPKEAGENMOENPETYEDSYKRSNDNDNYVFTAPYFNKSGPGAYESGI	780							
QY	776	MVSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSVMDCVI	840							
DB	776	MVSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSVMDCVI	840							
QY	841	LDDGGFLLMANHDDYTNQIGREFGIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ	900							
DB	841	LDDGGFLLMANHDDYTNQIGREFGIDPSLMRHLVNIISVYAFNKSIDYQSVCEPGAAPKQ	900							
QY	896	GAGHRSAYVPSVADILQIGWATAAASWILQOFLSLTFPRLEAVEMEDDDFTASLSKQ	955							
DB	896	GAGHRSAYVPSVADILQIGWATAAASWILQOFLSLTFPRLEAVEMEDDDFTASLSKQ	955							
QY	961	SCITEQTYFFDNDKSKFSGLVDCGNCSTRIFHGKELMNTNLIIFIMVESKGTCTPCDTRLLI	1020							
DB	961	SCITEQTYFFDNDKSKFSGLVDCGNCSTRIFHGKELMNTNLIIFIMVESKGTCTPCDTRLLI	1020							
QY	1021	QAEQTSQGNPCDVKQPRYKGPDPVCFDNNVLEDYTDGCVS	1063							
DB	1021	QAEQTSQGNPCDVKQPRYKGPDPVCFDNNVLEDYTDGCVS	1063							

Db 1016 QABQTSQGNPCDMVKQPRYKGPVCFDNNVLEDYTDGCGVS 1058

RESULT 8  
US-08-223-305C-54  
; Sequence 54, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1086 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-223-305C-54

Query Match 99.3%; Score 5559.5; DB 2; Length 1086;  
Best Local Similarity 99.5%; Pred. No. 0;

	Matches 1058;	Conservative	0;	Mismatches	0;	Indels	5;	Gaps	1;
QY	1	MAAGCLLALTLT	FOSLLIGPSSEPP	SAVTIKSWDKMQEDL	VLAKTASGVNQLVDI	60			
DB	1	MAAGCLLALTLT	FOSLLIGPSSEPP	SAVTIKSWDKMQEDL	VLAKTASGVNQLVDI	60			
QY	61	YEKYQDLTYVEP	NNARQLVEIAARDI	EKLLSNRSKALVSL	ALEAEKVQAAHQWREDFASN	120			
DB	61	YEKYQDLTYVEP	NNARQLVEIAARDI	EKLLSNRSKALVSL	ALEAEKVQAAHQWREDFASN	120			
QY	121	EVVYNKDDLDPE	KNDSEPGSQRKPV	IEDANFGRQISYQHA	AVHIPTDIYEGSTIVL	180			
DB	121	EVVYNKDDLDPE	KNDSEPGSQRKPV	IEDANFGRQISYQHA	AVHIPTDIYEGSTIVL	180			
QY	181	NELNMTSALDE	VFKKREEDPSLLQ	QVFGSAGLARYXP	ASPWDNSRTPNKIDLYDVR	240			
DB	181	NELNMTSALDE	VFKKREEDPSLLQ	QVFGSAGLARYXP	ASPWDNSRTPNKIDLYDVR	240			
QY	241	RPWYIQGAASPK	DMLILVDVSGVSG	LTLLKLRISVSEMLE	TLSDDDFYNVASFNSNAQD	300			
DB	241	RPWYIQGAASPK	DMLILVDVSGVSG	LTLLKLRISVSEMLE	TLSDDDFYNVASFNSNAQD	300			
QY	301	VSCFOHLVQAN	VRNKKVLKDAVNN	ITAKITDYKKGFSF	AFQOLLNYSRANCNKIIML	360			
DB	301	VSCFOHLVQAN	VRNKKVLKDAVNN	ITAKITDYKKGFSF	AFQOLLNYSRANCNKIIML	360			
QY	361	FTDGGEEERAQ	EIFNKYKDKVVR	FESYGOHNYERGP	IOWMACENKGYIETPSIGAIR	420			
DB	361	FTDGGEEERAQ	EIFNKYKDKVVR	FESYGOHNYERGP	IOWMACENKGYIETPSIGAIR	420			
QY	421	INTQEYLDVLR	PMVLADGKAKQV	QWNTNVLDALEL	GLVITGTPLPVENITGOFENKTNLK	480			
DB	421	INTQEYLDVLR	PMVLADGKAKQV	QWNTNVLDALEL	GLVITGTPLPVENITGOFENKTNLK	480			
QY	481	NOLILGVMGV	DVSLDIKRLTPR	FLCPNGYIFAIDP	NGVLLHPNLQPNKPSQBPVIL	540			
DB	481	NOLILGVMGV	DVSLDIKRLTPR	FLCPNGYIFAIDP	NGVLLHPNLQPNKPSQBPVIL	540			
QY	541	DELDAELENDI	KVEIRNKMDGSE	GKERTLVKSDERY	IDKGNRTYTPTVNGDYSL	600			
DB	536	DELDAELENDI	KVEIRNKMDGSE	GKERTLVKSDERY	IDKGNRTYTPTVNGDYSL	595			
QY	601	ALVLPYSEYI	IKALEETITQARS	KKGMKDSSETL	KPNFESGYTFIAPRDYCNLDKI	660			
DB	596	ALVLPYSEYI	IKALEETITQARS	KKGMKDSSETL	KPNFESGYTFIAPRDYCNLDKI	655			
QY	661	SDNTEFLNFE	NFIDRKTPNPN	SCNADLINRVLL	DAGFTNELVQNYWSKQNIKGVKAR	720			
DB	656	SDNTEFLNFE	NFIDRKTPNPN	SCNADLINRVLL	DAGFTNELVQNYWSKQNIKGVKAR	715			
QY	721	FVYTDGGITR	VYPKEAGENQEN	PETEDSFYKRS	LDNDNYVETAPYENKSGPGAYESGI	780			
DB	716	FVYTDGGITR	VYPKEAGENQEN	PETEDSFYKRS	LDNDNYVETAPYENKSGPGAYESGI	775			
QY	781	MYSKAVEIYI	IQGLKLPVAVGI	KIDVNSWIENT	FKTISIRDPACAPVCDCKRNSDVMDCVI	840			
DB	776	MYSKAVEIYI	IQGLKLPVAVGI	KIDVNSWIENT	FKTISIRDPACAPVCDCKRNSDVMDCVI	835			
QY	841	LDDGGFLMAN	HDDYTNQIGR	FFGEIDPSLMR	HLVNI SYAFNKS YDYQSVCEPGAAPKQ	900			
DB	836	LDDGGFLMAN	HDDYTNQIGR	FFGEIDPSLMR	HLVNI SYAFNKS YDYQSVCEPGAAPKQ	895			
QY	901	GAGHRSAYVP	SVADILQIGW	MTAAAWSI	ILQQFLLSITPPRLLEAVEMEDDDFTASLSKQ	960			
DB	896	GAGHRSAYVP	SVADILQIGW	MTAAAWSI	ILQQFLLSITPPRLLEAVEMEDDDFTASLSKQ	955			
QY	961	SCITEQTQY	FFDNDKSF	SGVLDGNC	SRIFHGEKLMNTNLIFIMVESKGTCPCDTRLLI	1020			
DB	956	SCITEQTQY	FFDNDKSF	SGVLDGNC	SRIFHGEKLMNTNLIFIMVESKGTCPCDTRLLI	1015			
QY	1021	QABQTSQGNP	CDMVKQPRYKGP	VDVCFDNNVLEDY	TDGCGVS 1063				
DB	1016	QABQTSQGNP	CDMVKQPRYKGP	VDVCFDNNVLEDY	TDGCGVS 1058				

Mon Jul 23 08:36:36 2001

RESULT 9  
 US-08-455-543A-56  
 ; Sequence 56, Application US/08455543A  
 ; Patent No. 5792846  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harpold, Michael  
 ; APPLICANT: Ellis, Steven  
 ; APPLICANT: Williams, Mark  
 ; APPLICANT: Feldman, Daniel  
 ; APPLICANT: McCue, Ann  
 ; APPLICANT: Brenner, Robert  
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 ; TITLE OF INVENTION: METHODS  
 ; NUMBER OF SEQUENCES: 57  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Brown, Martin, Haller & McClain  
 ; STREET: 1660 Union Street  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92101-2926  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/455,543A  
 ; FILING DATE: May 31, 1995  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/223,305  
 ; FILING DATE: April 4, 1994  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/868,354  
 ; FILING DATE: April 10, 1992  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/745,206  
 ; FILING DATE: 15-AUG-1991  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/620,250  
 ; FILING DATE: 30-NOV-1990  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/482,384  
 ; FILING DATE: 20-FEB-1990  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/603,751  
 ; FILING DATE: 04-APR-1989  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/US89/01408  
 ; FILING DATE: 04-APR-1989  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/176,899  
 ; FILING DATE: 04-APR-1988  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Seidman, Stephanie L.  
 ; REGISTRATION NUMBER: 33,779  
 ; REFERENCE/DOCKET NUMBER: 6362-52517  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619)238-0999  
 ; TELEFAX: (619)238-0062  
 ; INFORMATION FOR SEQ ID NO: 56:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1084 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-08-455-543A-56

Query Match 99.0%; Score 5542.5; DB 1; Length 1084;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY	1	MAAGCLLALTTLFQSL	IGPSEEP	PPSAVTIKSWDKMQEDLVT	LAKTASGVNQLVDI	60
DB	1	MAAGCLLALTTLFQSL	IGPSEEP	PPSAVTIKSWDKMQEDLVT	LAKTASGVNQLVDI	60
QY	61	YEQYQDLYTVEPNNA	RQLVFIAR	DIKLLSNRSKALVSLALAEK	VQAAHQWREDFASN	120
DB	61	YEQYQDLYTVEPNNA	RQLVFIAR	DIKLLSNRSKALVSLALAEK	VQAAHQWREDFASN	120
QY	121	EVVYINAKDDLDPEK	NDSEPGSQRIKPV	FIEDANFGRIQISYQHA	AVHIPTDIYEGSTIVL	180
DB	121	EVVYINAKDDLDPEK	NDSEPGSQRIKPV	FIEDANFGRIQISYQHA	AVHIPTDIYEGSTIVL	180
QY	181	NELNWTISALDEVFK	KNREEDPSLLQV	FGSATGLARYYPAS	PWDNSRTPNKIDLYDVR	240
DB	181	NELNWTISALDEVFK	KNREEDPSLLQV	FGSATGLARYYPAS	PWDNSRTPNKIDLYDVR	240
QY	241	RPWYIQGAASPKDML	ILVDVSGVSGLT	KLIRTSVSEMLET	LSDDDFNVASFNSAQD	300
DB	241	RPWYIQGAASPKDML	ILVDVSGVSGLT	KLIRTSVSEMLET	LSDDDFNVASFNSAQD	300
QY	301	VSCFQHLVQANVRN	KKVLDVNNITAK	GITDYKGFSAFQ	QLLNYNVSRANCKNIIML	360
DB	301	VSCFQHLVQANVRN	KKVLDVNNITAK	GITDYKGFSAFQ	QLLNYNVSRANCKNIIML	360
QY	361	FTDGGEEARAEI	FNKYNKDKVR	FRFSVQGHNYER	GPIQWACENKGYIYEIP	420
DB	361	FTDGGEEARAEI	FNKYNKDKVR	FRFSVQGHNYER	GPIQWACENKGYIYEIP	420
QY	421	INTQEYLDVLRPM	LAGDKAKQVQW	TNYLDALGLVIT	GTLPVFNITGTFENKTNL	480
DB	421	INTQEYLDVLRPM	LAGDKAKQVQW	TNYLDALGLVIT	GTLPVFNITGTFENKTNL	480
QY	481	NQILGVMGVDV	SLEDIKRLTP	RTCPNGYFAIDP	NGVYLLHPLNQPNKPSQ	540
DB	481	NQILGVMGVDV	SLEDIKRLTP	RTCPNGYFAIDP	NGVYLLHPLNQPNKPSQ	540
QY	541	DFLDAELENDI	KVEIRNKMID	GESGEKTFRLV	KSQDERYIDKGNRTYT	600
DB	541	DFLDAELENDI	KVEIRNKMID	GESGEKTFRLV	KSQDERYIDKGNRTYT	600
QY	601	ALVLPYTSFYI	IKAKLEETI	QARSKKGKMDSE	TLPADNFEESGYTFIAP	660
DB	601	ALVLPYTSFYI	IKAKLEETI	QARSKKGKMDSE	TLPADNFEESGYTFIAP	660
QY	661	SDNTEFLLN	FEINERIDR	KTPNPNPCNAD	LINRVLLDAGFTNELV	720
DB	661	SDNTEFLLN	FEINERIDR	KTPNPNPCNAD	LINRVLLDAGFTNELV	720
QY	721	FVITDGGITRV	YPKEAGENW	ENPETYEDSFY	KRSNDNDNVFTAPY	780
DB	721	FVITDGGITRV	YPKEAGENW	ENPETYEDSFY	KRSNDNDNVFTAPY	780
QY	781	MYSKAVEIY	IQGKLLKPA	VVGKIDVNSW	IENTFTTSIRDP	840
DB	781	MYSKAVEIY	IQGKLLKPA	VVGKIDVNSW	IENTFTTSIRDP	840
QY	841	LDGGFLLMAN	HDDYTNQIG	REFGEIDP	SLMRHLNYSVYAFN	900
DB	841	LDGGFLLMAN	HDDYTNQIG	REFGEIDP	SLMRHLNYSVYAFN	900
QY	901	GAGHSAYVPS	VADILQIGW	ATAAWSILQO	FLSLTPRLLAEVEM	960
DB	901	GAGHSAYVPS	VADILQIGW	ATAAWSILQO	FLSLTPRLLAEVEM	960
QY	961	SCITEQTQY	FFDNDN	SKSFGVLDC	GNCSRIFPHGEK	1020
DB	961	SCITEQTQY	FFDNDN	SKSFGVLDC	GNCSRIFPHGEK	1020
QY	1021	QAEQTS	SDGNPCDM	VQPKRYE	KGPDVCFDNNVLE	1060
DB	1021	QAEQTS	SDGNPCDM	VQPKRYE	KGPDVCFDNNVLE	1060

Db 1014 QAEQTSDEPNCDMVKQPRYRKGPVCFDNNVLEDTDCGGVS 1056

RESULT 10  
US-08-223-305C-56  
; Sequence 56, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223.305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1084 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-223-305C-56

Query Match 99.0%; Score 5542.5; DB 2; Length 1084;

Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gaps 1;  
Qy 1 MAAGCLLALTLTLFQSLIGSPSEPPSPSAVTIKSWDKMOEDLVTAKTAGSVNQLYDI 60  
Db 1 MAAGCLLALTLTLFQSLIGSPSEPPSPSAVTIKSWDKMOEDLVTAKTAGSVNQLYDI 60  
Qy 61 YEKYODLYTVEPNNAQOLVEIAARDIEKLLNSRKALVSLALEAKVQAAHQRDFASN 120  
Db 61 YEKYODLYTVEPNNAQOLVEIAARDIEKLLNSRKALVSLALEAKVQAAHQRDFASN 120  
Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180  
Qy 181 NELNWTSDALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPDWDSRTPNKIDLYDVR 240  
Db 181 NELNWTSDALDEVFKKNREEDPSLLWQVFGSATGLARYYPASPDWDSRTPNKIDLYDVR 240  
Qy 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPWYIOGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Qy 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGIDYKKGFSFAFEPQLLNNVSRANCKIIML 360  
Db 301 VSCFQHLVQANVRNKKVYLKDAVNNTAKGIDYKKGFSFAFEPQLLNNVSRANCKIIML 360  
Qy 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSGQHNYPGRPIOWMACENKGYEYIPEISGAIR 420  
Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSGQHNYPGRPIOWMACENKGYEYIPEISGAIR 420  
Qy 421 INTOEYLDVLRPMVLADGKAKOVQNTNVYLDALBELGVITGTLVFNITGOFENKTNLK 480  
Db 421 INTOEYLDVLRPMVLADGKAKOVQNTNVYLDALBELGVITGTLVFNITGOFENKTNLK 480  
Qy 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFADPNGYVLLHPLNLPKPKSQEPVTL 540  
Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFADPNGYVLLHPLNLPKPKSQEPVTL 540  
Qy 541 DFLDAELENDIKVEIRNKMIDGESGEKFTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGESGEKFTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
Qy 601 ALVLPYTFYIKAKLEETITQARSKKGMKDSKSEKLPKPNFESGYTFIAPRDYCNDLKI 660  
Db 601 ALVLPYTFYIKAKLEETITQARY-----SEFLKPNFESGYTFIAPRDYCNDLKI 653  
Qy 661 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLDAGFTNELVQNYWSKQKNIKGVKAR 720  
Db 654 SDNTEFLNFEFIDRKTTPNPNPCNADLINRVLDAGFTNELVQNYWSKQKNIKGVKAR 713  
Qy 721 FVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNNYFTAPYFNKSGPGAYESGI 780  
Db 714 FVVTGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNNYFTAPYFNKSGPGAYESGI 773  
Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSKIENFTTSTDPDPCAGPVCDCRNSDYMDCVI 840  
Db 774 MYSKAVEIYIOGKLLKPAVVGKIDVNSKIENFTTSTIRDPDPCAGPVCDCRNSDYMDCVI 833  
Qy 841 LDDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPAAKQ 900  
Db 834 LDDGGFLLMANHDDYTNOIGRFFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPAAKQ 893  
Qy 901 GAGHRSAYVPSVADILQIGWATAAAWSILOQLFLSLTFPRRLEAVEMEDDDFTASLSKQ 960  
Db 894 GAGHRSAYVPSVADILQIGWATAAAWSILOQLFLSLTFPRRLEAVEMEDDDFTASLSKQ 953  
Qy 961 SCITEQTQYFFDNDKSFSGVLDGNCNRIFPHGEKLMNTNLIFIMVESKGTCCPTRLLI 1020  
Db 954 SCITEQTQYFFDNDKSFSGVLDGNCNRIFPHGEKLMNTNLIFIMVESKGTCCPTRLLI 1013  
Qy 1021 QAEQTSDEPNCDMVKQPRYRKGPVCFDNNVLEDTDCGGVS 1063  
Db 1014 QAEQTSDEPNCDMVKQPRYRKGPVCFDNNVLEDTDCGGVS 1056



Db 1014 QAEQSDGPNPCDMVOPRYRKGPVCFDNNVLEDYDCGGVS 1056

RESULT 11

US-08-455-543A-53

; Sequence 53, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; METHODS

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,543A

; FILING DATE: May 31, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/223,305

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/869,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/176,899

; FILING DATE: 04-APR-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 6362-52517

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)238-0082

; TELEFAX: (619)238-0999

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1103 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-455-543A-53

Query Match 98.6%; Score 5523; DB 1; Length 1103;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1055; Conservative 0; Mismatches 1; Indels 26; Gaps 2;  
Qy 1 MAAGCLLALTLTQSLIGSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGVGNQVLDI 60  
Db 1 MAAGCLLALTLTQSLIGSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGVGNQVLDI 60  
Qy 61 YEKYODLYTVPNNARQVETAAARDIEKLLSNRSKALVSLALEAEKQAAHQRDEFASN 120  
Db 61 YEKYODLYTVPNNARQVETAAARDIEKLLSNRSKALVSLALEAEKQAAHQRDEFASN 120  
Qy 121 EVVYVNAKDDLDPKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 EVVYVNAKDDLDPKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
Qy 181 NELNMTSALDEYFKKNREEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
Db 181 NELNMTSALDEYFKKNREEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240  
Qy 241 RPYIQGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLETSLSDDDFVNVSFNSNAQ 300  
Db 241 RPYIQGAASPKDMLILVDVSGVSGTLTKLIRTSVSEMLETSLSDDDFVNVSFNSNAQ 300  
Qy 301 VSCFQHLVQANVRNKKVLDVANNITAKGITYDKKGFSAFEOQLLNYSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDVANNITAKGITYDKKGFSAFEOQLLNYSRANCNKIIML 360  
Qy 361 FTGGERAQEIENKYNKDKKRVFRFVSGOHNYERGIQWACENKGGYIYEPSIGAIR 420  
Db 361 FTGGERAQEIENKYNKDKKRVFRFVSGOHNYERGIQWACENKGGYIYEPSIGAIR 420  
Qy 421 INTQEYLDVLGRPMVLAGDKAKOVQWNTNVYLDALGLVITGTLPVFNITGQFENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLAGDKAKOVQWNTNVYLDALGLVITGTLPVFNITGQFENKTNLK 480  
Qy 481 NQLILGVNGVDVSLIEDIKRLTPRETLPNGYFFAIDPNGYVLLHPNLPQK 540  
Db 481 NQLILGVNGVDVSLIEDIKRLTPRETLPNGYFFAIDPNGYVLLHPNLPQK 540  
Qy 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYI 581  
Db 541 LRKRRPNIQNPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYI 600  
Qy 582 DKGNRITYTWPVNGDYSLALVLPITYFYIYAKLEETITQARSKKGMKSEILKPNF 641  
Db 601 DKGNRITYTWPVNGDYSLALVLPITYFYIYAKLEETITQARSKKGMKSEILKPNF 653  
Qy 642 EESGYTFIAPRDYCNLDKISDNNTTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 701  
Db 654 EESGYTFIAPRDYCNLDKISDNNTTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 713  
Qy 702 ELVQYWSKQKNIKGVARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSLDNDNY 761  
Db 714 ELVQYWSKQKNIKGVARFVTDGGITRVYPKEAGENQENPEYEDSFYKRSLDNDNY 773  
Qy 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGIIKIDVNSWTENTKTSIRDP 821  
Db 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGIIKIDVNSWTENTKTSIRDP 833  
Qy 822 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYA 881  
Db 834 CAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYA 893  
Qy 882 FNKSYDYQSVCEPGAAPKOGAGHRSAYVSVADILQIGWATAAAWSILQOQLLSLTFPR 941  
Db 894 FNKSYDYQSVCEPGAAPKOGAGHRSAYVSVADILQIGWATAAAWSILQOQLLSLTFPR 953  
Qy 942 LLEAVEMEDDDFTASLSKQSCITEQTYQFFDNDKSKFSFSGVLDGCGNCSRIFPHGKLMNTNL 1001  
Db 954 LLEAVEMEDDDFTASLSKQSCITEQTYQFFDNDKSKFSFSGVLDGCGNCSRIFPHGKLMNTNL 1013

QY 1002 IFIWKSGKTCPCDTRLLIQABQTSDBGNPCDMVKOPRYRKGDVCFDNNVLEDYTDGCG 1061  
Db 1014 IFIWKSGKTCPCDTRLLIQABQTSDBGNPCDMVKOPRYRKGDVCFDNNVLEDYTDGCG 1073  
QY 1062 VS 1063  
Db 1074 VS 1075

RESULT 12  
US-08-223-305C-53  
Sequence 53, Application US/08223305C  
Patent No. 5851824  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/223,305C  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
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APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

FRAGMENT TYPE: internal  
US-08-223-305C-53

Query Match 98.6%; Score 5523; DB 2; Length 1103;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1055; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLFQSLLLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
Db 1 MAAGCLLALTTLFQSLLLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHOWREDFASN 120  
Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHOWREDFASN 120  
QY 121 EYVYNNAKDDLPKNDSEPPGSGRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTIVL 180  
Db 121 EYVYNNAKDDLPKNDSEPPGSGRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTIVL 180  
QY 181 NELNMTSALDEVPKKNREEDPSLLQVFGSATGLARYYPASPMVDNSRTPNKIDLDVRR 240  
Db 181 NELNMTSALDEVPKKNREEDPSLLQVFGSATGLARYYPASPMVDNSRTPNKIDLDVRR 240  
QY 241 RPWYIQGAASPDKMLILVDVSGSVGLTLKLI RTSYSEMLETLSDDDFVNVASFNSNAQD 300  
Db 241 RPWYIQGAASPDKMLILVDVSGSVGLTLKLI RTSYSEMLETLSDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYKKGFSFAFEOQLLNNVSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYKKGFSFAFEOQLLNNVSRANCNKIIML 360  
QY 361 FTDGGEERAQELFNKYNKDKKVRFRFSYGOHNYERGPIQWACENKGGYIYEPSIGAIR 420  
Db 361 FTDGGEERAQELFNKYNKDKKVRFRFSYGOHNYERGPIQWACENKGGYIYEPSIGAIR 420  
QY 421 INTQEYLDVLGRPMVLADGKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLADGKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480  
QY 481 NQILGVMGVDVSLEDIKRLTPRTLCPNGYIFAIDPNGVVLHPNLQPK-----530  
Db 481 NQILGVMGVDVSLEDIKRLTPRTLCPNGYIFAIDPNGVVLHPNLQPK-----530  
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRKNMIDGESGEKTFRLVKSQDERYI 581  
Db 531 -----NPKSQEPVTLDFDAELENDIKVEIRKNMIDGESGEKTFRLVKSQDERYI 581  
QY 581 LKRRRNIONPKSQEPVTLDFDAELENDIKVEIRKNMIDGESGEKTFRLVKSQDERYI 600  
Db 581 LKRRRNIONPKSQEPVTLDFDAELENDIKVEIRKNMIDGESGEKTFRLVKSQDERYI 600  
QY 601 DKGNTYTTVPVNGTDYSLALVLPYTFYIYKAKLEETITQARY-----SETLKPDNF 641  
Db 601 DKGNTYTTVPVNGTDYSLALVLPYTFYIYKAKLEETITQARY-----SETLKPDNF 641  
QY 642 EESGYTFIAPRDYCNLDKISDNTEFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 701  
Db 642 EESGYTFIAPRDYCNLDKISDNTEFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTN 701  
QY 701 ELVQNTWSKQKNIKGVKARFVVDGGITRVYPKEAGENWQENPETEYDSFYKSLSDNDNY 761  
Db 701 ELVQNTWSKQKNIKGVKARFVVDGGITRVYPKEAGENWQENPETEYDSFYKSLSDNDNY 761  
QY 761 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 821  
Db 761 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 821  
QY 822 CAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGIDPSLMRHLVNISVYA 881  
Db 822 CAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGIDPSLMRHLVNISVYA 881  
QY 882 FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADILQIGWATAAANSILOQFLLSLTFPR 941  
Db 882 FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADILQIGWATAAANSILOQFLLSLTFPR 941  
QY 894 FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADILQIGWATAAANSILOQFLLSLTFPR 953  
Db 894 FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADILQIGWATAAANSILOQFLLSLTFPR 953  
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFPFDNDSKSFSGVLDCGNC-SRIFPHGEKLMNTNL 1001  
Db 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFPFDNDSKSFSGVLDCGNC-SRIFPHGEKLMNTNL 1001

SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-455-543A-55

Query Match 98.3%; Score 5503; DB 1; Length 1079;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1050; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

QY 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
DB 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
QY 121 EYVYNKADDDLPKNDSEPGSQRIKPVIEDANFGROISYOHAAVHIPTDIYEGSTIVL 180  
DB 121 EYVYNKADDDLPKNDSEPGSQRIKPVIEDANFGROISYOHAAVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEVEFKKNREEDPSLLQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR 240  
DB 181 NELNWTSSALDEVEFKKNREEDPSLLQVFGSATGLARYYPASVPWVNSRTPNKIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFNVASFNSNAQD 300  
DB 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSEAFEOALLNVNVRNCRNKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSEAFEOALLNVNVRNCRNKIIML 360  
QY 361 FTDGGEERAQEIENKYNKDKKVRVFRFVSGQHNHYERGPIOMMACENKGYIYEIPSGAIR 420  
DB 361 FTDGGEERAQEIENKYNKDKKVRVFRFVSGQHNHYERGPIOMMACENKGYIYEIPSGAIR 420  
QY 421 INTQEVLDVLRPMVLGADRAKQVQNTNVDLALGLGLVITGILPVFNITGQENKTNLK 480  
DB 421 INTQEVLDVLRPMVLGADRAKQVQNTNVDLALGLGLVITGILPVFNITGQENKTNLK 480  
QY 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYIFADPNQYVLLHPNLQPKNSQEPVTL 540  
DB 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYIFADPNQYVLLHPNLQPKNSQEPVTL 540  
QY 541 DFDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDYSL 600  
DB 541 DFDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDYSL 600  
QY 595 DFDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDYSL 595  
DB 595 DFDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTTWTPVNGTDYSL 595  
QY 601 ALVLPYTSFYIKAKLEETITQARSKKGKMKDSITLKPDPNFEESGYFTIAPRDCNDLKI 660  
DB 601 ALVLPYTSFYIKAKLEETITQARSKKGKMKDSITLKPDPNFEESGYFTIAPRDCNDLKI 660  
QY 648 ALVLPYTSFYIKAKLEETITQARY-----SETLKPDPNFEESGYFTIAPRDCNDLKI 648  
DB 648 ALVLPYTSFYIKAKLEETITQARY-----SETLKPDPNFEESGYFTIAPRDCNDLKI 648  
QY 720 SDNNTFLLNPNFIDRKTNNPCNADLINRVLLDAGFTNELQVYWSKOKNKGKVAR 720  
DB 720 SDNNTFLLNPNFIDRKTNNPCNADLINRVLLDAGFTNELQVYWSKOKNKGKVAR 720  
QY 708 SDNNTFLLNPNFIDRKTNNPCNADLINRVLLDAGFTNELQVYWSKOKNKGKVAR 708  
DB 708 SDNNTFLLNPNFIDRKTNNPCNADLINRVLLDAGFTNELQVYWSKOKNKGKVAR 708  
QY 780 FVVTGGITRVYKPEAGENWQENPETEYDSFYKRSLDNDNVFVAPYFNKSGPGAYESGI 780  
DB 780 FVVTGGITRVYKPEAGENWQENPETEYDSFYKRSLDNDNVFVAPYFNKSGPGAYESGI 780  
QY 768 FVVTGGITRVYKPEAGENWQENPETEYDSFYKRSLDNDNVFVAPYFNKSGPGAYESGI 768  
DB 768 FVVTGGITRVYKPEAGENWQENPETEYDSFYKRSLDNDNVFVAPYFNKSGPGAYESGI 768  
QY 840 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGVPCDKRNSVDMCVI 840  
DB 840 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGVPCDKRNSVDMCVI 840  
QY 900 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSYDQSVCEPAAAPKQ 900  
DB 900 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSYDQSVCEPAAAPKQ 900  
QY 888 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSYDQSVCEPAAAPKQ 888  
DB 888 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSYDQSVCEPAAAPKQ 888

RESULT 13  
US-08-455-543A-55  
; Sequence 55, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,543A  
; FILING DATE: May 31, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/223,305  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; NAME: Seigman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-52517  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 55:

QY 901 GAGHSAYPSVADILQIGWATAAWSILOQFLLSLTTPRLLAEVEMEDDDFTASLSKO 960  
Db 889 GAGHSAYPSVADILQIGWATAAWSILOQFLLSLTTPRLLAEVEMEDDDFTASLSKO 948  
QY 961 SCITEQTYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020  
Db 949 SCITEQTYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1008  
QY 1021 QABQTSQGNPCDMVKOPRYRGPDVCFDNNVLEDYTDGCGVS 1063  
Db 1009 QABQTSQGNPCDMVKOPRYRGPDVCFDNNVLEDYTDGCGVS 1051

## RESULT 14

US-08-223-305C-55  
; Sequence 55, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1079 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-223-305C-55

Query Match 98.3%; Score 5503; DB 2; Length 1079;

Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1050; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

QY 1 MAAGCILLALTTLFOSLLIGPSSERPSPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
Db 1 MAAGCILLALTTLFOSLLIGPSSERPSPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSALAEAEKVQAAHQWREDFASN 120  
Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSALAEAEKVQAAHQWREDFASN 120  
QY 121 EYVYNKADLDPEKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EYVYNKADLDPEKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSAIDVEFKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKLIDLDVRR 240  
Db 181 NELNWTSAIDVEFKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKLIDLDVRR 240  
QY 241 RPWYIQGAASPDKMLILVDVSGVSGTLTKLIRTSVSEMLETSLSDDDFVNVASFNSNAOD 300  
Db 241 RPWYIQGAASPDKMLILVDVSGVSGTLTKLIRTSVSEMLETSLSDDDFVNVASFNSNAOD 300  
QY 301 VSCFQHLVOANVRNKKVLDVANNITAKGITDYKKGFSFAFQOLLNYSRANCNKIIML 360  
Db 301 VSCFQHLVOANVRNKKVLDVANNITAKGITDYKKGFSFAFQOLLNYSRANCNKIIML 360  
QY 361 FTDGGERAQEIFNKYKDKKVRFRFSVGQHNRYERGPIQWMACENKGYIYEPSIGAIR 420  
Db 361 FTDGGERAQEIFNKYKDKKVRFRFSVGQHNRYERGPIQWMACENKGYIYEPSIGAIR 420  
QY 421 INTQEYLDVLGRPMVLADGKAKQVQNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLADGKAKQVQNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480  
QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPNGVYLHPNLPKNPQSQBPTVL 540  
Db 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPNGVYLHPNLPKNPQSQBPTVL 540  
QY 541 DFLDAELENDDIKVEIRNKMIDGESGKFTTLVKSDERYIDKGNRTYTTWTPVNGTDYSL 600  
Db 541 DFLDAELENDDIKVEIRNKMIDGESGKFTTLVKSDERYIDKGNRTYTTWTPVNGTDYSL 600  
QY 596 ALVLPYISFYIKAKLEETITQARSKKGMKMSSETLKPDNFEESGYTFIAPRDYCNLDKI 648  
Db 596 ALVLPYISFYIKAKLEETITQARSKKGMKMSSETLKPDNFEESGYTFIAPRDYCNLDKI 648  
QY 661 SDNTEFLNFEFIDRKTPNPNPCSNADLINRVLLDAGFTNELVQNYWSKQKIKGVKAR 720  
Db 661 SDNTEFLNFEFIDRKTPNPNPCSNADLINRVLLDAGFTNELVQNYWSKQKIKGVKAR 720  
QY 708 SDNTEFLNFEFIDRKTPNPNPCSNADLINRVLLDAGFTNELVQNYWSKQKIKGVKAR 708  
Db 708 SDNTEFLNFEFIDRKTPNPNPCSNADLINRVLLDAGFTNELVQNYWSKQKIKGVKAR 708  
QY 721 FVYTDGGLTRVYPKEAGENWOENPETEYDSFYKRSLDNDNYVFTAPVFNKSGPGAESGI 780  
Db 721 FVYTDGGLTRVYPKEAGENWOENPETEYDSFYKRSLDNDNYVFTAPVFNKSGPGAESGI 780  
QY 769 MYSKAVEIYIQGLKLPVAVGVIKIDVNSWIENTFKTSIRDPACGVCDCCKRNSDVMDCVI 840  
Db 769 MYSKAVEIYIQGLKLPVAVGVIKIDVNSWIENTFKTSIRDPACGVCDCCKRNSDVMDCVI 840  
QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSITYDSVCEPAAKQ 900  
Db 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSITYDSVCEPAAKQ 900  
QY 888 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSITYDSVCEPAAKQ 888  
Db 888 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISVAFNKSITYDSVCEPAAKQ 888



Mon Jul 23 08:36:36 2001

Search completed: July 23, 2001, 07:39:25  
Job time: 552 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:38:14 ; Search time 84.28 Seconds  
(without alignments)  
960.768 Million cell updates/sec

Title: US-09-397-548-17  
Perfect score: 5599  
Sequence: 1 MAAGCLLALTLFQSLIIG.....PDVCFDNNVLEDTDCGGVS 1063

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5599	100.0	1091	2 JH0565	calcium channel al
2	5390	96.3	1091	2 A4147	calcium channel pr
3	5380.5	96.1	1106	1 CHRBA2	calcium channel pr
4	1119.5	20.0	1091	2 T30256	calcium channel al
5	607	10.8	734	2 S44617	C50C3.11 protein
6	580.5	10.4	1148	2 T18770	probable calcium c
7	198	3.5	1450	2 C66880	inter-alpha-trypsi
8	194.5	3.5	886	2 S54355	inter-alpha-trypsi
9	185	3.3	885	2 S30350	inter-alpha-trypsi
10	164.5	2.9	889	2 JC5576	variant-specific s
11	161	2.9	2706	2 T28155	p-type cation tran
12	159	2.8	1984	2 A44396	hypothetical prote
13	157.5	2.8	575	2 D64958	RAD2 endonuclease
14	155	2.8	2364	2 E71619	cytotoxin L - Clos
15	155	2.8	946	1 IYH084	inter-alpha-trypsi
16	154.5	2.8	1315	2 T28679	fibrinogen-binding
17	154.5	2.8	932	2 JC5953	inter-alpha-inhibi
18	153	2.7	1291	2 S46431	botulinum neurotox
19	152	2.7	1291	2 A49777	hypothetical prote
20	152	2.7	1291	2 S76691	inter-alpha-trypsi
21	151.5	2.7	420	2 JC4625	methyl-accepting c
22	150.5	2.7	921	2 A69656	proteinase (EC 3.4
23	150	2.7	654	2 F64688	inter-alpha-trypsi
24	149	2.7	459	2 JX0368	rhodopy protein -
25	149	2.7	930	2 T28676	DNA-directed DNA p
26	148.5	2.7	2401	2 S25855	hypothetical prote
27	148	2.6	964	2 B72420	hypothetical prote
28	146.5	2.6	1285	2 S24885	hypothetical prote
29	146	2.6	4688	2 F82885	hypothetical prote

hypothetical prote  
probable retroelem  
hypothetical prote  
cellulose 1,4-beta  
fibronectin-binding  
inter-alpha-trypsi  
hypothetical prote  
C50C3.10 protein -  
P115 homolog - Met  
glucosyltransferas  
reticulocyte-bind  
rhodopy protein -  
toxin A - Clostrid  
apolipoprotein prec  
protective antigen  
parasporal crystal

30 145.5 2.6 676 2 T47637  
31 145.5 2.6 689 2 F84811  
32 145.5 2.6 5005 2 F82884  
33 144 2.6 1087 1 S41797  
34 144 2.6 1091 2 S33850  
35 143 2.6 946 2 JC5575  
36 143 2.6 1864 2 T18485  
37 142.5 2.5 382 2 S44618  
38 142 2.5 1169 2 A64505  
39 142 2.5 1599 2 S22737  
40 141 2.5 1252 2 B42771  
41 140.5 2.5 2269 2 T28677  
42 140 2.5 2710 2 A37052  
43 140 2.5 3305 2 T18358  
44 139.5 2.5 764 2 T19934  
45 139 2.5 1180 2 A26858

ALIGNMENTS

RESULT 1  
JH0565  
calcium channel alpha-2b chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999  
C:Accession: JH0565  
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B.  
Neuron 8, 71-84, 1992  
A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of  
A:Reference number: JH0564; MUID:92110010  
A:Accession: JH0565  
A:Molecule type: mRNA  
A:Residues: 1-1091 <WIL>  
A:Cross-references: GB:M76559; NID:gl79761; PIDN:AAA51903.1; PID:gl79762  
A:Experimental source: basal ganglia  
A:Note: Several conflicts are found between GenBank submission, authors' translation  
C:Comment: This protein is a subunit of the voltage dependent calcium channel.  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: glycoprotein; phosphoprotein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>  
F;32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase  
F;91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #  
F;92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca  
F;501/Binding site: phosphate (Thr) (covalent) #status predicted  
F;833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 100.0%; Score 5599; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFQSLIIGPSSEPPSPSATYIKSWDKMOEDLVTLAKTAGSNQLYDI 60  
|||||  
DB 1 MAAGCLLALTLFQSLIIGPSSEPPSPSATYIKSWDKMOEDLVTLAKTAGSNQLYDI 60  
|||||

QY 61 YEKQDLYTFVFNARQIVETAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120  
|||||

DB 61 YEKQDLYTFVFNARQIVETAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120  
|||||

QY 121 EYVYNNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
|||||

DB 121 EYVYNNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
|||||

QY 181 NELNNTSALDEYFKKNREDDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
|||||

DB 181 NELNNTSALDEYFKKNREDDPSLLMQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240  
|||||

QY 241 RPWYTOGAASPKDMLILVDVSGVSLTLKLTITSVSEMLETISDDDFVNFASFNSNAOD 300  
|||||

DB 241 RPWYTOGAASPKDMLILVDVSGVSLTLKLTITSVSEMLETISDDDFVNFASFNSNAOD 300  
|||||



QY 301 VSCFHLVQVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLLNLYNVRANCNKIIML 360  
Db 301 VSCFHLVQVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLLNLYNVRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKYNKDKKVRFRFVSQGHNYERGPQIOWMACENKGYEYIPIPSIGAIR 420  
Db 361 FTDGGEERAQEIFNKYNKDKKVRFRFVSQGHNYERGPQIOWMACENKGYEYIPIPSIGAIR 420  
QY 421 INTQYLDVLGRPMVLGADKAKQVQWNTVYLDALGLVITGTLVPFNITGQFENKTNLK 480  
Db 421 INTQYLDVLGRPMVLGADKAKQVQWNTVYLDALGLVITGTLVPFNITGQFENKTNLK 480  
QY 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPQLKPKSQEPVTL 540  
Db 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPQLKPKSQEPVTL 540  
QY 541 DFLDAELENKDIKVEIRNKMIDGESGEKFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELENKDIKVEIRNKMIDGESGEKFTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFTIAPRDYCNLKI 660  
Db 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFTIAPRDYCNLKI 660  
QY 661 SDNNTFELLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720  
Db 661 SDNNTFELLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720  
QY 721 FVVTGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNDYFTAPYFNKSGPGAYESGI 780  
Db 721 FVVTGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNDYFTAPYFNKSGPGAYESGI 780  
QY 781 MYSKAVEIYIQGLKLPKPAVVGKIDVNSWIENTFTKTSIRDCAGPVCCKRNSDVMDCVI 840  
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Db 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 900  
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Db 901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
QY 961 SCITETQYFFDNDKSGVGLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
Db 961 SCITETQYFFDNDKSGVGLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLLI 1020  
QY 1021 QAEQTSQDGNPCDMVKQPRYKGPDPVCPDNNVLEDTDCGGVS 1063  
Db 1021 QAEQTSQDGNPCDMVKQPRYKGPDPVCPDNNVLEDTDCGGVS 1063

RESULT 2  
A44147  
calcium channel protein alpha-2 chain precursor - rat  
N:Alternate names: dihydropyridine-sensitive L-type  
N:Contains: calcium channel alpha-2 chain  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 20-Aug-1999  
C:Accession: A44147  
R:Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.  
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992  
A:Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive  
A:Reference number: A44147  
A:Accession: A44147  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1091 <KIT>  
A:Cross-references: GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 96.3%; Score 5390; DB 2; Length 1091;  
Best Local Similarity 95.8%; Pred. No. 0;  
Matches 1019; Conservative 24; Mismatches 19; Indels 2; Gaps 2;

QY 1 MAAGCLLALTTLTFLSLLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVQNLVDI 60  
Db 1 MAAGCLLALTTLTFLSLLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVQNLVDI 60  
QY 61 YEKYODLYATVPENNAQOLVETAAARDIEKLLSNRSKALYSALAEAEKVQAAHWRDEFASN 120  
Db 61 YEKYODLYATVPENNAQOLVETAAARDIEKLLSNRSKALYSALAEAEKVQAAHWRDEFASN 120  
QY 121 EVVYNNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYNNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKLIDLYDVR 240  
Db 181 NELNWTALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKLIDLYDVR 240  
QY 241 RPWYTOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETSLDDDFYNVASFNSNAOD 300  
Db 241 RPWYTOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETSLDDDFYNVASFNSNAOD 300  
QY 301 VSCFHLVQVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLLNLYNVRANCNKIIML 360  
Db 301 VSCFHLVQVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLLNLYNVRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKYNKDKKVRFRFVSQGHNYERGPQIOWMACENKGYEYIPIPSIGAIR 420  
Db 361 FTDGGEERAQEIFNKYNKDKKVRFRFVSQGHNYERGPQIOWMACENKGYEYIPIPSIGAIR 420  
QY 421 INTQYLDVLGRPMVLGADKAKQVQWNTVYLDALGLVITGTLVPFNITGQFENKTNLK 480  
Db 421 INTQYLDVLGRPMVLGADKAKQVQWNTVYLDALGLVITGTLVPFNITGQFENKTNLK 480  
QY 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPQLKPKSQEPVTL 540  
Db 481 NQILILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPQLKPKSQEPVTL 540  
QY 541 DFLDAELENKDIKVEIRNKMIDGESGEKFTLVKSQDERYIDKGNRTYTWTPVNGTDY 599  
Db 541 DFLDAELENKDIKVEIRNKMIDGESGEKFTLVKSQDERYIDKGNRTYTWTPVNGTDY 599  
QY 600 LALVLPYTFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFTIAPRDYCNL 659  
Db 600 LALVLPYTFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFTIAPRDYCNL 659  
QY 660 ISDNTEFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIKGVK 719  
Db 660 ISDNTEFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIKGVK 719  
QY 720 RVVVTGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNDYFTAPYFNKSGPGAYES 779  
Db 720 RVVVTGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNDYFTAPYFNKSGPGAYES 779  
QY 780 IMVSXAVEIYIQGLKLPKPAVVGKIDVNSWIENTFTKTSIRDCAGPVCCKRNSDVMDCV 839  
Db 780 IMVSXAVEIYIQGLKLPKPAVVGKIDVNSWIENTFTKTSIRDCAGPVCCKRNSDVMDCV 839  
QY 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPGAAPK 899  
Db 840 ILDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPGAAPK 899  
QY 900 QGAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLAEVEMEDDDFTASLSK 959  
Db 900 QGAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLAEVEMEDDDFTASLSK 959  
QY 960 QSCITEQYFFDNDKSGVGLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLL 1019  
Db 960 QSCITEQYFFDNDKSGVGLDCGNCRIHFHGEKLMNTNLIIFIMVESKGTGCPDTRLL 1019

QY 1020 IQAETSDGPNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCVS 1063  
 Db 1020 MQAETSDGPNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCVS 1063  
 RESULT 3  
 CHRNA2  
 calcium channel protein alpha-2 chain precursor - rabbit  
 N:Alternate names: dihydropyridine-binding protein, 140K  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 22-Jun-1999  
 C:Accession: S10579; A33409  
 R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell  
 Science 241, 1661-1664, 1988  
 A:Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of  
 A:Reference number: S10579; MUID:88336904  
 A:Accession: S10579  
 A:Molecule type: mRNA  
 A:Residues: 1-1106 <ELL>  
 A:Cross-references: EMBL:M21948; NID:g164762; PID:AA81562.1; PID:g164763  
 A:Note: This sequence represents the amino end of a glycosylated peptide that appears at  
 e at the amino end and identical molecular weights (17K) following deglycosylation  
 R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.  
 Biochemistry 28, 7820-7828, 1989  
 A:Title: Subunit composition of the purified dihydropyridine binding protein from skelet  
 A:Reference number: A39518; MUID:91131638  
 A:Accession: A39518  
 A:Molecule type: protein  
 A:Residues: 961-973 <JAY>  
 A:Note: This sequence represents the amino end of a glycosylated peptide that appears at  
 e at the amino end and identical molecular weights (17K) following deglycosylation  
 R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.  
 Biochemistry 28, 7820-7828, 1989  
 A:Title: Subunit composition of the purified dihydropyridine binding protein from skelet  
 A:Reference number: A33409; MUID:9012765  
 A:Accession: A33409  
 A:Molecule type: protein  
 A:Residues: 27-44, 'S', 46-47 <HAW>  
 C:Superfamily: calcium channel alpha-2 chain  
 C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph  
 F:1-26/Domain: signal sequence status predicted <SIG>  
 F:27-1106/Product: calcium channel alpha-2 chain status predicted <MAT>  
 F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:  
 Query Match 96.1%; Score 5380.5; DB 1; Length 1106;  
 Best Local Similarity 94.8%; Pred. No. 0;  
 Matches 1029; Conservative 15; Mismatches 12; Indels 29; Gaps 4;  
 QY 1 MAAGCLLALTLTQFQ--LLIGPSSEPPFPFSAVTIKSWDKMQEDLVTLAKTASGVNQLV 58  
 Db 1 MAAGRPLAWTLTQWMLLIGPSSEPPFPFSAVTIKSWDKMQEDLVTLAKTASGVHQLV 60  
 QY 59 DIYEKYQDLTYVEPNNAQLVEIARIEKLLSNRSLVSLALEAEKVAQAAHQWREDF 118  
 Db 61 DIYEKYQDLTYVEPNNAQLVEIARIEKLLSNRSLVSLALEAEKVAQAAHQWREDF 120  
 QY 119 SNEVYVNAKDDLPENKDDSPGSGRIKPVIEDANFGRIQSYQHAHVHIPTDIYEGSTI 178  
 Db 121 SNEVYVNAKDDLPENKDDSPGSGRIKPVIEDANFGRIQSYQHAHVHIPTDIYEGSTI 180  
 QY 179 VINELNWT-SALDEVFKKREDDPSLLMQVFGSATGLARYYPASVPWDSRTPNKIDLYDV 238  
 Db 181 VINELNWT-SALDEVFKKREDDPSLLMQVFGSATGLARYYPASVPWDSRTPNKIDLYDV 240  
 QY 239 RRRPWTIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETISDDDEVNVAFSNSA 298  
 Db 241 RRRPWTIOGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETISDDDEVNVAFSNSA 300  
 QY 299 QDVSCFOHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNVNVRANCKII 358  
 Db 301 QDVSCFOHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAFEQLLNVNVRANCKII 360  
 Query Match 20.0%; Score 1119.5; DB 2; Length 1091;  
 RESULT 4  
 T30256  
 calcium channel alpha-2-delta-C chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 20-Jun-2000  
 A:Accession: T30256  
 R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.  
 J. Neurosci. 19, 648-691, 1999  
 A:Title: Molecular diversity of the calcium channel alpha2delta subunit.  
 A:Reference number: 220794  
 A:Accession: T30256  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1091 <KLU>  
 A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1  
 A:Experimental source: brain  
 C:Superfamily: calcium channel alpha-2 chain

Best Local Similarity 28.5%; Pred. No. 2.3e-59;		Matches 321; Conservative 230; Mismatches 443; Indels 131; Gaps 41;	
QY	3	AGCLLALTTLFOSLIGSPSEPPFSATVITKSWDKMOEDLVTLAKTAGSGVNLVDIYE	62
Db	14	ASALLA-TALLYAALGDVVRSEQIPLSV-VKLWAFSGEIKSIAKYSGSOLLQKKYK	71
QY	63	KYQDLVTVPEPNARQVLVEIAARDIEKLLNSRKALVSLALEAKVQAQAHQWRDFASNEV	122
Db	72	EYKQVAIEIDGLQVLKLAIMEEMFKKSEAVRLVEAABEHLKHEFDADL--QY	128
QY	123	VYNAK--DDLDEKNDSEPGSORIIPVTFEDANFR-QISYQHAHVHPTDIEGSTIV	179
Db	129	EYFNAVILNERDDGNFLELKGFEI--LAPNDHFNNLPVNISLSDVQVPTNNYKDPAI	185
QY	180	LNELNLTALDEYFKKNNREDPSLLWQVFSATGLARIYPASPWVDNSRTPNKLIDYVR	239
Db	186	VNGVWSESLNKVFDVDFDRPSLIWQVFSAGKFFRQVPGIKWEPD--NGVIAFDCR	242
QY	240	RRPWYIOGAASPKDMLILVDVSGVSGLTLLKLRISVSEMLETISDDDFVNASPNSNAQ	299
Db	243	NRWYIOGAATSPKDVVTLVDVSGSMKGLRTIAKQTVSSILDTLGDDEFNIITYNEELH	302
QY	300	DVS-CFQ-HLVQANVRNKKVYLKDAVNNTAKGTYDKKGFSEAFQOLLNVNVRAN--CN	355
Db	303	YVEPCLNGTLVQADRTNKEHREHLDKLFRAGIGMLDIALNEAFNILSDFNHTGQSICS	362
QY	356	KIIMFLTDGGEERAQEIFNKYN-KDKKVRVFRFSVGQHNRYERGIOWMACENKGYIYEIP	414
Db	363	QAIMLITDGAVDYDTIFAKYNWDRKVRIFTYILIGREAAAFADNLKWMACANKGFFQIS	422
QY	415	SIGAIRNTQBYLDVGRPWVLAGDKAKQVQWTVYLD-----ALEGLVI--TGT	463
Db	423	TLADVQNVMEYHLVSRPKVI--DQEHVVTVEAYIDSTLPQAQKLADQGLVMTVA	480
QY	464	LPVNITQGFENKTNLKNOLITGVMGVDVSLDEIKRTPRTPLCPNGYIYFADPNGVLL	523
Db	481	MPVFS---KQNETRSG-ILLGVVGTDVVKELLKIPYKLGIIHYAFATNNGVILT	535
QY	524	HPNLQP---KNPKSQEP--VTLDFDLAELENDIKVEIRNKMIDGESGKTRTLVKSQDE	578
Db	536	HPELRPLYEECKRRKPNYSVDLSEVEDRDOV-LRNAMVRNKTGK--FSMEVK----	588
QY	579	RYIDKGNPT-----YWPVTVNGTDYSLALVLPY-YEFYIYKALETITQARSKKGMK	631
Db	589	KTVDKGRVLVMTNDYITDITKGFPSLGVALSRGHGKIYF-----RGNTV	634
QY	632	DSETLKPDPNEESGYTFIAPRDCN-DLKISDNTEFLNFEFIDRKTNNPNSCNADLI	690
Db	635	IEEGL--HDLEHPDVSLADEWSYCNLDLHPHRHLSQLEAIKLYLKKEP--LLQCDKELI	691
QY	691	NRVLIDAGFTNELVQNYWS-----KQNKIGVKARFVVTDDGTRVYP-----	733
Db	692	QEVLFDA-VVSAPTEAYWTSALAKNSDNDKGVAFVLTGTGLSRINLRFVGAQLTNQD	750
QY	734	KEAGENQENPETYEDSFYKRSLDN--DNYVFTAPY-----FNKSGPGAYESGIWVSKAV	786
Db	751	FLKAGDKENIFNADHFLPWRARAEQIAGSFVYSIPFSTGTGNKS-----NVVTASTSI	804
QY	787	EIYIOGKLLKPAVGIKIDVNSWTFNFKTIRDPACGVPVCDKRNVDVDCVILDDGGF	846
Db	805	QLLDERKSPVVAAGVQMKLEFFORKEFTWASROCASLDGKCSICDDDETVCNYCLIDNNGF	864
QY	847	LIAMNHDYTNQIGRFGCEIDPSLMRHLVNTSVAFNKSIDYQSVCEPGAAPKOGAGHRS	906
Db	865	ILVS--EDIT-OTGDFEFGVAGVANKLMTMGSKFRITLYIQAMCR---ANKSSDSAH	918
QY	907	AYXPSVADILQIGWATAAASILQOFTLLSTFPRLLEAVEMEDDDFTASLSK-----QS	961
Db	919	GLLDYPYKAFL-----SAAKWIMTELVLFLVEF-----NLCSSWHSMDTAKAQLKQLEP	968
QY	962	CITEQOTQFFDNDNSKFSGLVDCGNCRIFFHGEKLMNTNLIFFIVESKGTCPCDRLLIQ	1021
Db			
Db	969	CDTEYPAFVSERTIKETTGNACDCSKSFVIQIIPSSNLFVWVVD--SCLCESVAPIT	1026
QY	1022	ABQTSQDPN---PCDMVKQPRYRKGPVDFCDNNVLEDDYTDGCGVS	1063
Db	1027	MAPIEIRYNESLKCEKRLKAKRRRPSCHGPFPEENARECGGAS	1071
RESULT 5			
S44617			
C50C3.11 protein - Caenorhabditis elegans			
C:Species: Caenorhabditis elegans			
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001			
C:Accession: S44617			
R:Favell, A.D.			
submitted to the EMBL Data Library, May 1993			
A:Description: Sequence of the C. elegans cosmid C50C3.			
A:Reference number: S44618			
A:Accession: S44617			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-734 <PAV>			
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650			
C:Genetics:			
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3			
Query Match 10.8%; Score 607; DB 2; Length 734;			
Best Local Similarity 26.8%; Pred. No. 9.6e-29;			
Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;			
QY	47	LAKTASGNVLVDIYEKYQDLVTVPEPNARQVLVEIAARDIEKLLNSRS----	KALVSLAL 102
Db	36	MKETFSKISHETILKQNYEKLVEEEDFPAELKSKKHRIEDYLKVSQFAYKAKIS--L	93
QY	103	EAEKVQAAHQWRDFASNEVYVYNAKDDLDPEK-NDSEPGSQRIKP-----VFIEDANP	155
Db	94	EARSVRNDSTVNDPQSKSFIRFMSAKQGNDCGTTIYESNHLGKRLKVNRETKSFNLTQANF	153
QY	156	-GROISYQHAHVHPTDIEYEGSTIVLNELNWTSALDEVEKKNNREEDPSLLWQVFGSATGL	214
Db	154	YTLPTSSVSSAVHPTFLYDRNEDLLKIDW-SIDAVYRTNRETKDLAFQLFCSEAGY	212
QY	215	ARYYPASFPW-DNSRTPNKLIDYVRRRPWYIOGAASPKDMLILVDVSGVSGYJTLKLIR	273
Db	213	MRYYPASWFDNQ--DEHLDLFCRNTWYINSATNSKVNILMDNGSMLGQRYEVAK	270
QY	274	TSVSEMLETISDDDFVNVASNSNA---QDVSCFQHLVQANVRNKKVCLKDAVNITAKGI	330
Db	271	QTTEAILETLSHNDYFNIMTFSKNTFLDGCNGTNGLIQATMRNKKALRRKMDTYQSEK	330
QY	331	TDYKGFSAFEQLNLYN-----VSRANCNKLIMFLTDGGEERAQEIFNKYNKDKKVRVF	385
Db	331	AEYEKALPLAFSVLLDINNNGGDNNGACENVIMLTDGAPNAYKKIYFDMNADKKRVF	390
QY	386	RFSVQGNHYERGIOWMACENKGYIYEIPSIGAIRINTQEYL----DVLGRPMVLADGKA	441
Db	391	TFVLGDEAIDNEVREMACNNGRVVHVANMADVDEKTHHVRMSRVVGRHYKESGOLS	450
QY	442	KOVQWTVNVLDALEGL--VITGLPVFNITQGFENKTN-----	478
Db	451	---WTVGVYRERLYLPRPEIFAEPVPIITNQSFVAVNKKASRRKIRLQKSEARSFVITV	507
QY	479	----LKNQLILGVMGVDVSLDIKRLTRPFLTCPNGYIYFADPNGYVLLHPNLQPNP--	532
Db	508	SYPVTVNETFGVAANIPLTEVAQKSHPANIGSKSYFFMLDQNGFVMTHPQLRPIDPFT	567
QY	533	--KQEPVYTLDFD-----	561
Db	568	KYHKQNYNNMDLLEVEGQGNVRSQKSAQVSDLVCSGGANYACVDDLRKAVRKMID	627
QY	562	GESGKTRTLVKSODERY----IDK---GNRTYTWTPVNGTDYSLALVPLTYSYPIKA	614
Db	628	CDNSD-----VQQLDVLVYATLLELDVYTPQINTYYAEICINHANFVLGLAVAKGDDYRVVK	681

QY 615 KLEETITQARSKKGMK 631  
| : : : : :  
Db 682 K-----QKKYDFGRVK 692

RESULT 6  
T18770  
probable calcium channel protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T18770; T25249  
R:Sulston, J.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z19019  
A:Accession: T18770  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1148 <W1>  
A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN000020; CESP:T24F1.6  
A:Experimental source: clone B0491  
R:Chui, C.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z20004  
A:Accession: T25249  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1148 <W12>  
A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN000020; CESP:T24F1.6  
A:Experimental source: clone T24F1  
C:Genetics:  
A:Gene: CESP:T24F1.6  
A:Map position: 2  
A:Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.4%; Score 580.5; DB 2; Length 1148;  
Best Local Similarity 21.2%; Pred. No. 7.7e-27;  
Matches 244; Conservative 217; Mismatches 437; Indels 251; Gaps 43;

QY 37 VDKMQEDVTLA-----KTASGVNOLVDIYEKYQDLYTVPEPNARQLVEIARDI 86  
| : : : : :  
Db 99 VDIIEAPASIAQFSANILRDFQTSRFSLVQEEFKLPDIKSKEDAAEKLRVATEHL 158  
| : : : : :  
QY 87 EKLNSRKALVSLALEAEKVAQHQWREDFASNEVYVYNAKDDLDPKNDSEPGSOR-- 144  
| : : : : :  
Db 159 DRLVTNRVDALKLASSAESAFAVE-----DEYDDQAVAVPADKRC 201  
| : : : : :  
QY 145 --TKPVFIEDANTGROISQIHOH---AAVHIPTDIYEGSTIVLNLNWTSA--LDEVFKNR 197  
| : : : : :  
Db 202 AYMKKNESDMHFVSNM-VEHNSKSGIHITVESYQCDPRVYRDFWTGTGKHLKTSNDK 260  
| : : : : :  
QY 198 EEDPSLLQVFGSATGLARYIPASPVVDNSRTENKIDLYDVRPRPYIQAASPKDMLIL 257  
| : : : : :  
Db 261 EKAPENGHQVIGYISGLTRMYPRRH- KVEPTITIDLPDRFPVFNASVPKDLVFL 319  
| : : : : :  
QY 258 VDVSGVSGTLKIRTSVSEMLETSDDDFVNVSFNSNAQD-VSCFQH-LVQANYRK 315  
| : : : : :  
Db 320 LDYSGVKGPTMLIKITMYILSTLSPNDYFPGVFNHFNFIISCANTEMPTATSNK 379  
| : : : : :  
QY 316 KVLKDAVNNTAKIYDYKGFSAFEQL---LNVNVS-----RANCKIMLFTDGGEE 367  
| : : : : :  
Db 380 KVFPELGMLEEKDOAHFATPLAFSLDLVLRGNLDSNQLSFADYRSEGHKLLIIFTGVDE 439  
| : : : : :  
QY 368 RAQEIFEN---KYNKDKKVRVERFVSQOHNVGPIQWACENKGYIYEIPISGAIRINTO 424  
| : : : : :  
Db 440 WPHQIDEEFQTNSEILIRIFGFSMGYGTSLPLPQQYMACKSHGYSYSEIDSIMDVQPQR 499  
| : : : : :  
QY 425 EYLDVLGRPNVLADGKAK-----QVQNTNVYLDALGLVITGLTPVFNITGQFENKT 477  
| : : : : :  
Db 500 TIONVLSQ---VRGDELKGTNAEKRPSTWOLYNEQGGPIVITLSLPILT-----SEQR 551  
| : : : : :  
QY 478 NLKNQLILGVMGVDVSLEDIKRLTPRTLCPNGYIFADPNPGVYLLHPNLQ-PKNPK--- 533  
| : : : : :

Db 552 IWRDQKLAGVVAIDISIKETKHLP--TSSEQMVGIVDNNGMILYHPQLQIPKTEVHCV 609  
| : : : : :  
QY 534 -----SQEPV-----TIDFLDAELENIDIKVIRN 557  
| : : : : :  
Db 610 RRSACYDAQVKQKAGSGLRVHYGFSDEVRVRLGLDLSIPTLDMYDLEGDSTAIRDLR 669  
| : : : : :  
QY 558 KMIDGESGKTRFLVKQSDERYIDKNRNYTTPVNGTYSALV--LPTYSFYIYKAK 615  
| : : : : :  
Db 670 -----RITTKCYEEAIKDNSKEYHCSHKIDSPFTLVIVNNIOLKTYVYDSDV 717  
| : : : : :  
QY 616 LESTITQ-----ARSKGKMKDSETLKPDNFEESGYTFIAPRDYC--NDLKISDNNT 665  
| : : : : :  
Db 718 QELGLTDNKLVTFFPRDVCQMKLDEYAAHDFRV--WSDISEKEICAQDDMLPRAFT 775  
| : : : : :  
QY 666 EFLINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQVNSKQKNIRKVGARFVYTD 725  
| : : : : :  
Db 776 KGLSMTQSWPKSDIEHTC-----LLAQYPENASVPHYNS-----FVHTR 817  
| : : : : :  
QY 726 GGTRVYPKEAGENQWQENPTYEDSFYKRSLDNDNYYTAPYFNKSGPGAYESIMVSKA 785  
| : : : : :  
Db 818 SKLTAFYPTCTSSHDMKAVNKKFDEEI--KLTDNDFV---QFSMR-----SESLIYRT 866  
| : : : : :  
QY 786 VEIYIOGKLLKPAVVGKIDVN---SWIENFTKTSIRPCAGPVCDCRNSD-----VMD 837  
| : : : : :  
Db 867 IADYDNNRL---AVVGQWKENFDFQYDFDNT-----RQNPDMKICRQKE 908  
| : : : : :  
QY 838 CVILDDGGFLIMAHDDYTNQIGRFFGEIDPSLMRHLNISVAFNKSVDYQSVCEPGAA 897  
| : : : : :  
Db 909 CSIITRNGHVIIASSAHRAHAKLAF---DPQLFESLVKYNLVSTNSWTEVQSECK---- 960  
| : : : : :  
QY 898 PKOGAGHRSAYVPSVADILQIGWATAA--AWSILOQLLSLTFPRLEAVEMEDDDFTA 955  
| : : : : :  
Db 961 -----AKRVAPWSSAAGSSSILRYFTVTSI-----FKLAKTSFWR 995  
| : : : : :  
QY 956 SLSKQSCITEQTOYFFDNDSDKSPGVLDGNC-SRIHGEKLMNTNLIFFIWESKGC-- 1012  
| : : : : :  
Db 996 NLLESALTLDVADQSPMTGNTCTTQKIKPFERCFMKFFHYRMTLNITK-QLQLTGMSTCSR 1054  
| : : : : :  
QY 1013 -----PCDTRLLIOAEQTSQGNP-----CDMVKQPRYRKGPVDCFD--N 1050  
| : : : : :  
Db 1055 YAKLYPVPHTTLSLIITADRACSYRPRKIFESPRKLEKCDVV-HSHARRPDALNDWKI 1113  
| : : : : :  
QY 1051 NVLEDYDC 1059  
| : : : : :  
Db 1114 DLQNKHVDC 1122

RESULT 7  
C86880  
hypothetical protein yvvc [imported] - Lactococcus lactis subsp. lactis (strain IL140  
C:Species: Lactococcus lactis subsp. lactis  
C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: C86880  
R:Solotkin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Eh  
Genome Res. in press, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium.  
A:Reference number: A86625  
A:Accession: C86880  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1450 <STO>  
A:Cross-references: GB:AE005176; NID:gl2725093; PIDN:AAK06141.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: yvvc

Query Match 3.5%; Score 198; DB 2; Length 1450;  
Best Local Similarity 21.0%; Pred. No. 0.0013;  
Matches 242; Conservative 149; Mismatches 439; Indels 322; Gaps 56;

QY 37 VDKMQEDVTLAKTAGVGNOLVDIYEKYQDLYTVPEPNARQLVEIARDIEK-----L 89  
| : : : : :

Db 69 INKTENKELKLFSPGNOPIEIEE--NESWLKENT-----IISDFEKEGKIVL 120  
QY 90 LSNRSKALVLALEAEKVOAHQWR---EDFA-----SNEVYYNA 127  
Db 121 RANNSISLLNLEIQADAKLIENDQEVISEDILAKKESTIFSLVIPPENKADSEKDNKNT 180  
QY 128 KDDLDPEKNDSEPGSORIKP---VFIEDANFGQISVQHAHVH-----167  
Db 181 EEVLNNESSOEETVQKQDSQAFSPNFGIKASPNDLAQNENISPIYRODETGISP 240  
QY 168 ---IPTDIIEGSTIVLNELNWTSALDEVEFKKNEEDPSLLQWFGSATGLARYPASPW 223  
Db 241 NHSWIPT---GNTVVNVHOGWNSF-----SSQWDGVNSWN---GEATWLENSYIEYAG 287  
QY 224 VDN-----STPNKIDLY-DVRRPWWYIOGAASPKDMLILVDVSGVSGITLK 270  
Db 288 VNNPVPFALRKYAKETETPGDYLVNVRGN---VQNPKPVDVLVIDMSGMOGAKET 344  
QY 271 LIKTSVSEMLETISDD---DFVNV--ASFNSAODVSCFOHLVQANVRNKKVLKD---A 321  
Db 345 AVROGVSDFTSTONTAYADYVNVGVISPGNYVTGASGYITVPI--DKVSESEHVKS 402  
QY 322 VNNITA---KGITDYKKGFSFAFEQOLLNVNVRANCKIIMLFTDGGEEAQAQIFNKYNK 378  
Db 403 INQALAPQFSGGTFTQLGRKGTML---EQDSSDNQKMMILMTDG---VPTFSYKVN 455  
QY 379 DKVVR---VFRFSVQGHNYERG---PIQ---WMAENKGYIYEI-----PSGAIKRNTOQE 425  
Db 456 ASKVDNVIYQSGFAESRDEPGNTSKISPYVVKDINGSGNIEIRDTWAATLGEAEISKQE 515  
QY 426 YLDVLGRPMVLAD-----KAKQVQWNVNVLDALEGLVITGLTPVFNITQCFE 474  
Db 516 ISEIHTLGIQMGNDGYSLSOEVEKSRFTSLIATGLYQDANSAN-----DITDYLK 565  
QY 475 NKTN-----LKNQILGVMGVDVSLDIEKRLTPFTLCPNGYVFAIDPNGYVLLHPN 526  
Db 566 NQANVLRSFNTITNGILLDPLGAQFEYKTK-----PEINSVG-----604  
QY 527 LQPNKPSQSPVLDLFDLAELNDIKVEIRNKMIDGESGKTEFTLVKSODEYIDKGNR 586  
Db 605 -----EDSIDNLPKTINEKGLEISNLNI--GNQEVQIHYQVRLNTETDDFKTNY 653  
QY 587 TY-----TTPVNGT--DYSLALVPTYFYIKAKLE-----ETIQARSKK 627  
Db 654 WYQMGTEITLP--NGSPDNKNVFGPSAKSGINLTLEKOWLANSENIPENVELLIGR 712  
QY 628 GKMKDSE-----TLKPDNFEESGYFTIAPRDYCNLDKISDNNTFEFLNFNEFIDRKTNN 682  
Db 713 SAQISSDWTKVTILKEDEWRSQLENLPKYSILGEEFYIEIKDEIVLN--SEIYDWITIGE 771  
QY 683 PSCHADLINRVLD-----AGFTNELVQNVYWSKOKNIKGVKARFVVDGTRVYPKEAGE 738  
Db 772 DKTTIANIEKFRLOIKTSNHDNEPLSEVEFVLKNSOGEEIDKAVTN-----EKGE 822  
QY 739 -NWQENETVEDSFYKSLONDVNVFTAPFNKSGPAYESGYNVSK-----AVEIYIQ 791  
Db 823 ILFDKTRNLNGEEYQLHEIKSPHSGLEGPKTKT---EFENGQPIIKVDGEQIALDEHYN 879  
QY 792 GKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGVPCDKRNSDVMDCVILD---DG-- 844  
Db 880 KFMIS---LNTINDIN--VVEF-----RNSVTIDKRAVDSEKLDGAV 917  
QY 845 -GFLLMANHDYTNQIGRFTGEIDPDSLMRHLNIVSYAFNKSVDYQSCVCPGAAPKOGAG 903  
Db 918 FNLYQIESVDDELTKPL--EITNLLPLGL-----YALQESVSPNGYIRDEV 964  
QY 904 H--RSAVPSVADILQGWATAAANSILOQFL-----LSITF- 939  
Db 965 HFRVKNGSVIAITGSEG-----IDIPFLDENESKNGLVNBEENGDLHLTLIFY 1015  
QY 940 ---PRLEAVEMEDDDFTASLSKQSC--ITEQTYQFPDNDG---KSFSGVLDCGNCRI 990

Db 1016 NQAVPPLQLEVDKIDDDFTSPLAGVSFELTRLGRKSTDSVSKRINSFDRILAKTN--NE 1073  
QY 991 FHGEKL-MMTNL 1001  
Db 1074 FTGETIALKSNL 1085  
RESULT 8  
S54355  
inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 04-Feb-2000  
C:Accession: S54355  
R:Chan, P.; Risler, J.L.; Raguenes, G.; Salier, J.P.  
Biochem. J. 306, 505-512, 1995  
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mou  
A:Reference number: S54353; MUID:95194326  
A:Accession: S54355  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-886 <CHLA>  
A:Cross-references: EMBL:X70993; NID:g695635; PIDN:CAA49843.1; PID:g695636  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match 3.5%; Score 194.5; DB 2; Length 886;  
Best Local Similarity 19.9%; Pred. No. 0.00094;  
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;  
QY 27 FPSAVTIKSVMDKQEDLVLTAKTASGVNQLVDIYKYQDLYTVPEPNARQLVEIAARDI 86  
Db 98 YPGNVKEVEQAQYKAVSQGTAG---LVKASGRKLEKFTVSVNVAAGSKVTFELTY 153  
QY 87 EKLSSRSKALVSLALEAEKVOAHQWRDFAENVEVYVNAKDDLDPEKNDSEPGSORIK 146  
Db 154 EELL-KRNKGKYEMLKVQPKQLVRHFEID-----AHIFEP-----Q 189  
QY 147 PVIEDANFGQISVQHAHVHPTDIYEGSTIVLNELNWTSALDEVEFKKNEEDPSLLQW 206  
Db 190 GISMLDAE-----ASFITNDL-LGSALTQSF-----214  
QY 207 VFGSATGLARYYPASPVWDNSRT-PNKID-----LYDVRRRP-----WYI-- 245  
Db 215 -----SGKKGHVSKFSLDQORSCPTCTDSLLNGDFITVDVNRSPGNVQVINGYVHF 269  
QY 246 ---QG-AASPKDMLILVDVSGVSGITLKLIKRTSVSMLTSLDDEFFVNVASNSNQDV 301  
Db 270 FAPQGLPVVPKNIVFVIDVSGMSGRKIQTREALLKILDVKKEDDYLNELFST---DV 326  
QY 302 SCFQ-HLVQANVRNKKVLKDAVNITAKGITDYKKGFSFAFEQOLLNVNVRAN-----C 354  
Db 327 TTWKDHLVQATPANLKEAKTFVKNIHQDSMTNINDGLLKGIEML---NKAREDHVTPERS 383  
QY 355 NKIIMLTGQ---GEERAQEIENKYNK---DKKVRFRFSVQGHNYERGPIQWMACENKG 408  
Db 384 TSIIMLTGQDANTGESRPEKIQENVRNAIGKPELYNLGFG-NLNLNFEILELLENHG 442  
QY 409 YVEIPISGAIRINTOEYLDVLRPMVLGADKAKQVQWNTVYLDALGLL-VITGLPV 466  
Db 443 LARRIVEDSDANLOQGYEEVANPLL-----TNVEVEYEPENAILDLTRNSYPH 491  
QY 467 FNTIGFENKTNLKNQLILGVGVDSLEDIKRLTPFTLCPNGYVFAIDPNGYVLLHPN 526  
Db 492 F-----YDG-----SEIVVAGRLVDRNMDN-----FKADVKGHGALN-- 523  
QY 527 LQPNKPSQSPVLDLFDLAELNDIKVEIRNKMIDGESGK--TFRTLVKSQBERYIDKG 584  
Db 524 ----DLTFTFEVDNEEMDAALK-----EQYIFGDIYERLWAYLTIEQLLEKRNKAG 572  
QY 585 NRTYTWTPVNGTDYSLA--DVLPTYFYIYKAKLEETITQARSKKGMKMDSET-----LK 637  
Db 573 DEKENIT-AEALDLSLKYHEVTPLTSMVVTKPEDNEQDTSIADNAGEEAPAEITMTSFLT 631

QY 638 PDNFESGYTFIADPYCNDLKISDNTEYELLNFNEIDRKTNPNSCNADLINRVLLDA 697  
 Db 632 TQSQSQSPYIV-----DGPHEFIQI-----PGKNDSCIFNIDEKP 668  
 QY 698 GFTNELVQNTYMSKOKNIKGVKAREVVDGGITRVYPKKEAGENWOENPETVEDSFYKRLSD 757  
 Db 669 GTVLRLIQD-----PVT--GIT-VTGQIIGD-----KRS-- 694  
 QY 758 NDNTVFTAPIFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTS 817  
 Db 695 NASSRTGKTGYFGKLGITNANWDFRVEVTEKILG-----TGAELSTESWLDIVTVQ 747  
 QY 818 IRDPCAGVCDCKRNSDVCVILDDG-GELLMAN-----HDDYTNQIGRFFGEIDP 868  
 Db 748 -----TGLSVTINRKNMV--VSFGDGISFVILHQVKKRHPVHQDFLG-----FYVDS 795  
 QY 869 SLMRHLNIVISVYAFNKSVDYQSV-CEPGAAP 898  
 Db 796 HRMSAQTHGLLGQFFQFDFKVGIRGSDP 826

RESULT 9  
 S30350  
 N; alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy  
 C; Species: Homo sapiens (man)  
 C; Date: 03-May-1994 #sequence\_revision 20-Feb-1995 #text\_change 04-Feb-2000  
 C; Accession: S30350; S02141; D34245; A39079; S50133; B53642; A59167  
 R; Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin,  
 Eur. J. Biochem. 212, 771-776, 1993  
 A; Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-  
 A; Reference number: S30350; MUID:93215656  
 A; Accession: S30350  
 A; Molecule type: mRNA  
 A; Residues: 1-885 <BOU1>  
 R; Bourguignon, J.  
 A; Cross-references: EMBL:X67055; NID:g288562  
 submitted to the EMBL Data Library, June 1992  
 A; Reference number: S34123  
 A; Accession: S34123  
 A; Molecule type: mRNA  
 A; Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
 A; Cross-references: EMBL:X67055; NID:g288562; PIDN:CAA47439.1; PID:g288563  
 R; Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattei, M.G.; Passage, E.; Salier,  
 Eur. J. Biochem. 179, 147-154, 1989  
 A; Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three ch  
 A; Reference number: S02141; MUID:89137072  
 A; Accession: S02141  
 A; Status: not compared with conceptual translation  
 A; Molecule type: mRNA  
 A; Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIA1>  
 A; Cross-references: EMBL:X14690; NID:g35464; PIDN:CAA32821.1; PID:g35465  
 R; Enghild, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.  
 J. Biol. Chem. 264, 15975-15981, 1989  
 A; Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-a  
 A; Reference number: A92736; MUID:89380192  
 A; Accession: D34245  
 A; Molecule type: protein  
 A; Residues: 30-49 <ENGL>  
 R; Enghild, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S.V.  
 J. Biol. Chem. 266, 747-751, 1991  
 A; Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot  
 A; Reference number: A39079; MUID:91093267  
 A; Accession: A39079  
 A; Molecule type: protein  
 A; Residues: 631-647 <ENG2>  
 R; Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Bon  
 Biochim. Biophys. Acta 1219, 551-554, 1994  
 A; Title: Tandem Orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 g  
 A; Reference number: S50133; MUID:95002176  
 A; Accession: S50133  
 A; Status: preliminary  
 A; Molecule type: DNA

A; Residues: 1-27 <DIA2>  
 A; Cross-references: EMBL:X75318  
 R; Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.  
 Biochemistry 33, 7423-7429, 1994  
 A; Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable co  
 A; Reference number: A53642; MUID:9421799  
 A; Accession: B53642  
 A; Molecule type: protein  
 A; Residues: 30-34, 'X' <WIS>  
 R; Jessen, T.E.; Faarvang, K.L.; Ploug, M.  
 FEBS Lett. 230, 195-200, 1988  
 A; Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a  
 A; Reference number: S02431; MUID:88167187  
 A; Accession: A59167  
 A; Molecule type: protein  
 A; Residues: 30-32, 'GEKEQAVDT' <JES>  
 C; Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondro  
 C; Genetics:  
 A; Gene: GDB:ITIH3  
 A; Cross-references: GDB:120109; OMIM:146650  
 A; Map position: 3p13-3p12  
 C; Superfamily: Inter-alpha-trypsin inhibitor complex component II  
 C; Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase I  
 F; 1-19/Domain: signal sequence #status predicted <SIG>  
 F; 20-29/Domain: propeptide #status predicted <PRO>  
 F; 30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M  
 F; 648-885/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
 F; 87-576/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F; 647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s

Query Match 3.3%; Score 185; DB 2; Length 885;  
 Best Local Similarity 20.9%; Pred. No. 0.0035;  
 Matches 137; Conservative 101; Mismatches 239; Indels 180; Gaps 34;

QY 27 FPSAVTIKSWDKQEDLVTLAKTAGSNQVLVDIYKYQDLYTVEPNNAQLVEIAARDI 86  
 Db 97 YPGNVKEVAKQYKAVSQGTAG-----LVKASGRKL 131  
 QY 87 EKLLSNRSKAL---VSLALEAKVQAQAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSQ 143  
 Db 132 EKRTVSYNVAAGSKVTFELTYEELLRKHGK-----YEMLYKVQPK-----Q 173  
 QY 144 RIKPVEDIANFGKQISYQAAHVHPTDIYEGSTIVLNELNWTSALDEVEFKNREEDPSL 203  
 Db 174 LVKHFIE-----VDIFEPOGI-----SMLD-----AEASFI 200  
 QY 204 LMQVFGSA-----TGLARYYPASPPWVDSRT-PNKID-----LYDVRRP----- 242  
 Db 201 TNDLLGSALT KSFSGKKGHVSPKPSLDQORSCPTCTDLSLNGDFTTYDYNRESPGNVQI 260  
 QY 243 ---WYI-----QG-AASPRDMLLVDSVSGSLTGLKLTSTVSEMLETSDDDFVNVA 293  
 Db 261 VNGFYVHFPAQGLPVVPKNVAVVIDISGMAGRKLEQTKAALLRILEDMQEDYLNFIL 320  
 QY 294 FNSNAQDVSCF--GHLVQVARNKKVLKDAVNNITAKGIDYKGFSAFAPQLLNYSVR- 351  
 Db 321 FSG---DVSTWKEHLVQAPENLQEAFTVKSMEDKMTNIDGLLRGISML---NKARE 374  
 QY 352 -----ANCKNIIMFLTDG-----GEERAQEIFNKYNK--DKKVVFRFVSQGHYERGP 400  
 Db 375 EHRIPERSTSVIMLTGDGANVGSPEKIQENVRNVAIGKFFLYNLGFG--NNLNYNFLE 433  
 QY 401 WMAENKGYIYEPSIGAIRINQEVLDVLRPWLVLGADKAKQOVNTVYVLDALD----- 455  
 Db 434 NMALENHGFAIRIYEDSDADLQGGFYEEVANPL-LTGVEMEYPE--NAILDLTQNTYQH 490  
 QY 456 ---LGLVITGTLVPVNIQTGFENKNLK-----NOLILGVMGVDYSLEDIKRLTFRFTL 506  
 Db 491 FIDGSEIVVAGRL-VDEDNNSF--KADVGHGATNDL---TFTEFVDMKEMEK-----AL 539  
 QY 507 CPNGYIFAIDPN-----GYVLHPNLPQK---NPKSQEPVTLDFDAELENDIKVEIRN 557



Db 540 QERDYIFG---NYIERLWAYLTIEQLLEKRNKNAHGEERENLTARALDLSLKYHFVTPPLTS 596  
QY 558 KMIDGESGKTRTLVKQODERYI--DKGNRIYVTPVN-GTDYSALVLPYFSFYI 612  
Db 597 MVTKPE-----DNEDERAIAKPGCEADAEATPVSPAMSYLTSYQPPQNPYYIV 644

RESULT 10  
JC5576  
Inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 17-Mar-1999  
C:Accession: JC5576; PC4486  
J.Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinochara, H.  
R. Biochem. 122, 71-82, 1997  
A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors  
sin inhibitor heavy chain family.  
A:Reference number: JC5574; MUID:97420688  
A:Accession: JC5576  
A:Molecule type: mRNA  
A:Residues: 1-869 <NA>  
A:Cross-references: DDBJ:D89287  
A:Experimental source: liver  
A:Accession: PC4486  
A:Molecule type: protein  
A:Residues: 34-53,449-475;509-526 <NA2>  
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were  
that the complexes play important role for pancreatic cancer.  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
F:236-239,664-865/Disulfide bonds: #status predicted

Query Match 2.9%; Score 164.5; DB 2; Length 889;  
Best Local Similarity 23.2%; Pred. No. 0.061;  
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLWVFGSATGLARYIPASPVDSRT--PNKID-----LYDVRRL--PWYIOGA-- 248  
Db 211 SALTQSFSGKKHGVSEKPS--LDQRSCTCTDLSLNGDFIVDVNRSEGNVQVNG 267  
QY 249 -----ASPKDMILVDVSGSVSGLTLKLRISVSEMLETSLDDDFVNVASFNS 296  
Db 268 YFVHFAPQGLPVPKNIVFVDISGSMAGRIQOTRVALLKILDDMKQDYLNFILFST 327  
QY 297 NQDVSCFQHLVQANRKNKVLKDVANNITAGITDYKKGFSFAFEQLLN-----YNSRA 352  
Db 328 GV--TTWKDSLVOATPANLEEARFVRSISDQGMNTINDGLLRGINMLTDAREQHTVPER 385  
QY 353 NCNKIIMLFTDG---GEERAQEIFNKNKRVFRFSVG--QHNRYERGPQWMAENK 407  
Db 386 STSIIML--TDGANTGESRPEKIQENVRKATGEPPLYNLFGNMLNFTLETHALENH 444  
QY 408 GYYEIPISGAIKRIHQEYLDVLRPMVLGDKAKOVQVNTVYLD 452  
Db 445 GVARRIYSDANLQIGFVEEVANELL-----TNVEVE 478

RESULT 11  
T28155  
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum) (fragments  
N:Alternate names: erythrocyte membrane binding protein 1 (EMPI)  
C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T28155  
R; Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.  
Nature 388, 292-295, 1997  
A:Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and requires complement  
A:Reference number: Z20477; MUID:97373957  
A:Accession: T28155  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-2706 <ROW>  
A:Cross-references: EMBL:Y13402; PIDN:CAA73831.1

A:Experimental source: strain IT 4/25/5  
C:Genetics:  
A:Introns: 2493/3  
A:Note: R29R+var1

Query Match 2.9%; Score 161; DB 2; Length 2706;  
Best Local Similarity 18.2%; Pred. No. 0.57;  
Matches 183; Conservative 137; Mismatches 345; Indels 338; Gaps 46;

QY 36 WDKMQEDLVTLAKTASGVNLVDIYKQDIYVEPNNA-----RQL 78  
Db 308 WFDEWAEFCRIRKI-----KLENVKECRD-----EBNNKYCSGDHCKRTYLKDNITF 358  
QY 79 VEIARDEIKLLSNRSKALVSLALEAEKVAQAHOREDPASNEVYVYNAKDDLDDEKNS 138  
Db 359 IDLNCPRCENACSNYTK-----WIEQRKFQDKRRK--YMEI---KIKTWNINNDK 408  
QY 139 E-----PGSORIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVLNLNMTSALDE 191  
Db 409 EYENLDKGYSTIN--TFLESNLHGKQCQ-----DN 438  
QY 192 VFKNREEDPSLLWVFGSATGLARYIPASP-----WDNSRTPNKI 233  
Db 439 IDKKNKTNFKNL--ETFGP-----SGYCEACPIYGVKCSNEKCTPVTEWNSNNRLPTDT 493  
QY 234 DLYDVRPWPYIOGAASPKDMLLLVDVSGSVSGLTLKLRISVSEMLETSLDDDFVNVAS 293  
Db 494 STKNLN-----ATNIDMLVNDGIGNAI----- 515  
QY 294 FNSNAQDVSCFQHLVQANVRNK-----VLKDVANNITAKGITDYKKGFSFAFEQLL 345  
Db 516 --DNELEKCTKYGLKIGKKQKQWCOYLNNIDQCKINNVMNSGYFDNKIAFNVLFRWL 573  
QY 346 NYNVRANCKNIIMLTGDEGEAEQEIFNKNKDKKRVFRFSVGOHNTYERGPQWMAE 405  
Db 574 RYFVRDHRNLK-----EKIDVICIKENINENICIKCKTN-----CE 610  
QY 406 NKGYEIPISGAIKRI-----NTQEVLDVLRPMVLGDKAKOVQVNTVYLDALGLVIT 461  
Db 611 CVGKLEKEAEWDKINQHNQKNHIMFLIPIYWTGYEK--ITPNDFFKALE-----DV 665  
QY 462 GLPVENITGPFENKTLNQLILGYMGVDVSLDEDIKRLTPRFTLCPNGYIFAIDPNGYV 521  
Db 666 DFINVLDLTKECQD--THCKIEKIRSI--DVDLIKEILISWLNKIEVCKS--HHDEKHEYC 721  
QY 522 LHLNLPKNPKSQPVTLDLFLDAELENDIKVEIRKNKMDIGSEGEKT-----FRT 571  
Db 722 C---DILPKSVDDDEDD--EYDDEKEESSQTTKRN--ISQKGGTKSASCVKGACAIVKG 775  
QY 572 LVKSQDERVID---KGNRTYTW-----TPVNGTD-----YSLALVLPYFS 609  
Db 776 VLOQKNGSIDMCKNAKRNKKNWQCDKNTFVDGNEGVCMPPRKSKICINHLTLEEQTKK 835  
QY 610 Y-----YIKAKLEET--ITQARSKKGMKDSITLK-----PDNFEE--SGYTFIAPRDYC--N 656  
Db 836 YQLREAFIKCAAKETNLLWDKYKNDKNEAEELKKGKIPEDFMRIYFTFGDFRDCLEN 895  
QY 657 DL-----KTSNNTEPLNPNFIDRK-----TPNPFSC--NADLINRVLVDAGTNNEL 703  
Db 896 DMGKDVKVKKNINKVFNNSKRGPKKIDPNWNNWNGPQIWNMGMLCALIHADTKOSIKN 955  
QY 704 VQNY-----W-----SKOKNIKGVKARFVV 723  
Db 956 KONYKYKVTILAKRDGSGNGMTLSEFAKPKFLURFVEMTDDYCKERQKVLTEVASTCKS 1015  
QY 724 TDGGITRV-----YKPEAGENWQENPETEYDSFYKRSLDN-----DNIV-- 762  
Db 1016 IDGGQLKCDRCGNCKDEYKKNRKKKEEWNLDQKYKDKRENKIDKGPIGIIVKDYVL 1075  
QY 763 -----FTAPYKNSGPGAYESGIMVSKAVETIYOGKLLKPAVGIKIDVNSWI-- 810  
Db 1076 ANAKYLLKKKFTASCVTSSGKAQNSATEEYKKNIELLEEYQ-----YDADQYCGC 1126





QY 392 HNYERGPIQWACENKGGYVYIPISGAIIRINTQEVLDVGRPMVL--AGDKAKOVQ--- 445  
Db 355 SNYENAMVRADVNGNGYVIDTSL--BAQVLNEMKROMLITVAKDVKAQIENPA 410  
QY 446 WTNVYLDALGLVITGTPVFNITGOFENKTNLKNQILGVMGV--VSLBDI---KRLT 501  
Db 411 WVTEY---RQIG-----YE-----KRLRVEHENNDVAGDIGAGKHIT 447  
QY 502 PRFTLCPNGYFAIDPNQYVLLHNPQLPKPKSQE 536  
Db 448 LIFELTLNGKASIDKLRYA--PDNKLAKSDKTRE 480  
RESULT 14  
E71619  
RAD2 endonuclease PFB0265c - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
C:Accession: E71619  
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;  
Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.  
Science 282, 1126-1132, 1998  
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A:Reference number: A71600; MUID:99021743  
A:Accession: E71619  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1516 <GAR>  
A:Cross-references: GB:AB001383; GB:AB001362; NID:g3845135; PIDN:AAC71842.1; PID:g384513  
A:Experimental source: clone 3D7  
C:Genetics:  
A:Gene: PFB0265c

Query Match 2.8%; Score 155; DB 2; Length 1516;  
Best Local Similarity 18.9%; Pred. No. 0.53;  
Matches 178; Conservative 133; Mismatches 291; Indels 340; Gaps 52;  
QY 119 SNEVYVYNAKDL--PEKNDSEPGSRKPVIFEDANFRQISYQHAHVHPTDIYEGS 176  
Db 517 NNDVIEHNKNNMNIYDKYVNECSSEKINDNGISKNIN-----ILEPNNL-DTS 567  
QY 177 TIVNELNWTSLDE--VFKNREDDPSLLV-----QVFGSATGLARYPPSPWDNERT 229  
Db 568 NIFL-----EGKDEKYVYVYVNEKEIRIPLKEINKEIF-----EKL 603  
QY 230 PNKID--LYDVRRRPWY----IOGAAPKDMILVDVSGVSGLT-LKLIRT----- 274  
Db 604 PUKLQYILQDIKEE-WYTDNRKAIKSKDDM----DVSQVQLETYYVMIKTDFEIEKL 658  
QY 275 --SVSEMLFTLSDDDFVN---VASFNSNAQDVSCFQHLVQANVRNKKVLDKAVN--NIT 326  
Db 659 KIKMAENIQSVGELLINKLDSKNTDNINIKDYVNLQK-KSKSKKKKFLNDILNTYNT 717  
QY 327 A-----KGITYKGFSAFQOLL--NYNVSRANCNKIIMLTGDCGEEAQQEIP 373  
Db 718 TESKYQDLVYKGEESKEDIKIDFVTOCYERNNDIIRDTHDK-----SDIF 764  
QY 374 N--KYNKDKKVRVERFSVGOH-----NYERGPQWACENKGYVYIPIGAIIRNTOE 425  
Db 765 NIKIDNNKKYIYNLEDSQEBEINKKNYNNND-----SNKTFP-----LKIENEF 812  
QY 426 YLDVLRPMVLGADK-----AKQVMT-----NYYLDALEGLVITGLPVENIT 470  
Db 813 KNDLLDDSQIFGDSLLADIKYVNTADNLNENKSLYEDGENF---ITRNEP---IT 866  
QY 471 GQENKTNL-----KNQILGVMGVVSLDIDKRLTPFTLCPN-----G 510  
Db 867 NEYEEKNNIYISDEQYNEEDIIFDKIKKEKKNNDSSDDFENCVSQOEKIYVNEKIE 926  
QY 511 YYPAD---PNGVLLHNPQLPKPKSQEPVT-----LDLFD--AELEN-----DI 551

Db 927 YNNKNDKSSSSSIILEEIKYKKEKDELVSPNCLVLLDEFHSNDLENNYISVSSDDM 986  
QY 552 KVEIRNKWIDGSEKFRITLVKSQDERYIDKGNRTWTTPVNGTDYSALVLPTSYFY 611  
Db 987 KTNVSKNITG-----VK---ENKVDKTNVEY----- 1010  
QY 612 IKAKLEETITQARSKKG-----KMKDSETLKPDNFEESGYTF-----IAPRDYCN 656  
Db 1011 -----DKGDDGVIEISFEDSHKLEESKFDNNNNIYDNDDELEKLSKDYIS 1057  
QY 657 DLKISDNNTEFLNF-----NEFTDRKTPNAPS-----CNADL 689  
Db 1058 D--VDKHNVNINIERGEDERENEFVENKIQSTESHKSNEFICTENKSLRKQYNSKEDI 1115  
QY 690 IN-RVLLDAGFTNELVONYSKQKNIGKVRKVFVVTGGITRVYPKAGENKQENPETYE 748  
Db 1116 SNVRILKSDDDNNLSKNYFE-----ILLD-----KKQVMDNFQMNIEQNN 1156  
QY 749 DSFYKRSILDNDNYVFTAPYFNKSGPGAYESGIMYSKAVEIYI-----OGKLLK 796  
Db 1157 DKLEADKLE-----GAYFEYLEDNKIIDSYIKETKNEEELIKEYKKLK 1201  
QY 797 PAVYGIKIDVNSWIE---NFTKTS-IRDPD-AGPVCDCKRSDVMDCVILDDGGFLLMAN 851  
Db 1202 KNNTIEINDEMDDIKLLNFRFGIPIYIQSPCEAAEQCSYLNKNKNTCDAIISDDSVLVFSG 1261  
QY 852 HDDTYNQIGREFGE-----IDPSL---MRHLVNSIV 879  
Db 1262 ----KTIVKFNFKKKTVEVYEKRAIEKGLGYQELINISL 1299  
RESULT 15  
I40884  
cytotoxin L - Clostridium sordellii  
C:Species: Clostridium sordellii  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 15-Oct-1999  
C:Accession: I40884  
R:Green, G.A.; Schue, V.; Montell, H.  
Gene 161, 57-61, 1995  
A:Title: Cloning and characterization of the cytotoxin L-encoding gene of Clostridium  
A:Reference number: I40884; MUID:95369733  
A:Accession: I40884  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2364 <RES>  
A:Cross-references: EMBL:X82638; NID:g1000694; PIDN:CAA57959.1; PID:g1000695  
C:Superfamily: cpl repeat homology  
C:Keywords: cytotoxin  
Query Match 2.8%; Score 155; DB 2; Length 2364;  
Best Local Similarity 18.7%; Pred. No. 1.1;  
Matches 217; Conservative 132; Mismatches 342; Indels 468; Gaps 57;  
QY 12 TLFQSLILGPSSEEPFSAVTTKSWDKMQEDLVTLAKTASGVNQLVDIYKIQDYTYE 71  
Db 1137 TLDDKIIMPQDD-----LVLSIED-FNNNSIYLGKC-----EIWRAE 1173  
QY 72 PNNARQLVEIARADIEKLSNRS-----KALVS-----LALAEKVQAAHQRDFASNEVV 123  
Db 1174 GSGGHTLD---DIDHFFSSPSITRKPWLSIYDVNLNKKKEI-----DFSKDLAV 1221  
QY 124 YYNKD-----DLDPKNDSEPGSRKIP-----VFIEDANFGR- 157  
Db 1222 LPNAPNRFVGEWGTTPGFRSLD---NDGTKLDDRIRDHVGEQFYWRVFAFDALITKL 1278  
QY 158 QISYQHAHVHPTBIYEGSTIVLNLNMTSALDVEFKKREDDPSLLMQVFGSATGLARY 217  
Db 1279 KPRYEDTNVRINLDGNTSRFIV-----PVIETEQRKN-----LSYFYGSG--GGSVS 1324  
QY 218 YPASPWONSRTPNKIDLYDVRRRPWYIQGAASPKDMLILVDVSGVSGLTGLKLRISVS 277  
Db 1325 LSLSPYNNM-----IDLNLVENDTW-----VIDVDNVVKNITTESIEIQKG 1365



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:48:25 ; Search time 66.28 seconds  
(without alignments)

549.390 Million cell updates/sec

Title: US-09-397-548-17

Perfect score: 5599

Sequence: 1 MAAGCLLALTLFQSLIG.....PDVCFDNNVLEDTDCGGVS 1063

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5599	100.0	1091	1	CIC2 HUMAN
2	5390	96.3	1091	2	CIC2 RAT
3	5380.5	96.1	1106	1	CIC2 RABIT
4	607	10.8	734	1	UN36 CAEL
5	194.5	3.5	886	1	ITH3 MOUSE
6	182	3.3	885	1	ITH3 HUMAN
7	180.5	3.2	887	1	ITH3 RAT
8	164.5	2.9	886	1	ITH3 MSAU
9	161	2.9	1829	1	DPOL THEST
10	159	2.8	1956	1	ATX1 PLAF
11	157.5	2.8	575	1	YFBK ECOLI
12	154.5	2.8	946	1	ITH2 HUMAN
13	152	2.7	1290	1	BXCI CLOBO
14	151.5	2.7	420	1	103 SYNY3
15	150.5	2.7	921	1	ITH4 PIG
16	150	2.7	854	1	MCPC BACSU
17	149	2.7	930	1	ITH4 HUMAN
18	148	2.6	964	1	DPOL CBEPV
19	144	2.6	1087	1	YXNX CLOTM
20	143	2.6	946	1	ITH2 MSAU
21	142.5	2.5	382	1	YLJ0 CAEL
22	141	2.5	1251	1	RBP2 PLAVB
23	140.5	2.5	935	1	ITH2 PIG
24	140	2.5	2710	1	TOXA CLODI
25	140	2.5	3305	1	APLP MANSE
26	139.5	2.5	764	1	PAG BACAN
27	139	2.5	1513	1	STUL YEAST
28	138	2.5	1180	1	CA4A BACTI
29	137	2.4	984	1	HYSA STRAG
30	136.5	2.4	3063	1	CAIC HUMAN
31	135.5	2.4	946	1	ITH2 MOUSE
32	134.5	2.4	2077	1	TEGU HSB6U
33	133	2.4	862	1	MUTS BORBU

34	133	2.4	1323	1	ADRI YEAST	P07248	saccharomyc
35	132.5	2.4	547	1	SYM BUCAI	P57210	buchnera ap
36	132.5	2.4	929	1	CAIC NOTVI	O91145	notophthalm
37	132.5	2.4	1679	1	YIO9 YEAST	P40457	saccharomyc
38	132	2.4	697	1	YE9C SCHPO	O13773	schizosacch
39	131.5	2.3	1018	1	YC14 METJA	Q58611	methanococc
40	131	2.3	1634	1	DPOL METJA	Q58295	methanococc
41	131	2.3	1658	1	YM67 YEAST	Q03661	saccharomyc
42	130.5	2.3	987	1	YD94 METJA	Q58789	methanococc
43	129	2.3	1244	1	X307 MYCPN	P75342	mycoplasma
44	128.5	2.3	1254	1	UBPC YEAST	P39538	saccharomyc
45	128	2.3	1113	1	Y140 MYCPN	P75033	mycoplasma

## ALIGNMENTS

RESULT 1							
CIC2_HUMAN							
ID	CIC2_HUMAN	STANDARD;	PRT;	1091 AA.			
AC	P54289;						
DT	01-OCT-1996 (Rel. 34, Created)						
DT	01-OCT-1996 (Rel. 34, Last sequence update)						
DT	01-OCT-2000 (Rel. 40, Last annotation update)						
DE	DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA						
DE	SUBUNITS PRECURSOR.						
GN	CACNA2D1 OR CACNL2A OR CCHL2A.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
OX	NCBI_TaxID=9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=92110010; Pubmed=1309651;						
RA	Williams M.E., Feldman D.H., McCue A.F., Brenner R.,						
RA	Valicielebi G., Ellis S.B., Harpold M.M.;						
RT	"Structure and functional expression of alpha 1, alpha 2, and beta						
RT	subunits of a novel human neuronal calcium channel subtype.";						
RL	Neuron 8:71-84(1992).						
CC	-1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN						
CC	EXCITATION-CONTRACTION COUPLING.						
CC	-1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:						
CC	ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS						
CC	HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).						
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.						
CC	-1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND						
CC	AORTA TISSUES						
CC	-1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM						
CC	A PRECURSOR FORM (BY SIMILARITY).						
CC	-1- SIMILARITY: TO OTHER SPECIES ALPHA-2 SUBUNIT.						
CC	-----						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration						
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).						
CC	-----						
DR	EMBL: M76559; AAA51903.1; -						
DR	MTM; 114204; -						
DR	InterPro: IPR002035; -						
DR	Pfam: PF00092; vwa; 1.						
DR	PROSITE: PS0234; VWFA DOMAIN; 1.						
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;						
FT	Calcium channel; Glycoprotein; Phosphorylation; Signal.						
FT	SIGNAL	1	24	POTENTIAL.			
FT	CHAIN	25	944	L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT			
FT				(BY SIMILARITY).			
FT	CHAIN	945	1091	L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY			
FT				SIMILARITY).			
FT	TRANSMEM	446	469	POTENTIAL.			
FT	TRANSMEM	906	930	POTENTIAL.			

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FT TRANSMEM 1067 1086 POTENTIAL.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 563 663 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 769 769 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 883 883 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 973 973 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 986 986 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT MOD_RES 501 501 PHOSPHORYLATION (BY CAPK)
FT FT (BY SIMILARITY)
FT MOD_RES 833 833 PHOSPHORYLATION (BY CAPK)
FT FT (BY SIMILARITY)
FT SEQUENCE 1091 AA; 123183 MW; 284E13EE29A47837 CRC64;

Query Match 100.0%; Score 5599; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLFQSLIGSPSSPEPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLFQSLIGSPSSPEPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60
QY 61 YEKQDLYTEPNARQLVEAARDIEKLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
DB 61 YEKQDLYTEPNARQLVEAARDIEKLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
QY 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRQISVQHAHVHPTDIYEGSTIVL 180
DB 121 EVVYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGRQISVQHAHVHPTDIYEGSTIVL 180
QY 181 NELNWTSALEDFVFKNREDEPSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
DB 181 NELNWTSALEDFVFKNREDEPSLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
QY 241 RPWTIQGAASPKDMLLVDSVSGSGTLKLRITSVSEMLETLSDDDFVNVSFNSNAQD 300
DB 241 RPWTIQGAASPKDMLLVDSVSGSGTLKLRITSVSEMLETLSDDDFVNVSFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIITDYKKGFSFAPEQLLNYSRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIITDYKKGFSFAPEQLLNYSRANCKIIML 360
QY 361 FTDGEERAQEIFNKNYKDKKVRVFRFSVGOHNYERGPQIWMACENKGYEIPSGAIR 420
DB 361 FTDGEERAQEIFNKNYKDKKVRVFRFSVGOHNYERGPQIWMACENKGYEIPSGAIR 420
QY 421 INTOEYLDVLRPMVLADKAKQVQWNVYLDLEGLVITGTLVPVNTGQFENKTNLK 480
DB 421 INTOEYLDVLRPMVLADKAKQVQWNVYLDLEGLVITGTLVPVNTGQFENKTNLK 480
QY 481 NQLILGVGVDSLEIDKRLPRTCLPNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540
DB 481 NQLILGVGVDSLEIDKRLPRTCLPNGYFFAIDPNGYVLLHPNLPKNPKSQEPVTL 540
QY 541 DFLDALENDIKVEIRNMKIDGESGKTFRLVKSQDERYIDKGNRYITWTVPVNGTDYSL 600
DB 541 DFLDALENDIKVEIRNMKIDGESGKTFRLVKSQDERYIDKGNRYITWTVPVNGTDYSL 600
QY 601 ALVLPYTFYIKAKLETITQAKSKGKMKDSETLPKDPNFEESGYTFIAPRDCNDLKI 660
DB 601 ALVLPYTFYIKAKLETITQAKSKGKMKDSETLPKDPNFEESGYTFIAPRDCNDLKI 660
QY 661 SDNNTFLLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIGVKAR 720
DB 661 SDNNTFLLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIGVKAR 720
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DB 661 SDNNTFLLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIGVKAR 720
QY 721 FVYTDGGITRVYPKEAGENQENPETVEDSFYKRSNDNDNVFTAPYFNKSGPGAYESGI 780
DB 721 FVYTDGGITRVYPKEAGENQENPETVEDSFYKRSNDNDNVFTAPYFNKSGPGAYESGI 780
QY 781 MVSKAVEIYIQGKLLPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840
DB 781 MVSKAVEIYIQGKLLPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840
QY 841 LDGGGFLMANHDDYTNQIGRFGEDIPSLMRHLVNLVSVAFNKSYDYSVCEPGAAPKQ 900
DB 841 LDGGGFLMANHDDYTNQIGRFGEDIPSLMRHLVNLVSVAFNKSYDYSVCEPGAAPKQ 900
QY 901 GAGHSRAYSVPVADILQIGWATAAASILQOFLSLTFPRLLEAVEMEDDDFTASLSKQ 960
DB 901 GAGHSRAYSVPVADILQIGWATAAASILQOFLSLTFPRLLEAVEMEDDDFTASLSKQ 960
QY 961 SCITEQTYFFDNDKDSFSGVLDGCGNSRIFHGKLMNTNLIIFIMVESKGTGCPDTRLI 1020
DB 961 SCITEQTYFFDNDKDSFSGVLDGCGNSRIFHGKLMNTNLIIFIMVESKGTGCPDTRLI 1020
QY 1021 QABQTSQGNPCDMVKQPRYRKGPVDFVFNVDNVEDYTDGCGVS 1063
DB 1021 QABQTSQGNPCDMVKQPRYRKGPVDFVFNVDNVEDYTDGCGVS 1063

RESULT 2
CIC2_RAT
ID CIC2_RAT STANDARD; PRT; 1091 AA.
AC P54290;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9228762; PubMed=1314383;
RX Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
RL dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CC EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC A PRECURSOR FORM (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
CC -----
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CC -----
CC EMBL: M86621; AAA1088.1;
CC InterPro: IPR002035;
CC Pfam: PF00092; vwa; 1.
CC PROSITE: PS50234; VWFA_DOMAIN; 1.
CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW
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KW Calcium channel; Glycoprotein; Phosphorylation; Signal;  
KW Alternative splicing.

FT SIGNAL 1 24  
FT CHAIN 25 944  
FT  
FT  
FT CHAIN 945 1091  
FT  
FT  
FT TRANSMEM 445 468  
FT TRANSMEM 906 930  
FT TRANSMEM 1067 1086  
FT CARBOHYD 92 92  
FT CARBOHYD 136 136  
FT CARBOHYD 184 184  
FT CARBOHYD 323 323  
FT CARBOHYD 347 347  
FT CARBOHYD 474 474  
FT CARBOHYD 584 584  
FT CARBOHYD 593 593  
FT CARBOHYD 663 663  
FT CARBOHYD 769 769  
FT CARBOHYD 812 812  
FT CARBOHYD 876 876  
FT CARBOHYD 883 883  
FT CARBOHYD 973 973  
FT CARBOHYD 986 986  
FT MOD\_RES 500 500  
FT  
FT MOD\_RES 833 833  
FT  
FT SEQUENCE 1091 AA; 123822 MW; 70549079D343B34 CRC64;

Query Match 96.3%; Score 5390; DB 1; Length 1091;  
Best Local Similarity 95.8%; Pred. No. 1.7e-302;  
Matches 1019; Conservative 24; Mismatches 19; Indels 2; Gaps 2;

QY 1 MAAGCLLALTLTFLQSLIGPSEEPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTLTFLQSLIGPSEEPSPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTEPNNAQVLEIARDTEKLSNRSKALYSALAEAKVQAQAHQREDPASN 120  
DB 61 YEKYQDLYTEPNNAQVLEIARDTEKLSNRSKALYSALAEAKVQAQAHQREDPASN 120  
QY 121 EVVYNAKDDLPDEKNDSEPGSQRIKPVFTEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
DB 121 EVVYNAKDDLPDEKNDSEPGSQRIKPVFTEDANFGQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSALEVEFKKNEEDPSLLQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
DB 181 NELNWTSALEVEFKKNEEDPSLLQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
QY 241 RPNYIOGAASPKDMLILVDYSGVSGTLKLTISVSEMLETISDDDFVNVASFNSNAQD 300  
DB 240 RPNYIOGAASPKDMLILVDYSGVSGTLKLTISVSEMLETISDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVKNKYLKDAVNNTAKGITYDKKGFSAFQELLNYSRANCNKIIML 360  
DB 300 VSCFQHLVQANVKNKYLKDAVNNTAKGITYDKKGFSAFQELLNYSRANCNKIIML 360  
QY 361 FTGGEERAQEIFKNYKDKKVRFRFSVGQHNRYERGPIQWACENKGYIYEIPSGAIR 420  
DB 360 FTGGEERAQEIFKNYKDKKVRFRFSVGQHNRYERGPIQWACENKGYIYEIPSGAIR 420  
QY 421 INTQEYLDVLRPNVLADGAKQVQNTNLYDLAELGLVITGLPVENITGQFENKTNLK 480  
DB 420 INTQEYLDVLRPNVLADGAKQVQNTNLYDLAELGLVITGLPVENITGQFENKTNLK 480  
QY 481 NQILGVMGVDVLEIDIKRLTPFTLCPCNGYIYFAIDPNGVLLHPNLPKNPKSOEPTVL 540  
DB 480 NQILGVMGVDVLEIDIKRLTPFTLCPCNGYIYFAIDPNGVLLHPNLPKNPKSOEPTVL 540  
QY 541 DFLDAELENDIKVEIRNKMGIDGSEKFTFLVKSQDERYIDKGNRTYTWTPVNGTDYS- 599

DB 540 DFLDAELENDIKVEIRNKMGIDGSEKFTFLVKSQDERYIDKGNRTYTWTPVNGTDYR 599  
QY 600 LALVLPYSYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFTAPRYCNDLK 659  
DB 600 LALVLPYSYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFTAPRYCNDLK 659  
QY 660 ISDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNQLVQNSKQKNIGYKA 719  
DB 660 PSNNTTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNQLVQNSKQKNIGYKA 719  
QY 720 RFVVTGDIIRVYPKEAGENQENPETEYEDSFYKRSLDNPNYFTAPYFNKSGPAYESG 779  
DB 720 RFVVTGDIIRVYPKEAGENQENPETEYEDSFYKRSLDNPNYFTAPYFNKSGPAYESG 779  
QY 780 IMYSKAVEIYIQGLKLPVAVGKIDVNSMTENFTKTSIRDPACAGPVCDCKRNSDVMDCV 839  
DB 780 IMYSKAVEIYIQGLKLPVAVGKIDVNSMTENFTKTSIRDPACAGPVCDCKRNSDVMDCV 839  
QY 840 ILDDGGFLLMANHDDYTNQIGRFFGEIDPISLMRHLVNSIYAFNKSYDYQSVCEPAGAPK 899  
DB 840 ILDDGGFLLMANHDDYTNQIGRFFGEIDPISLMRHLVNSIYAFNKSYDYQSVCEPAGAPK 899  
QY 900 QGAGHRSAVPSVADILQIGWATAAAWSILQFLLSLTTPRLLAEVMEDEDDFTASLSK 959  
DB 900 QGAGHRSAVPSVADILQIGWATAAAWSILQFLLSLTTPRLLAEVMEDEDDFTASLSK 959  
QY 960 QSCITEQTVFFDNDSKSFVLDGNCGRIFHGKELMNTNLFIMVESGKTCPCDTRLL 1019  
DB 960 QSCITEQTVFFDNDSKSFVLDGNCGRIFHGKELMNTNLFIMVESGKTCPCDTRLL 1019  
QY 1020 IQAEQTSDEGPNCDMWKQPRYKGPVDFCNVLEDTDCGGVS 1063  
DB 1020 MQAEQTSDEGPNCDMWKQPRYKGPVDFCNVLEDTDCGGVS 1063  
RESULT 3  
CIC2\_RABIT STANDARD; PRT; 1106 AA.  
AC P13806;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA  
DE SUBUNITS PRECURSOR.  
GN CACNA2D1 OR CACNA2A OR CCHL2A.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88336904; PubMed=2458626;  
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,  
RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Rui A.,  
RA Schwartz A., Harpold M.M.;  
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2  
RT subunits of a DHP-sensitive calcium channel.";  
RL Science 241:1661-1664 (1988).  
RN [2]  
RP SEQUENCE OF 961-973.  
RX MEDLINE=91131638; PubMed=1847144;  
RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,  
RA Campbell K.P.;  
RT "Structural characterization of the dihydropyridine-sensitive calcium  
RT channel alpha 2-subunit and the associated delta peptides.";  
RL J. Biol. Chem. 266:3287-3293 (1991).  
RN [3]  
RP SEQUENCE OF 961-975; 992-1000 AND 1033-1050.  
RX MEDLINE=90368635; PubMed=2168391;  
RA de Jongh K.S., Warner C., Catterall W.A.;  
RT "Subunits of purified calcium channels. Alpha 2 and delta are encoded  
RT by the same gene.";

J. Biol. Chem. 265:14738-14741(1990).  
- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.  
- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS HETERODIMERS THAT ARE DISULFIDE-LINKED.  
- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.  
- TISSUE SPECIFICITY: SKELETAL MUSCLE.  
- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM.  
- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.  
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-----  
EMBL; M21948; AAA81562.1; -  
PIR; S10579; CHRA2.  
InterPro; IPR002035; -  
Pfam; PF00092; vwa; 1.  
PROSITE; PS0234; VWFA\_DOMAIN; 1.  
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Phosphorylation; Signal;  
KW  
KW  
FT SIGNAL 1 26  
FT CHAIN 27 960 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT.  
FT CHAIN 961 1106 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.  
FT TRANSMEM 448 471 POTENTIAL.  
FT TRANSMEM 921 945 POTENTIAL.  
FT TRANSMEM 1082 1101 POTENTIAL.  
FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 326 326 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 606 606 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 678 678 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 784 784 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 827 827 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 891 891 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 898 898 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 988 988 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1001 1001 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT MOD\_RES 503 503 PHOSPHORYLATION (BY CAPK)  
FT MOD\_RES 503 503 (POTENTIAL).  
FT MOD\_RES 848 848 PHOSPHORYLATION (BY CAPK)  
FT MOD\_RES 848 848 (POTENTIAL).  
FT SEQUENCE 1106 AA; 125042 MW; B00DE7F3C77B618 CRC64;  
  
Query Match 96.1%; Score 5380.5; DB 1; Length 1106;  
Best Local Similarity 94.8%; Pred. No. 6.2e-302;  
Matches 1029; Conservative 15; Mismatches 12; Indels 29; Gaps 4;  
  
QY 1 MAAGCULATLTLFQS--LLIGPSSEPPFSAVTTKSWVDKMQEDLVTLAKTASGVNQLV 58  
DB 1 MAAGRPLAWTLTLQAWLLIGPSSEPPFSAVTTKSWVDKMQEDLVTLAKTASGVHQLV 60  
  
QY 59 DIYEKYQDLYTVEPNNAQQLVETAAEDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFA 118  
DB 61 DIYEKYQDLYTVEPNNAQQLVETAAEDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFA 120  
  
QY 119 SNEWVYNAKDDLDPEKNDSEPGSQRIKVFIEDANFRQISVQHAHVHPTDIYEGSTI 178  
DB 121 SNEWVYNAKDDLDPEKNDSEPGSQRIKVPFIDANFRQISVQHAHVHPTDIYEGSTI 180

QY 179 VLNELNMTSALDEVEFKKNEEDPSLLMQVFGSATGLARYYPASPMWVNSRTPNKIDLDYV 238  
DB 181 VLNELNMTSALDDVFKKNEEDPSLLMQVFGSATGLARYYPASPMWVNSRTPNKIDLDYV 240  
QY 239 RRRPMYIOGAASPKDMLILVDVSGSVGLTLKLIRTSYSEMLETLSDDDFVNVASFNSA 298  
DB 241 RRRPMYIOGAASPKDMLILVDVSGSVGLTLKLIRTSYSEMLETLSDDDFVNVASFNSA 300  
QY 299 QDVSCFQHLVQANVYNNKVKLDAVNNITAKGTTDYKKKGFSAFECOLLNYSRANCNII 358  
DB 301 QDVSCFQHLVQANVYNNKVKLDAVNNITAKGTTDYKKKGFSAFECOLLNYSRANCNII 360  
QY 359 MLFTDGGERAQEIFKNKDKKRVFRFSVQGHNYERGIQWACENKGGYIEIPSIGA 418  
DB 361 MLFTDGGERAQEIFKNKDKKRVFRFSVQGHNYERGIQWACENKGGYIEIPSIGA 420  
QY 419 TRINTQEYLDVLRPMVLGAKQVQNTNLYDLALEGLVITGLPVFNITGQFENKTN 478  
DB 421 TRINTQEYLDVLRPMVLGAKQVQNTNLYDLALEGLVITGLPVFNITGQFENKTN 480  
QY 479 LKNQLILGVMGVDSLEDIKRLTPFTLCPNGYFFAIDPNGYVLLHPNLOPK----- 530  
DB 481 LKNQLILGVMGVDSLEDIKRLTPFTLCPNGYFFAIDPNGYVLLHPNLOPKIGVIGPT 540  
QY 531 -----NPKSQEPVTLDFDAELENDIKVIRKNMIDGESGEKTFRLVKSQDER 579  
DB 541 INLRKRRPNVQPKSQEPVTLDFDAELENDIKVIRKNMIDGESGEKTFRLVKSQDER 600  
QY 580 YIDKGNRTYTTVPNGTDY--SLALVLPYTFYIYKAKLEETITQARSKGKMKDSETLKP 638  
DB 601 YIDKGNRTYTTVPNGTDYSSALVLPYTFYIYKAKLEETITQARY-----SETLKP 653  
QY 639 DNFEESGTTFTAPROYCNDLKISDNNTFELNFEFIDRKTNNPCNADLINRVLLDAG 698  
DB 654 DNFEESGTTFTAPROYCNDLKISDNNTFELNFEFIDRKTNNPCNADLINRVLLDAG 713  
QY 699 FTNELVQNVWSKQKNIKGVKARFVTDGGITRVYPKEAGENQENPETVEDSFYKRSLDN 758  
DB 714 FTNELVQNVWSKQKNIKGVKARFVTDGGITRVYPKEAGENQENPETVEDSFYKRSLDN 773  
QY 759 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSI 818  
DB 774 DNYVFTAPYFNKSGPAYESGIMVSKAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSI 833  
QY 819 RDPACAGVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI 878  
DB 834 RDPACAGVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI 893  
QY 879 VYAFNKSVDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAASIIQQFLLSUT 938  
DB 894 VYAFNKSVDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGWATAAASIIQQFLLSUT 953  
QY 939 FPRLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSKFSGLVDCGNCGRIFHGEKLN 998  
DB 954 FPRLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSKFSGLVDCGNCGRIFHGEKLN 1013  
QY 999 TNLIFIMVESKTCPCDTRLLIQAQOTSDGNPCDMVKOPRYRKGPVCFDNNVLEDYTD 1058  
DB 1014 TNLIFIMVESKTCPCDTRLLIQAQOTSDGNPCDMVKOPRYRKGPVCFDNNVLEDYTD 1073  
QY 1059 CGGVS 1063  
DB 1074 CGGVS 1078  
  
RESULT 4  
UN36\_CAEEL  
ID UN36\_CAEEL STANDARD; PRT; 734 AA.  
AC P34374;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)



```

DE UNC-36 PROTEIN.
GN UNC-36 OR UNC-72 OR C50C3.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RA [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Favello A., Frazer A.,
RA Craxton M., Dear S., Du Z., Durbin R., Hawkins T., Hillier L., Jier M.,
RA Fulton L., Gardner A., Green P., Hawkes J., Kirsten J., Laiister N.,
RA Johnston L., Jones M., Kerhaw J., Kirsten J., Mortimore B., O'Callaghan M.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., Saunders D., Showkhen R.,
RA Parsons J., Percy C., Rifken L., Roopra A., Smith M., Sonhammer E., Staden R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin W., Vaughan K.,
RA Waterson R., Watson A., Weinstein L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans."
CC -----
CC Nature 368:32-38(1994).
CC -I- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L14433; AAA27969.1; -
DR PIR: S44617; S44617.
DR WormPep: C50C3.11; CE00117.
DR InterPro: IPR002035; -.
DR Pfam: PF00092; vwa; 1.
DR PROSITE: PS50234; VWFA_DOMAIN; 1.
DR KW Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;
KW Glycoprotein.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. . ) (POTENTIAL).
FT SEQUENCE 734 AA; 85034 MW; CCFB78CDBE4B71F CRC64;
QY Query Match 10.8%; Score 607; DB 1; Length 734;
BY Best Local Similarity 26.8%; Pred. No. 1.3e-27;
MM Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;
QY 47 LAKTAGVNLVDIEKYQDIYTPNPNAQLVETIAARDIEKLISNRS----KALVSIAL 102
DB : : | : : : : : : : : : : : : | : | : | : | : | : | : | :
QY 36 MKETFISKISHETILKONYEKIVEEQDPRAELKSKHRIEDYLKVSQFAYKAKIS--L 93
QY 103 EAERQVAAHQWRDFASNEVVYYNAKDLDPEK-NDSPEGSQRTP-----VFIEDANF 155
DB || : : : : : : : : : : : : | : | : | : | : | : | : | :
QY 94 EARSVRNDSTVNDPSQSFIRFMSAKQGNDGTITYESNHGLKRLKVNETKSFNLTQNANF 153
QY 156 -GROISQHAHVHTPTDIYGSTIVNELNWTLSALDEVFKKNREDESLLMQVFGSATGL 214
DB : : | : | : | : : : : : : : : : : | : | : | : | : | : | : | :
QY 154 YTLPTS SVSSAVHTPTPLYRDNEIDLRLKDW-SDIDAVITRNREETDLAFQLFCSEAGY 212
QY 215 ARYPASPFW-DNSRTENKIDLYDVRRPPWIOGAAPKMDLIIVDVGSGVSLGTLKLIR 273
DB ||||| : : | : | : | : | : | : | : | : | : | : | : | : :
QY 213 MRYIPAAASWFWDNQ--DEHLDLFCRTEWTSATNSKNVLIMLDMSGMLGQRYEVAK 270
QY 274 TSVSEMLETLLSDDDFVNVAFSNSNA---QDVSCFPQLHVQANRVKKLVKDAVNNITAKGI 330
DB : : : : | : : : : : : : : : : : : | : | : | : | : | : | : | :

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EMBL: X70393; CAA49843.1; -  
MGD; MGI:96620; Itih3.  
InterPro: IPR002035; -  
Pfam: PF00092; vwa; 1.  
DR PROSITE; PS0234; VWFA\_DOMAIN; 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
glycoprotein.  
FT SIGNAL 1 18 POTENTIAL.  
FT PROPEP 19 30 BY SIMILARITY.  
FT CHAIN 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
H3.  
FT PROPEP 647 886 BY SIMILARITY.  
FT DOMAIN 279 439 VWFA.  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT BINDING 646 646 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
(BY SIMILARITY).  
SQ SEQUENCE 886 AA; 98977 MW; 15955308C7F5030A CRC64;

Query Match 3.5%; Score 194.5; DB 1; Length 886;  
Best Local Similarity 19.9%; Pred. No. 0.00089;  
Matches 185; Conservative 138; Mismatches 347; Indels 261; Gaps 44;  
QY 27 FPSAVTKSWDKMDEDVTLAKTAGSNQVLYVEKYQDLYTYEPNNARQLVEIAARDI 86  
DB 98 YPGNVKEVAQKQEKAVSGOKTAG----LVKASGRKLEKFTVSVNVAAGSKVTFELTY 153  
QY 87 EKLNSNRKALVSLALEAKYQAAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSRIK 146  
DB 154 EELL-KRNKGYEMLYKQPKQLVRHFEID-----AHIFEP-----Q 189  
QY 147 PVFIDANFGROIYQHOAHVHPTDIYEGSTIVNELNWTGALDEVFKNKEEDPSLLMQ 206  
DB 130 GISMLDAE-----ASFITNDL-LGSALATKSF----- 214  
QY 207 VEGSATGLARYYPASPWNST-PNKTID-----LYDVRERP-----WYI-- 245  
DB 215 -----SGKKGHVSFKPSLDQQRSCPTCDLSLLNGDFTIVDVNRESPOVINGYFVHF 269  
QY 246 ---QG-AASPDMILTVDSVSGSLTLKLRITSYSEMLETSLDDDFVNVASFNSAQDV 301  
DB 270 FAPQGLPVVPANIVFIDVSGSMGRKIQOTREALKLLDDVDKEDDYLNFLFST---DV 326  
QY 302 SOFQ-HLVQANVRNKKVLYKDAVNNITAKGIDYKKGFSFAFEQLLYNVSRAN-----C 354  
DB 327 TTKDKHLVQATPANLKEAKTEFKVNIHQDSMTNINDGLLKGIEML---NKAREDHVTPERS 383  
QY 355 NKIIMLFTDG-----GEERAQELFKYK-NKKVRFVRFSGVQHYERGPQWACENKG 408  
DB 384 TSIIIMLTGDGANTGESPEKIQENVRNAIGKFPFLYNLGFG-NLNLNFTLETALEHNG 442  
QY 409 YYPEIPSGAIRINTQEVLDVLRGPMVLGDKAKQVQNTVYLDALGLL---VIITGLPV 466  
DB 443 LARIYEDSDANLQGGVEEVANPLL-----TNEVEPEPNAIDLTRNSYPH 491  
QY 467 FNITQFQENKTNKQLILGVGVDSVLEDIKRLTPFTCLPNGYFFAIDPNGYVLLHPN 526  
DB 492 F-----YDG-----SEIVVAGRLVDRNMDN-----FKADVKGHCALN-- 523  
QY 527 LQPKNPKSOEPTVDFLDAELENLKVIRKNMIDGESGEK--FPTLVKSODERYIDKG 584  
DB 524 ----DLTETEEDVMEEMDAALK-----EQGYIFGDYIERLWALYLTIEQLLEKRNKAG 572  
QY 585 NRTYTWTPVNGVDYSLA--LVLPYTFYVYIRAKLEETITQARSKGKMKDSEI-----LK 637

DB 573 DEKENIT-AEALDLSLKYHFVPLTSMVTKPEDNEQDTSIADNAGEFAETMTMSFLT 631  
QY 638 PDNEESGYFIAPRDYCNLDKISDNTTELLNFEIDRKTTPNPNCSNADLINRVLLDA 697  
DB 632 TQOSSQSPYIYV-----DGPFIHQI-----PGKNSICNIDEKP 668  
QY 698 GFTNELQNTYWSKQKNIKVKAREVVDGTTIRYVPKEAGENWQENPETYBDSFYKRSLD 757  
DB 669 GTVLRLIQD-----PVT--GIT-VTGQIIGD-----KRS-- 694  
QY 758 NDNVFTAPIFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVGKIDVNSWIENFTKTS 817  
DB 695 NASRTGKTIFYGKLGITNAWMDRFEVTEKIILG-----TGAELSTFSLDVTVTQ 747  
QY 818 IRDPCAGPVCDCKNSDVMDCVILDDG--GFLLMAN-----HDDVTNQIGRFFGEIDP 868  
DB 748 -----TGLSVTINKKNV--VSEFGDGLISFVIIHQVKKHPVHQDFLG-----FYVDS 795  
QY 869 SLMRHLVNIISVYAFNKSVDYQSV-CEFGAAP 898  
DB 796 HRMSAQTHGLLGQFFQDFKVFGRPGSDP 826  
RESULT 6  
ITIH3\_HUMAN STANDARD; PRT; 885 AA.  
AC Q06033; Q99085;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY  
CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).  
GN ITIH3  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93215656; PubMed=7681778;  
RA Bourguignon J., Diarra-Mehrpour M., Thiberville L., Bost F.,  
RA Sesboue R., Martin J.P.;  
RT "Human pre-alpha-trypsin inhibitor-precursor heavy chain. cDNA and  
RT deduced amino-acid sequence".  
RL Eur. J. Biochem. 212:771-776(1993).  
RN [2]  
RP SEQUENCE OF 341-885 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=89137072; PubMed=2465147;  
RA Diarra-Mehrpour M., Bourguignon J., Sesboue R., Mattei M.-G.,  
RA Passage E., Sallier J.P., Martin J.P.;  
RT "Human plasma inter-alpha-trypsin inhibitor is encoded by four genes  
RT on three chromosomes".  
RL Eur. J. Biochem. 179:147-154(1989).  
RN [3]  
RP SEQUENCE OF 30-49; 463-477 AND 497-515.  
RX MEDLINE=89380192; PubMed=2476436;  
RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin  
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma".  
RL J. Biol. Chem. 264:15975-15981(1989).  
RN [4]  
RP SEQUENCE OF 631-647, AND CROSS-LINKAGE SITE TO BIKUNIN.  
RX MEDLINE=91093267; PubMed=1898736;  
RA Enghild J.J., Salvesen G., Hefta S.A., Thøgersen I.B.,  
RA Rutherford S., Pizzo S.V.;  
RT "Chondroitin 4-sulfate covalently cross-links the chains of the  
RT human blood protein pre-alpha-inhibitor".  
RL J. Biol. Chem. 266:747-751(1991).  
CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE

[illegible]

375	EHRIPEPSTSVIMLTGDGANTVGSERPEKIQENVRNATGGKFFLYNLGFG--NLLNYNFE	433
401	WMACENKGYVYIPISGAIKINTQBYLDVLRPMVLGAKAKQVQWNTVYLDALD	455
434	NMALEHNHGFARRIYEDSDADLQGFYERAVNPL-LTGVEMEYPE--NAILDITONTQYH	490
456	----LGLVTGILPVFNITGQENKTNLK-----NQLILGVMGVDVSLDIKRLTPFTL	506
491	FYDGSIVVAGRL-VDEDMNSF--RADVKHGATNDL---TFTEEVDKMEK-----AL	539
507	CPNGYFYAIDPN-----GYVLLHNPLOPK---NPKSQEPVTLDFLDAELENDIKVEIRN	557
540	QERDYIFG--NVIERLWAYLITIEQLLEKRNKAHGEKENLTARALDLSLKYHFVTPLTS	596
558	KMIDSGSEKTPRTLKVSQDERYI-DKGNRTVYTPVNV-GTDYSIALVLPTVSFYFI	612
597	MVYTKPE-----DNEDERAIDKPGEDAEATPSPAMSYLTSYQPPQNPYYIV	644
DB	RESULT 7	
QY	ITH3_RAT	
DB	ID ITH3_RAT STANDARD; PRT; 887 AA.	
QY	AC Q63416;	
DB	DT 15-JUL-1998 (Rel. 36, Created)	
QY	DT 15-JUL-1998 (Rel. 36, Last sequence update)	
DB	DT 01-OCT-2000 (Rel. 40, Last annotation update)	
QY	DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3).	
DB	GN ITIH3.	
QY	OS Rattus norvegicus (Rat).	
DB	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
QY	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
DB	ON NCBI_TaxID=10116;	
QY	RX [1]	
DB	RP SEQUENCE FROM N.A.	
QY	RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;	
DB	RA Blom A., Fries E.;	
QY	RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.	
DB	CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).	
QY	CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.	
DB	CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).	
QY	CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.	
DB	CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.	
QY	CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announcement/">http://www.isb-sib.ch/announcement/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
DB	CC EMBL; X83231; CAA58233.1; -	
QY	CC InterPro; IPR002035; -	
DB	CC Pfam; PF00092; vwa; 1.	
QY	CC PROSITE; PS50234; VWFA_DOMAIN; 1.	
DB	CC Serine protease inhibitor; Repeat; Signal; Multigene family;	
QY	CC Glycoprotein. 1 21 POTENTIAL.	
DB	CC SIGNAL 22 33 BY SIMILARITY.	
QY	CC FT PROPEP 34 647 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3.	
DB	CC FT CHAIN	

Mon Jul 23 08:36:42 2001

FT	PROPEP	648	887	BY SIMILARITY.
FT	DOMAIN	282	442	WFVA.
FT	CARBOHYD	91	91	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	580	580	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	BINDING	647	647	CHONDROITIN 4-SULFATE, CROSS-LINK SITE (BY SIMILARITY).
SQ	SEQUENCE	887 AA;	99097 MW;	3B9FOFF96D514096 CRC64;
Query Match 3.2%; Score 180.5; DB 1; Length 887;				
Best Local Similarity 18.5%; Pred. No. 0.0056;				
Matches 173; Conservative 139; Mismatches 350; Indels 275; Gaps 39;				
QY	27	FPSAVTIKSWDKQDLVTLAKTASGVNQLVDIYEKYQDLTYTVEPNNAQVLEIAARDI	86	
Db	101	YPGSVKEVAQKQYKAVSQKTAG---LVKASGRKLEKFTSVNVAAAGSKVIFELTY	156	
QY	87	EKLNSRKALVSLALEAEKVAQAQWRED---FASNEVYVYNAKDDLDPEKNDEPGSQ	143	
Db	157	EELL-KRNRKGYEMYLKQVFKQVLRHFEIDAHIPEQGISMLDA-----	199	
QY	144	RKPVIEDANFGQISYQAAVHIPTDIYEGSTIVLNELNMTSALDEVEFKKNREDDPSL	203	
Db	200	-----DASF-----ITNDL-LGSALTKEF-----	217	
QY	204	LMQVFGSATGLARYYPASPVDNSRT-PNKID-----LYDVRRRP-----WY	244	
Db	218	-----SGKKHVSFKPSLDOORSCPTCTDSLLNGDEFTIVYDVNRSPGNQVIYNGYF	269	
QY	245	I-----QG-AASFKDMLLVDSVSGSLTKLIRYSVSEMLETSLDSDPFVNVASNSNA	298	
Db	270	VHFFAPQGLPVPKNTAFYIDVSGSGRKIQOTRALUKILDDMKEDLYNLFSTGV	329	
QY	299	QDVSCFHLQVQANRNVKVLKDAVNNTAKGITDYKKGFSFAFEQLNLYNVRAN----	353	
Db	330	--TWKDLHLVATPANLEEARAFVKNIORDSMFNINDGLLGIEML---NKAREDLHVE	384	
QY	354	-CNKIIMLFTD---GEERAQEIFNKNKDKVVRFRFSVG-OHNVERGPIOWMACENK	407	
Db	385	RSTSILVMTDGOANTGESRPEKIQENVRNAIRGKFPYLNLFNGNLLYNFLESALENH	444	
QY	408	GYEIEISGAIRINTEYLDVLRGPMVLADKAKQVQWNTNVLDALEGL--VITGTLF	465	
Db	445	GFARIYEDSDASLOLQGFVEEVANPLL-----TNVEYFENAILDLTRNSYP	493	
QY	466	VFNITGFENKTNKLNOLILGVMGVDSLEDIKRLTPFTLCPNGYYFAIDPNGYVLLHP	525	
Db	494	HF-----YDG-----SEIVVAGRLVDRVDN-----FKADVKGHGALN-	526	
QY	526	NLOPKNPKSQBPVTLDFDLAELENDIKVEIRNKNMIDGESKEKT-----RTLKVSQDER	579	
Db	527	-----DLTFTTEEDVMKEMDAALK-----EQGYIFGDYIERLWAYLTIEQLLEKRNAR	574	
QY	580	YIDKGNRTYTTPVNGTDYSLA--LVLPYTSFYIYKAKLEETIQARSKGKMKDSET--	635	
Db	575	GDEKENIT-----AEALELSLKYHFVPLTSMVYTKPEDNEDQTAIDKPGEEAISASTA	629	
QY	636	-LKPDPNFEESGYTFIAPRDYCNLDKISDNNTFFLLNF---NEFIDRKTTPNPNPCNADLIN	691	
Db	630	YLTQSQSSHSPIYV-----DCDHPHFIQVQKNDTCFNDKPKGVLSLIQ	677	
QY	692	RVLLDAGETNELVQWNSKQNKIKGVKARFVVTGDTITRVYKPEAGENWQNPETYEDSF	751	
Db	678	DPVTGIATVGQII-----GEKGNNASSRTGKT-----	704	
QY	752	YKRLSDNDNVFTAPYFNKSGPGAYESIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIE	811	
Db	705	-----YFKGLGTANAWMDFRIEVTEKILGN-----GDALSTFSLWD	742	
QY	812	NFTKTSIRDPCAGPVCDCKRNSDVMCDVILDDG-GFLMAN-----HDDYTNQIGRF	862	
Db	743	TVTVTQ-----TGLSVTINRKNKMV--VSFEDGISFVILHVQWKKHPVHQDFLG-----	790	

QY	863	FGEIDPSLMRLHVNISVYAFNKNSDYQSV-CEPGAAP	898	
Db	791	FYVDVSHRMSAQTHGLLQGFQFPDFEKVFDVVRPGSDP	827	
RESULT 8				
ITH3_MESAU	8			
ID	ITH3_MESAU	STANDARD;	PRT;	886 AA.
AC	P97280;			
DT	15-JUL-1998	(Rel. 36, Created)		
DT	15-JUL-1998	(Rel. 36, Last sequence update)		
DT	01-OCT-2000	(Rel. 40, Last annotation update)		
DE	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) (HC3).			
GN	ITIH3.			
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus.			
OX	NCBI_TaxID=10036;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=97420688; PubMed=9276673;			
RA	Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;			
RT	"Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family."			
RT	J. Biochem. 122:71-82(1997).			
CC	FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).			
CC	SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.			
CC	PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).			
CC	SIMILARITY: BELONGS TO THE ITIH FAMILY.			
CC	SIMILARITY: CONTAINS 1 WFVA DOMAIN			
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CC	EMBL: D89287; BAAL3940.1;			
DR	InterPro: IPR002035;			
DR	Protein: PF00092; WVA; 1.			
DR	PROSITE: PS0234; WFVA_DOMAIN; 1.			
KW	Serine protease inhibitor; Repeat; Signal; Multigene family; Glycoprotein.			
FT	SIGNAL	1	18	POTENTIAL.
FT	PROPEP	19	30	BY SIMILARITY.
FT	CHAIN	31	646	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3.
FT	PROPEP	647	886	BY SIMILARITY.
FT	DOMAIN	279	439	WFVA.
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	577	577	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	BINDING	646	646	CHONDROITIN 4-SULFATE, CROSS-LINK SITE (BY SIMILARITY).
SQ	SEQUENCE	886 AA;	99018 MW;	AC0594C685257688 CRC64;

Query Match 2.9%; Score 164.5; DB 1; Length 886;  
Best Local Similarity 23.2%; Pred. No. 0.047;  
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;

QY 202 SLLWVFGSATGLARYIPASPVWDSNR-PNKID-----LYDVRER-PWYIOGA-- 248  
DB 208 SALTSGFGKGGHVFKEF-----LDQORSCPTCTDSSLNGDFTIVYDVNRSPGNVQVYVNG 264  
QY 249 -----ASPKDMLILVDVSGVSGTLKLRISVSSEMLETSLDDDFVNVASFNS 296  
DB 265 YVHFFAFOGLPVVPEKIVFVIDISSMAGRKIQOTRVALKILDDMKQDDYLNILFEST 324  
QY 297 NAQDVSCQHLVQVNRKVLKDAVNITAKGIDYKKGSAFAEQLLN-----YVNSRA 352  
DB 325 GV-TTWKDSLVQAPANLEEARTEVRSISQGMNTINDLGLRMLTDAREQHTVPER 382  
QY 353 NCKNIMLFTDQ-----GEARQEIFNKDKKVVRFVSFG-QHNYERGPIQWACENK 407  
DB 383 STSIILML-TGDANTGESREKIQENVRKALEGFPPIYLGFGNNLNYFLETMALENH 441  
QY 408 GYVEIPSIGAIRINTQBYDLVGRPMVLADGKAKQVQVNTNYLD 452  
DB 442 GVARRIEDSDANLQLOQFYEVANPLL-----TNVEVE 475

RESULT 9  
DPOL\_THEST STANDARD; PRT; 1829 AA.  
AC O33845;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE DNA POLYMERASE (EC 2.7.7.7).  
GN POL.  
OS Thermococcus sp. (strain TV).  
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.  
OX NCBI\_TaxID=86030;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98094267; PubMed=9434178;  
RA Niehaus F., Frey B., Antranikian G.  
RT "Cloning and characterisation of a thermostable alpha-DNA polymerase  
from the hyperthermophilic archaeon Thermococcus sp. TY.,"  
RL Gene 204:153-158(1997).  
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -  
N PYROPHOSPHATE + DNA(N).  
CC -1- PPM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES  
A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION  
(INTINS) FOLLOWED BY PEPTIDE LIGATION.  
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: Y13030; CAA73475.1;  
CC InterPro: IPR002064;  
CC InterPro: IPR002203;  
CC Pfam: PF001136; DNA\_pol\_B; 4.  
CC PRINTS: PR00379; INTEIN.  
CC PROSITE: PS00116; DNA\_POLYMERASE\_B; FALSE\_NEG.  
CC PROSITE: PS00881; PROTEIN\_SPLICING; 3.  
CC Transferrase; DNA-directed DNA polymerase; DNA replication;  
KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;  
KW Protein splicing.  
FT CHAIN 1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).  
FT CHAIN 410 769 INTEIN 1.  
FT CHAIN 770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).  
FT

FT CHAIN 856 1392 INTEIN 11.  
FT CHAIN 1393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).  
FT CHAIN 1442 1598 INTEIN 11.  
FT CHAIN 1599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).  
SQ SEQUENCE 1829 AA; 211875 MW; A113A8BC57EB9CB3 CRC64;

Query Match 2.9%; Score 161; DB 1; Length 1829;  
Best Local Similarity 20.1%; Pred. No. 0.21;  
Matches 172; Conservative 101; Mismatches 301; Indels 282; Gaps 39;

QY 16 SLLIGPSEEPSPS-----AVTIKSW-----DKMQEDLVTLA 48  
DB 229 TLLGRDRKHEPKIHRMGDSFAVEIKGRIHFDLFPVVRTINLPYTLAEVAVLGKT 288  
QY 49 KTASGVNQLVDIYKQDL-----YTVENNARQLVEIAARDIEKLLSNRSLALALE 103  
DB 289 KSKLGAEEAIAIWEETESMKLAQYSME--DARAYEL-----GKEFFPMEAE 334  
QY 104 AEKQAAHQWREDFAS--NEVVY-----NAKDDLDPEKNDSEPGSQRIKPVFI----- 150  
DB 335 LAKLIGQSVWDVSRSTGNLVEMYLRLVAYERNELAPKPDDEEYRRRLRTYILGYVKE 394  
QY 151 EDANFGROISTOHAHVHPTD---IYEGSTIV-----LNELNWTSALDEVFKKNREEDPSL 203  
DB 395 PERGLWENIAYLDFRCH-PADTKVIVKGGIVNISDVKEGDIYLGIDG----- 441  
QY 204 LMQVFGSATGLARYYPASPVWDSNR---TPN-KIDLYDVRERPWPVIOGAASPKDMLILVD 259  
DB 442 -WQ-----RVKVKWKYHIEGKLINGLKCTPNHKVPVVTENDRQTRI-----RDSLAKSF 491  
QY 260 VSGVSGTLKLRISVSSEMLETSLDDDFVNVASFNSN-----FEKTAEEKNKPSEELKLGSLIILAEGLT 537  
DB 492 LSGKVGK--KIITKL-----OHLVQVNV-RNKKVLKDAV-----NNTAKG----- 329  
QY 298 -AQDVSCF-----OHLVQVNV-RNKKVLKDAV-----NNTAKG----- 329  
DB 538 LRKIDIEYDSSRGKRKRISHOYRVEITIGENKEKELLERYIFDKLFGIRPSVKKKGDTNA 597  
QY 330 -ITDYKKGFSFAPBOLLNPNVSRANCKIIMLFTDGGEEARQAEIFNKYKDKKRVVRF 387  
DB 598 LKITTAKAVQLQIEELK-NIESLYAPAVLRGF-----FERDATYKNKRS 642  
QY 388 SV-----GQHNTERGPIQWACENKGY---YVEIPSIGAIRINTQBYDLVGRPMVLADGK 440  
DB 643 TIVTQGTNNKKIDIVAKLLDSLGLIPYSRYEYKVIENGKELTKHILITGED----- 695  
QY 441 AKQVQWTVNYLDALGLVITGTLPVFNITQGF-----NKTNLKNOLILGVMGVD 491  
DB 696 -----GLILFQTLVGFISSEKNEALEKAEIVRENNRNNKNSFYNLSTFE 739  
QY 492 VSLIEDIKRLTPRTLCPNGYFAIDPNGYVLLHNPLOPKNSQEPVTLDFDALENDI 551  
DB 740 VSSEYKGEVYDLLEGPNYIFA---NG-ILTHNSLYPSIIVTNH-VSPDILERE----- 789  
QY 552 KVEIRNKMGIDGSEKTEKTRTLVKSDQERYIDKGNRTYTPVNGTDTYSLALVLPYTFY 611  
DB 790 -----GCKNYDVAPIVG--YKCFKDFPG----F 811  
QY 612 IKAKLEETITQARSKGKMKDSEILKPDNFEEG-----TFTAPROYCNDLKTSD 662  
DB 812 IPSILGELITMRQETIKKMK--ATIDPIEKKMLDYRQRAVKLLANSILNPNE---LPIT 866  
QY 663 NNTFLLNNEFIDRKTPNPNPNSCNADLINRVLLDAGFTNELVQNVWSQKKNKGVKAREV 722  
DB 867 NGEYKFKVIGEFIDRYMEEQDKVTVTDNTEVLEVDNIFAFSLNKSSEIKKVKAL-- 924  
QY 723 VTDGGITRVYPKEAGE 738  
DB 925 -----IRHKYKGEAYE 935

RESULT 10

ATX1\_PLAFA STANDARD; PRT; 1956 AA.  
ID AC Q04956;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE PROBABLE CATION-TRANSPORTING ATPASE 1 (EC 3.6.1.-).  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=79/96;  
RX MEDLINE=93132070; PubMed=8421054;  
RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,  
RA Robson K.J.; cation ATPase-like molecules from Plasmodium  
RT "A family of cation ATPase-like molecules from Plasmodium  
RT falciparum.";  
RL J. Cell Biol. 120:385-398(1993).  
CC -|- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.  
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2  
CC ATPASES). SUBFAMILY V.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL: X65738; CAA6646.1; -  
DR InterPro: IPR001757; -  
DR Pfam: PF00122; E1-E2\_ATPase; 4. -  
DR PROSITE: PS00154; ATPASE\_E1\_E2; 1.  
KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.  
FT FT DOMAIN 1 35  
FT FT TRANSMEM 36 58  
FT FT DOMAIN 59 61  
FT FT TRANSMEM 62 80  
FT FT TRANSMEM 81 407  
FT FT TRANSMEM 408 427  
FT FT TRANSMEM 428 440  
FT FT TRANSMEM 441 462  
FT FT TRANSMEM 463 1818  
FT FT TRANSMEM 1819 1937  
FT FT TRANSMEM 1838 1845  
FT FT TRANSMEM 1846 1863  
FT FT TRANSMEM 1864 1881  
FT FT TRANSMEM 1882 1905  
FT FT TRANSMEM 1906 1928  
FT FT TRANSMEM 1929 1952  
FT FT TRANSMEM 1953 1956  
FT FT MOD\_RES 496 496  
FT FT METAL 1760 1760  
FT FT METAL 1764 1764  
FT FT TRANSMEM 246 251  
FT FT TRANSMEM 252 256  
FT FT TRANSMEM 937 941  
FT FT TRANSMEM 1344 1347  
FT FT TRANSMEM 1363 1372  
FT FT TRANSMEM 1680 1684  
SQ SEQUENCE 1956 AA; 230285 MW; AE708AAE99009335 CRC64;  
Query Match 2.8%; Score 159; DB 1; Length 1956;  
Best Local Similarity 17.1%; Pred. No. 0.3;  
Matches 179; Conservative 144; Mismatches 359; Indels 366; Gaps 45;  
OY 58 VDIEYQDIYVEPNAROLVFIARDIEKLLSNR-----SKALVSLALEAEK 106  
Db 100 INVYRYTSLYISS-----ELVPGDIYEIKNNMTIPCDTILSGSVTMSHMLTGES 152

107 VOAAHQWREDFASNEVVYNAKODLDPEKND-----SEPGSORIKPVFIEDANFGROIS 160  
153 V-PIHKERLPFEGNALINKNNKNDYSDERKDDYLRIYNNHASINMIKRNHLIETLGKKDR 211  
161 YQAAAHPTDIYEGSTIVLINELNW-TSALDEVFKKNREEDPSLLMQVFGSATGLARYTP 219  
212 EYKSNTH-----DLCSMKLCYINNTYDVHMKNNKM----- 244  
220 ASPWDNSRTPNPKIDLYDVRRRPWYTOGA-ASPKDMLILVDVSGSYGLTKLIRTSVSE 278  
245 ---YNNNNNNKKKKINLN-----FVKGYINSNLLY----- 275  
279 MLETLSDDDFEVNVASFNSSNAODVSCQHLVQAVNRKVKLDVANNITAKGIDYKKGFS 338  
276 -----DKIGVNIPE---DDVNNMKH--KFNORININYKDTNNL-----EYNNKHR 317  
339 FAFEQLLNVNVRANCKIIMLFDTGGEEAQAETFNKYNKDKKVRVRFVSGVGHYERGP 398  
318 IYDCLLKVEAISQKNKIY-----SNEDINKY----- 346  
399 IOWMACENKGYEYIPEISGAIRINTQYLDVLRPMVLG-----DKAKOV 444  
347 ---MLYGGTYVLSLYNINKIKYNNKEENRILGL-VIKTGFITTKGKIVNNILYHKKKL 401  
445 QWTNVYLDALGELGIVITGTLPVFNITQGFENKTNLKNQILG-----V 487  
402 NLINDSYKFLII-LIYALPSVFLIYTLSSNNEYTHIILIKCLDIITDAIPALPTILT 460  
488 MGVDSVLEDKRLTPRTPKNGVYFA-----IDPNGYVLLHPNLQ-----PKNPKSQ 535  
461 VGISIARLKKKESISCLCPHKINIAGIWNVFDKGT-TLTENNLFQIGITQNNKK 519  
536 EPVTLDFDLAELENDIKVEIRNKNMIDGESGKPTRTLVKSQDERYIDKGNRTYWTVPNG 595  
520 NMLS-DETHIK-----EMNTESYTHSRDDNNMHKN----- 549  
596 TDYSLALVLPFYFYIYKAKLEETITQARSKKMKMD-----SETLKPNDFEESG 645  
550 -----STISEYIKDNMKNLHTSSK-KKSTIKERSNLFVQTIKSCLLKDHVKEKK 599  
646 YTFIAPRDYCNLDKISDNN-TEFLIN-----FNEF--IDRKTNNPNSCNADLINRVLLD 696  
600 KEYTNTNYCNDLHINDSTCSSYLLNSETKDAYCEYNIH-----LCD---INKKND 650  
697 AGFTNELQNTWSKQKNIKGVKARPVVDGGITRYVPREAGENWQENPETYEDSYKRS 756  
651 INSKNELMGYSKNELMGKTIKNELM-----GKYSKNE 684  
757 DNDNVYFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVG-----IKIDVNSWI 810  
685 -----MGYSKNELMGYSKNELMGYSKNELMGYSKNELMGYSKNELMGYSKNELMGYSKNE 737  
811 ENFTKTSIRD-PCAGPVCDCKRNSDVMDCV-----ILDDGGFLLMANHDDYTNOIGRF--- 862  
738 MNCNDYNDYPCD---YNCNNDNTYHRLVHNKNSFNIPPEKNKSYNNISEHIKI 794  
863 -----FGEIDPSLMRHLVNIISVAF-----NEYSYDQ 889  
795 NYPLLFELACCHTSLSKVNMKIMGVLEILMFENFNCMDMLNNNSFIKEKKKNCYSYDQ 854  
890 SVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAWSILOQFLSLTLPRLLEAVE 949  
855 KI---DGDKNIGANDERCHLNN-----NLVSYNILARF----- 884  
950 DDDFTASLSKQSCITEQTQYFFDNDNSKS 977  
885 ---EFQSRLOQMSVYIKST-YGNNDNDNN 909

RESULT 11  
YFBK\_ECOLI  
ID YFBK\_ECOLI STANDARD; PRT; 575 AA.



P76481;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HYPOTHETICAL 63.6 KDA PROTEIN IN ELAD-NUON INTERGENIC REGION.  
GN YFBK.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
CC -1- SIMILARITY: TO SYNCHOCYSTIS PCC 6803 SLL0103.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AE000317; AAC75330.1;  
DR EcoGene; EG14095; yfbk.  
DR InterPro; IPR002035;  
DR Pfam; PF00092; ywa; 1.  
DR PROSITE; PS0234; VWFA\_DOMAIN; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 575 AA; 63634 MW; 7BB6A1A77A2BE111 CRC64;

Query Match 2.88; Score 157.5; DB 1; Length 575;  
Best Local Similarity 21.68; Pred. No. 0.063;  
Matches 111; Conservative 93; Mismatches 206; Indels 105; Gaps 25;

QY 71 EPNARQVETARDIEKILNSRKALVSLAEKVOAAHQWREDPASNEVYVNAKDD 130  
DB 22 QPENKESQQQPSPTPEQQVLAQAQAIAK---EAEQSA---AKALAQQEVOQYSDKQA 75  
QY 131 LDPEKND-----SEPGSORIKPVFIEDANFGRIQISYQHA---VHIPTDI 172  
DB 76 LOGRLQEAFTFAAAKAKATHIANPGTARYQQF---DDNPVQVAQNPLATFSLDVTGS 132  
QY 173 YEGSTIVLNE-----LNWTSALDEVEKKNREEDPSLLWQVFGSATGLARY 218  
DB 133 YANVRFLNQLGPPPPDAVREIVNVPSPDWI---KDKQSIASRPPIPMARYELA--- 187  
QY 219 PASPWNDSTPNKIDLYVRRPRTWQGAASPKDMLILVDVSGS-VSGTLKLRTSVS 277  
DB 188 PA-PW-NEQRTLLKVDILAKDRKSELPAS---NLVFLIDTSGSMISDBRLPIQSLK 241  
QY 278 EMLETLSDDDFVNVASFNNAQDVSCFQHLVQANVRNKKVLKDAVNNTAKGTDYKGF 337  
DB 242 LLVKELEQDNIAIVYAGDSRTA-----LPSISGSHKAEINAIDSLDAEGSTNGAGL 296  
QY 338 SFAFEOQLNYSRANCKIIMLFTDG-----GEERAQEIFKNYKNKKRVRFERSVGQ 391  
DB 297 ELAYQOATK-GFIKGINR-ILLATDGFNVGIDDPKSTESVKKKQRESGVLTSTFGVN 354  
QY 392 HNYVERPQIOWACENKGYEYIPSGAINTQYEDLVIGRPMVL--AGDKAKQVQ---- 445  
DB 355 SNTNEAMVRIADVGNNGNTSYIDTLS-----EAQKVLNSENRMQLITVADKVAQIEFNA 410  
QY 446 WTNVYLDALGLVITGLTPVFNITGQFENKYNLKNQLILGVNGVD-VSELDI---KRIT 501

DB 411 WTEY---RQIG-----YE-----KQLRVEHFNNDVNDAGDIGAGKHIT 447  
QY 502 PRFTLCNGYIFAIDPNGVYLLHPNLPKNPKSQE 536  
DB 448 LLFELTLNGKASIDKLRYA--PDNKLAKSDTKTE 480  
RESULT 12  
ITH2 HUMAN  
ID ITH2 HUMAN STANDARD; PRT; 946 AA.  
AC P19823; Q15484; Q14659;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY  
DE CHAIN H2) (INTER-ALPHA-TRYPSIN INHIBITOR COMPLEX COMPONENT II)  
DE (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).  
GN ITIH2 OR IGHEP2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=88152237; PubMed=2450046;  
RA Gebhard W., Schreitmuller T., Hochstrasser K., Wachter E.;  
RT "Complementary DNA and derived amino acid sequence of the precursor  
RT of one of the three protein components of the inter-alpha-trypsin  
RT inhibitor complex.";  
RL FEBS Lett. 229:63-67(1988).  
RN [2]  
RP SEQUENCE OF 384-865 FROM N.A.  
RX MEDLINE=88068576; PubMed=2446322;  
RA Salier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,  
RA Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.P.;  
RT "Isolation and characterization of cDNAs encoding the heavy chain of  
RT human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous  
RT evidence for multipolypeptide chain structure of I alpha TI.";  
RN Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).  
RN [3]  
RP SEQUENCE OF 384-766 FROM N.A.  
RX MEDLINE=89076497; PubMed=2462430;  
RA Salier J.P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,  
RA Martin J.P.;  
RT "Human inter-alpha-trypsin inhibitor. Isolation and characterization  
RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence  
RT of the H chain.";  
RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).  
RN [4]  
RP PARTIAL SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=88024442; PubMed=3663330;  
RA Schreitmuller T., Hochstrasser K., Resinger P.W.M., Wachter E.,  
RA Gebhard W.;  
RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses three  
RT different proteins.";  
RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).  
RN [5]  
RP SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.  
RX MEDLINE=89380192; PubMed=2476436;  
RA Engild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;  
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin  
RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.  
RT Polypeptide chain stoichiometry and assembly by glycan.";  
RL J. Biol. Chem. 264:15975-15981(1989).  
RN [6]  
RP SEQUENCE OF 55-64.  
RC TISSUE=Plasma;  
RX MEDLINE=93039735; PubMed=1384548;  
RA Malki N., Balduick M., Maes P., Capon C., Mizon C., Han K.K.,  
RA Tartar A., Fournet B., Mizon J.;  
RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor: their  
RT isolation, their identification by electrophoresis and partial



sequencing. Differential reactivity with concanavalin A.";  
 Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).  
 [7]  
 SEQUENCE OF 55-64 AND 681-702, AND CROSS-LINK STRUCTURE.  
 MEDLINE=9332026; PubMed=7682553;  
 RA Englund J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,  
 Pizzo S.V., Hefta S.A.;  
 RA "Presence of the protein-glycosaminoglycan-protein covalent cross-link  
 in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain  
 2/bikunin.";  
 J. Biol. Chem. 268:8711-8716(1993).  
 [8]  
 SEQUENCE OF 67-101, AND HYALURONAN BINDING.  
 TISSUE-Serum;  
 MEDLINE=94075371; PubMed=7504674;  
 RA Huang L., Yoneda M., Kimata K.;  
 RA "A serum-derived hyaluronan-associated protein (SHAP) is the heavy  
 chain of the inter-alpha-trypsin inhibitor.";  
 J. Biol. Chem. 268:26725-26730(1993).  
 [9]  
 SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.  
 TISSUE-Plasma;  
 MEDLINE=94229087; PubMed=7513643;  
 RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,  
 Michalski C., Fournet B., Mizon J.;  
 RA "Chondroitin sulphate covalently cross-links the three polypeptide  
 chains of inter-alpha-trypsin inhibitor.";  
 Eur. J. Biochem. 221:881-888(1994).  
 CC -!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
 CC -!- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,  
 BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE.  
 CC -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
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 CC -----  
 DR EMBL; X07173; CAA30160.1; ALT\_SEQ.  
 DR EMBL; M18193; AAA60558.1; -.  
 DR EMBL; M33033; AAA59195.1; -.  
 DR PIR; S00346; IYHU2.  
 DR PIR; B34245; B34245.  
 DR GlycoSuiteDB; P19823; -.  
 DR MIM; 146640; -.  
 DR InterPro; IPR002035; -.  
 DR Pfam; PF00092; vwa; 1.  
 DR PROSITE; PS0234; VWFA\_DOMAIN; 1.  
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
 KW Glycoprotein.  
 FT SIGNAL 1 18  
 FT PROPEP 19 54  
 FT CHAIN 55 702  
 FT INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN  
 FT H2.  
 FT PROPEP 703 946  
 FT DOMAIN 308 468  
 FT CARBOHYD 118 118  
 FT CARBOHYD 445 445  
 FT CARBOHYD 671 671  
 FT MOD\_RES 282 282  
 FT CARBOXYLATION.  
 FT MOD\_RES 282

FT MOD\_RES 283 283 CARBOXYLATION.  
 FT BINDING 702 702 CHONDROITIN-4-SULFATE, CROSS-LINK SITE.  
 FT CONFLICT 674 674 P -> A (IN REF. 2 AND 3).  
 FT CONFLICT 705 705 F -> S (IN REF. 2 AND 3).  
 FT CONFLICT 729 729 N -> D (IN REF. 2 AND 3).  
 FT CONFLICT 731 731 V -> A (IN REF. 2 AND 3).  
 FT CONFLICT 374 374 K -> L (IN REF. 5).  
 SQ SEQUENCE 946 AA; 106436 MW; 1478CF3B8F3BA776 CRC64;  
 Query Match 2.8%; Score 154.5; DB 1; Length 946;  
 Best Local Similarity 19.9%; Pred. No. 0.19;  
 Matches 133; Conservative 106; Mismatches 259; Indels 171; Gaps 29;  
 QY 33 IKSVDKMQEDLVTLAKTAGSGVNLVDIYEKYQDLTYTEPNARQLVETAAARDIEKLLSN 92  
 DB 26 LSEFVD--YEDIVEL---APGRFQLVAENRRYORSLPGESEEMEEVDQVTLYSYKQST 80  
 QY 93 RSKALVSLALEAEKVOAAHORE-----DFASN-----EV 122  
 DB 81 ITRMATMIQSKVNNSPQNVFVDVQIPKATISNFSMTVDGKTFRSSIKEKTVGRA 140  
 QY 123 VYNAK-----DDLPEKNDSE----PGSORIKPVFIEDANFORQISYOH---- 163  
 DB 141 LYAQAARAGKTAGLVRSASALDMENFTEVNLPGAKVQELHYQEVKWKRLGSEYHRIYL 200  
 QY 164 -----AAVHIPTDIYEGSTIVLNELNWTSLD-----EYFKKNREB-----DPSLLWQVF 208  
 DB 201 QPGLAKHLEVDVWVIEPQGLRFLHVPDTFEHFGVPIVSKGQOKAHVSFRPTVAQO-- 258  
 QY 209 GSATGLARYYPASPVDNSRTNPKIDLYDVRRP-----WYIOGAAS-----PK 252  
 DB 259 -----RICPSCR--ETAVDGLVVLVDVKKREKAGELEVNGFVHFAPDNLDPPIK 309  
 QY 253 DMLILDVSGVSGTLKILRTSVSEMLETSLDDDFVNVASFNASNAQDVSCFQHLVQANV 312  
 DB 310 NTLFVIDVSGSMGVMKQTVAMTKTILDLRAEDHFSVIDFNQIR--TWRNOLISATK 367  
 QY 313 RKKVKLDAVNNITAKGITYDKKGF---SFAFEQLNLYNVSRANCKNIIMLTG----G 365  
 DB 368 TQVADAKRYIEKIQPSGGTINEALLRAIFILNEANNLGLDPNSVSLILVSDGDPTVG 427  
 QY 366 ERAQEIFKNYKDKKVRVERFSGO-----HNYERGPIQWM-----ACENK 407  
 DB 428 ELKLSIKQKNWKENIQDNISLSLGMGFDVDYDFLKLRSNENHGAIRYIGNQDTSSQLK 487  
 QY 408 GYIYEI--PSIGAIRIN--TQEYLDVL-----GRPMVLG--DKAKQVQWNTNVIYL 452  
 DB 488 KFYQVSTPLLRNVQFNYPHTSVTDVTQNNFHYEGSGEIVVAGKFDPAK-----LD 539  
 QY 453 ALELGLVITGLTPVNTIGQFENKLNKQLILGVLGVGVDSLEDI-----KRLTPRPTLCP 508  
 DB 540 QIE--SVITA-----TSANTQLVLETLAQMDLQDLFLSKDKHADPQFTR-K 582  
 QY 509 NGYFEAPDNGVYLLHPNLQPKPKSQEPVTLDFLDAELENDIKVEIRKNKMGIDGSEGT 568  
 DB 583 LWAYLTIN---QLLAERSLAP-TAAAKRRITRSILOMSLDHHIVTPTLSLVINEAGDER 638  
 QY 569 FRTLKVSQD 577  
 DB 639 MLADAPPQD 647  
 RESULT 13  
 BXC1\_CLOBO  
 ID BXC1\_CLOBO STANDARD; PRT; 1290 AA.  
 AC P18640;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE BOTULINUM NEUROTOXIN TYPE C1 PRECURSOR (EC 3.4.24.69) (BONT/C1)  
 DE (BONTOKILYSIN C1).  
 OS Clostridium botulinum.

Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.  
NCBI\_TaxID=1491;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=90370487; PubMed=2204031;  
Hauser D., Eklund M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,  
Boquet P., Popoff M.R.;  
"Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";  
Nucleic Acids Res. 18:4924-4924(1990).  
[2]  
SEQUENCE FROM N.A.  
STRAIN=TYPE C STOCKHOLM / C-ST;  
MEDLINE=91024998; PubMed=2222445;  
Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,  
Yokosawa N., Takeshi K., Syuto B., Oguma K.;  
"The complete nucleotide sequence of the gene coding for botulinum  
type C1 toxin in the C-ST phase genome.";  
Biochem. Biophys. Res. Commun. 171:1304-1311(1990).  
[3]  
SEQUENCE OF 2-25.  
STRAIN=TYPE C STOCKHOLM / C-ST;  
MEDLINE=88153072; PubMed=2450068;  
Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,  
Oguma K.;  
"Establishment of a monoclonal antibody recognizing an antigenic site  
common to Clostridium botulinum type B, C1, D, and E toxins and  
tetanus toxin.";  
Infect. Immun. 56:898-902(1988).  
[4]  
IDENTIFICATION OF SUBSTRATE.  
MEDLINE=94038966; PubMed=7901002;  
Blasi J., Chapman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;  
"Botulinum neurotoxin C1 blocks neurotransmitter release by means of  
cleaving HPC-1/syntaxin.";  
EMBO J. 12:4821-4828(1993).  
-1- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER  
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED  
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD  
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT  
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC  
ENDOPETIDASE THAT CLEAVES SYNTAXIN.  
-1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A  
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,  
WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDATE CHANNEL  
FORMATION AND TOXIN BINDING, RESPECTIVELY.  
-1- SUBCELLULAR LOCATION: SECRETED.  
-1- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF  
BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.  
-1- MISCELLANEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C  
SPRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE  
BACTERIOPHAGE.  
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC  
METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN  
SUBFAMILY.  
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EMBL; X66433; CAA47060.1; -  
DR EMBL; X72793; CAA51313.1; -  
DR EMBL; X53751; CAA37780.1; -  
DR EMBL; D90210; BAA14235.1; -  
DR EMBL; X62389; CAA44263.1; -  
DR PIR; S11291; S11291. -  
DR PIR; A35396; A35396. -  
DR PIR; A43503; A43503. -  
DR MEROPS; M27\_002; -

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QY 698 -----GFTN-----ELVQYVW-----SKQNIKGVKARFVVTDDGTRVYPKAGE 738
Db 840 QNTIPFNISYNNLSLKDINEFNNINDSKILSLQNRKNTLDTSG-----YNAEVSE 894
QY 739 --NQENPETVEDSFYKRSLDNDNVETAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLK 796
Db 895 EGDVQLNP-----IF--PFDFKLGSGGEDRGKVIYTONENIVYNSMYE 935
QY 797 PAVYGIKIDVNSWNTENFKYSIRPCAGVCDCKRNSDVMDVLDLDDGGFLMANHD--- 853
Db 936 SFSISFWIRINKWVSLPGVTIID-----SVKNNSGWSIGIISNLFVTLTKQNESEQ 988
QY 854 -----DYTNQIGR-----FFGEIDPSLMRHLNVISVAFNKSVDYQSVCE 893
Db 989 SINFSDISNNAAGYNKWFVVTNNMGM---NMKIYNGKLIDTIKVE 1035

RESULT 14
Y103_SYNY3
ID Y103_SYNY3 STANDARD; PRT; 420 AA.
AC Q55874;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY
DE HYPOTHETICAL 45.8 KDA PROTEIN SLL0103.
GN SLL0103.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=9590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tanaka S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64 to 92% of the genome.";
RC DNA Res. 2:153-166(1995).
RL -1- SIMILARITY: TO E.COLI YF8K.
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CC -----
CC EMBL; D64004; BAA10635.1; -
CC InterPro; IPR002035; -
CC Pfam; PF00092; vwa; 1.
CC PROSITE; PS0234; VWFA_DOMAIN; 1.
CC KW Hypothetical protein.
SQ SEQUENCE 420 AA; 45849 MW; E7111B51478E74F3 CRC64;

Query Match 2.7%; Score 151.5; DB 1; Length 420;
Best Local Similarity 20.8%; Pred. No. 0.089;
Matches 85; Conservative 85; Mismatches 183; Indels 55; Gaps 16;

QY 251 PKDMLIVDVSGVSGGLIKLIRTSVEMLETLSDDDVFNVSFNSNAQDSCFQHLVQA 310
Db 41 PLNLGLVLDHSGMDGPLETVKSAALGLRLEDDRLSFIADHRAKIV-----IENQ 95
QY 311 NVYRNKVLKDAVNNITAGITDYKGFSAFPELLNLYNVSRANCKIIMLTDDGGEAAQ 370
Db 96 QVRNGAAKATERUKAGGGTAIDGLKLGQEAAGKEDRVS-----HFLTLDGENEHD 152
QY 371 E-----IFNKNYKDKVRVRFESVGOHNYERGPQIWMACENKG--YYYEIPSTGAIKINTQ 424
Db 153 NDRCLKLTGVASDYKLTVHTLFGFGDH-WNQDVLKLEIAAQAQSLSYIENPS-EALHTFRQ 210
QY 425 EYLDVIGRPMVLGAKAKQVQWNTVYLDALGLG-----LVITGLPVPVNTQGFENKTNLK 480
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Db 211 LF-----QMSNVGLINAHL-LLELAQAHAI--VKPVAQVSPETMDLT-VQ 254
QY 481 NQILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGLVLLHPNLPKNPKSQE----- 536
Db 255 NQGAIEVRLGDLMTDQERV-----LLNLNLYLDQLPGQHVIGQVQIRYDDDPASGQTNLL 309
QY 537 ----PVTLDFLDAELENDIKVEIRKNMIDGESGKT--FRTLVSQSDERYIDKNNRYTW 590
Db 310 SDPLPLFIQ-VQYQYQSDVQVOESILTLAKYRQTQIAETKLAAGRQGAATMLQTAAK 368
QY 591 TPVNGTDSYSLALVPTYFYFYIKAKLEETITQARSKKGKMDSETLRP 638
Db 369 TALQMGDKNGATILQTN-----TRLQSGEDLSEGRDKKTRMYSKTTLOP 413

RESULT 15
ITH4_PIG
ID ITH4_PIG STANDARD; PRT; 921 AA.
AC P79263;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY
DE CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED
DE PROTEIN) (IHRP) (MAJOR ACUTE PHASE PROTEIN) (MAP).
GN ITH4 OR IHRP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-36; 695-703 AND 710-722.
RX TISSUE=Liver;
RC MEDLINE=96271024; PubMed=8830057;
RA Hashimoto K., Tobe T., Sumiya J.-I., Sano Y., Choi-Mura N.-H.,
RA Ozawa A., Yasue H., Tomita M.;
RT "Primary structure of the pig homologue of human IHRP: inter-alpha-
RT trypsin inhibitor family heavy chain-related protein.";
RL J. Biochem. 119:577-584(1996).
RN [2]
RP PRELIMINARY SEQUENCE OF 267-556 FROM N.A.
RX TISSUE=Liver;
RC MEDLINE=90371455; PubMed=1697703;
RA Buchman T.G., Cabin D.B., Vickers S., Deutschman C.S., Delgado E.,
RA Sussman M.M., Bulkley G.B.;
RT "Molecular biology of circulatory shock. Part II. Expression of four
RT groups of hepatic genes is enhanced after resuscitation from
RT cardiogenic shock.";
RL Surgery 108:559-566(1990).
RN [3]
RP SEQUENCE OF 28-54 AND 223-240.
RX TISSUE=Serum;
RC MEDLINE=96013138; PubMed=7556597;
RA Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A.,
RA Garcia-Gil A., Lampreave F., Pineiro A.;
RT "The major acute phase serum protein in pigs is homologous to human
RT plasma kallikrein sensitive PK-120.";
RL FEBS Lett. 371:227-230(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.
CC -1- TISSUE SPECIFICITY: LIVER-SPECIFIC.
CC -1- INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC
CC SHOCK.
CC -1- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).
CC -1- PTM: CLEAVED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA
CC FRAGMENTS.
CC -1- SIMILARITY: BELONGS TO THE ITH4 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
CC -1- CAUTION: REF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER
CC SEQUENCING ERRORS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL: U43164; AAD00024.1; --  
DR EMBL: S82800; AAB46821.1; --  
DR EMBL: M29507; -- NOT\_ANNOTATED\_CDS.  
DR InterPro: IPR002035; --  
DR Pfam: PF00092; vwa; 1.  
DR PROSITE: P850234; VWFA DOMAIN; 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 27  
FT CHAIN 28 921 INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN  
FT H4.  
FT DOMAIN 270 428 VWFA.  
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 49 50 HT -> SK (IN REF. 3).  
FT CONFLICT 703 703 D -> H (IN REF. 1; AA SEQUENCE).  
SQ SEQUENCE 921 AA; 102146 MW; E2BF95925DE8D07C CRC64;

Query Match 2.7%; Score 150.5; DB 1; Length 921;  
Best Local Similarity 19.9%; Pred. No 0.31;  
Matches 156; Conservative 100; Mismatches 264; Indels 265; Gaps 36;

QY 4 GCLLATLT-----FSLIGPSEEPFPPSAVTKSWDK---MQED--- 43  
Db 10 GLLLVPLLLAVLQSTAHKNDINISLTVDKSVSRFAHTVTSRVNKGSAVQEAFTQ 69  
QY 44 -----LVTLAKAGVNLVDIYEK--YQDLYT-VEPNNAQLVETAAARDIEKL--- 89  
Db 70 MELPKAFITNFSMIDGVTYPGNIKEKAAQEQYSAVARGESAGLVRAVTRGTEQFQA 129  
QY 90 LSNRSKALVLALEAKVQAAHQWREDFASNEVYVYNAKDDLPKNDSEPGSQRKPKVF 149  
Db 130 VSVAPAAKVTFFELVYELLARH-----LGVYELLKIQPO-----QLVKHLQ 171  
QY 150 IEDANFGQ-ISKY-QHAAVHIPDIYEGSTIVLNE-----LNWTSALDEVFKKNEEDPSL 203  
Db 172 MDIHFEPOGISPLETFSTFMTNELAELTISQNTKAHIREKPTLSQQ-QKSPEQOETV 230  
QY 204 L-----MQVFGSATG-----LARYYPASPVWDNSRTNPKIDLYDVRPRPVIQ 247  
Db 231 LGNFIVRYDVRTVTGSGTQIENGTVHYFAPEVW----- 266  
QY 248 AASPCKMLILVDVSGVSGVGLTLKLTISVSEMLETSDDDVNVVASFNSNAQDVSCFOHL 307  
Db 267 SAIPKNVIFVIDTSGSWRGKIQOTREALIKILGDLGSDQDFNLVSFGSEAPR-----RRA 322  
QY 308 VQANVRKKVLDVANNITAKGTIDYKGFSAFEOQLLNVSRANCKI-----IM 359  
Db 323 VAASAENVEAKSYAAEIIHAQGTNINDAMLMAVQLL-----ERANRELLPARSVTFII 377  
QY 360 LFTDG-----GEERAQOIFNKNKDKVRV-----FRFSVGQHNHYERGPIQWMA 403  
Db 378 LFTDGSPTVGETNPSKI-----QKNVREAIQGHSLFCLGFGDFVPYAFLEK-----NA 426  
QY 404 CENKG-----YY-----YEIPSIGAIRNTQOYLDVL--GR 432  
Db 427 LENGGLARIYEDSDSALQLEDFQEVANPLRLKLVAFEYPS-NAVEEVTQDNPRFLFKGS 485  
QY 433 PMVLG---DKAKQOVQWNVNLDALGLVITGTLPVFNITQGFENKTNLKNOLILG--- 486  
Db 486 ELVAVGKLRDQSPDV-----LSAKVRQGLHMENTVFMESRVAEQAEFLSPKY 534  
QY 487 -----VMGVDSLEDI--KRUTPRFTLCPNGYFFAIDPNGYVLLHPNL 527

Db 535 IFHSEMERLWAYLTIOQLLAQTVVSASDAEKKALEARALSLSLNSYFVYPLTSMVITPEG 594  
QY 528 QPKNPKSQEPVTLDFLDAELENDIKVEIRKNKMDIGESGKTFRTLVKSQDERYIDKGNRT 587  
Db 595 QEQSQVAEKP-----VENGHRQGNTHSGHSF-----QFHSVGDRT 630  
QY 588 YTWTPVNGTDYSLALVLTPTYSFYIYKAKLEETITQARSKKGMKMDSETLKPDPNFESGYT 647  
Db 631 SRLTGGSSVD-----PVFS-----HRRGWKGQAQ-----GFEKMSY- 661  
QY 648 FIAPR 652  
Db 662 -LPPR 665

Search completed: July 23, 2001, 07:48:39  
Job time: 600 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:47:28 ; Search time 125.88 Seconds  
(without alignments)  
1117.256 Million cell updates/sec

Title: US-09-397-548-17  
Perfect score: 5599  
Sequence: 1 MAAGCLLALTFLFOSLLIG.....PDVCFDNNVLEDTDCGGVS 1063

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_unclassified.\*  
13: sp\_vertebrate.\*  
14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5565.5	99.4	1110	4 Q9UIU0	Q9ui0 homo sapien
2	5532	98.8	1091	6 O77773	O77773 sus scrofa
3	5447	97.3	1091	11 Q9ERS3	Q9ers3 rattus norv
4	5379	96.1	1103	11 O08532	O08532 mus musculu
5	3823	68.3	745	4 Q9UDQ3	Q9udq3 homo sapien
6	3045	54.4	1150	4 Q9NY47	Q9ny47 homo sapien
7	3017.5	53.9	1143	4 Q9NY48	Q9ny48 homo sapien
8	3015.5	53.9	1156	11 Q9EQG2	Q9eqg2 mus musculu
9	3004.5	53.7	1145	4 Q9Y268	Q9y268 homo sapien
10	2983.5	53.3	1076	4 Q9UEW0	Q9uew0 homo sapien
11	2814	50.3	975	4 Q9NSA6	Q9nsa6 homo sapien
12	1119.5	20.0	1091	11 Q9Z1L5	Q9z1l5 mus musculu
13	1045.5	18.7	997	4 Q9NY16	Q9ny16 homo sapien
14	937	16.7	2190	5 Q9NK64	Q9nk64 drosophila
15	920	16.4	2172	5 Q9VJW0	Q9vjw0 drosophila
16	896.5	16.0	1191	5 Q9VJN7	Q9vjn7 drosophila
17	891.5	15.9	1255	5 Q9NK83	Q9nk83 drosophila
18	875	15.6	170	4 Q9UDL7	Q9udl7 homo sapien
19	841	15.0	1022	5 Q9V6T7	Q9v6t7 drosophila

20	738.5	13.2	519	4 Q9NY18	Q9ny18 homo sapien
21	580.5	10.4	1148	5 Q17517	Q17517 caenorhabdi
22	514.5	9.2	104	4 Q9UD81	Q9ud81 homo sapien
23	506	9.0	100	6 Q9GLH1	Q9glh1 bos taurus
24	498.5	8.9	121	4 Q9UD82	Q9ud82 homo sapien
25	482	8.6	98	4 Q9UDU5	Q9udu5 homo sapien
26	465	8.3	97	4 Q9UD80	Q9ud80 homo sapien
27	452.5	8.3	223	11 Q9RI42	Q9ri42 mus musculu
28	402	7.2	77	4 Q95026	Q95026 homo sapien
29	344	6.1	1185	4 Q9HCJ9	Q9hcj9 homo sapien
30	223	4.0	1449	5 Q9V917	Q9v917 drosophila
31	170.5	3.0	494	5 Q9U7P4	Q9u7p4 eufolliculi
32	167	3.0	796	1 Q9HJRO	Q9hjr0 thermoplas
33	161	2.9	2708	5 Q15870	Q15870 plasmodium
34	156.5	2.8	903	6 Q9GLY3	Q9gly3 ocyctolagus
35	155	2.8	1516	5 Q96154	Q96154 plasmodium
36	155	2.8	2364	2 Q46342	Q46342 clostridium
37	154.5	2.8	1315	2 Q86488	Q86488 staphylococ
38	153	2.7	932	11 Q35802	Q35802 rattus norv
39	152.5	2.7	789	2 Q45793	Q45793 bacillus th
40	152	2.7	1105	14 Q9EMZ8	Q9emz8 ansacta moo
41	151.5	2.7	2867	5 Q9N2M3	Q9n2m3 plasmodium
42	150.5	2.7	2771	5 Q26216	Q26216 plasmodium
43	150	2.7	946	6 Q9GLY6	Q9gly6 ocyctolagus
44	149	2.7	459	2 Q25905	Q25905 helicobacte
45	149	2.7	930	4 Q9UQ54	Q9uq54 homo sapien

## ALIGNMENTS

RESULT 1

Q9UIU0 Q9UIU0 PRELIMINARY; PRT; 1110 AA.  
AC Q9UIU0;  
DT 01-MAY-2000 (TREMREL. 13, Created)  
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE DIHYDROPYRIDINE RECEPTOR ALPHA 2.SUBUNIT.  
GN CACNA2D1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20005942; PubMed=10534405;  
RA Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;  
RT "Genomic structure and functional expression of a human alpha(2)/delta  
RT calcium channel subunit gene (CACNA2).";  
RL Genomics 61:201-209(1999).  
DR EMBL; AF083854; AAF03259.1;  
DR EMBL; AF083817; AAF03259.1; JOINED.  
DR EMBL; AF083818; AAF03259.1; JOINED.  
DR EMBL; AF083819; AAF03259.1; JOINED.  
DR EMBL; AF083820; AAF03259.1; JOINED.  
DR EMBL; AF083821; AAF03259.1; JOINED.  
DR EMBL; AF083822; AAF03259.1; JOINED.  
DR EMBL; AF083823; AAF03259.1; JOINED.  
DR EMBL; AF083824; AAF03259.1; JOINED.  
DR EMBL; AF083825; AAF03259.1; JOINED.  
DR EMBL; AF083826; AAF03259.1; JOINED.  
DR EMBL; AF083827; AAF03259.1; JOINED.  
DR EMBL; AF083828; AAF03259.1; JOINED.  
DR EMBL; AF083829; AAF03259.1; JOINED.  
DR EMBL; AF083830; AAF03259.1; JOINED.  
DR EMBL; AF083831; AAF03259.1; JOINED.  
DR EMBL; AF083832; AAF03259.1; JOINED.  
DR EMBL; AF083833; AAF03259.1; JOINED.  
DR EMBL; AF083834; AAF03259.1; JOINED.  
DR EMBL; AF083835; AAF03259.1; JOINED.  
DR EMBL; AF083836; AAF03259.1; JOINED.  
DR EMBL; AF083837; AAF03259.1; JOINED.

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DR EMBL; AF083838; AAF03259.1; JOINED.
DR EMBL; AF083839; AAF03259.1; JOINED.
DR EMBL; AF083840; AAF03259.1; JOINED.
DR EMBL; AF083841; AAF03259.1; JOINED.
DR EMBL; AF083842; AAF03259.1; JOINED.
DR EMBL; AF083843; AAF03259.1; JOINED.
DR EMBL; AF083844; AAF03259.1; JOINED.
DR EMBL; AF083845; AAF03259.1; JOINED.
DR EMBL; AF083846; AAF03259.1; JOINED.
DR EMBL; AF083847; AAF03259.1; JOINED.
DR EMBL; AF083848; AAF03259.1; JOINED.
DR EMBL; AF083849; AAF03259.1; JOINED.
DR EMBL; AF083850; AAF03259.1; JOINED.
DR EMBL; AF083851; AAF03259.1; JOINED.
DR EMBL; AF083852; AAF03259.1; JOINED.
DR EMBL; AF083853; AAF03259.1; JOINED.
DR InterPro; IPR000885; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
DR ProDom; PD02078; -. 1.
KW Receptor.
SQ SEQUENCE 1110 AA; 125307 MW; 8358DC6AD489C074 CRC64;

Query Match          99.4%; Score 5565.5; DB 4; Length 1110;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1060; Conservative 1; Mismatches 2; Indels 19; Gaps 1;

Qy 1 MAAGCLLATLTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSGYNQLVDI 60
Db 1 MAAGCLLATLTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSGYNQLVDI 60
Qy 61 YEKYQDLYTVPNNARQLVEIAARDIEKLLNSRKALYSLEAEKVAQAQHWREDFASN 120
Db 61 YEKYQDLYTVPNNARQLVEIAARDIEKLLNSRKALYSLEAEKVAQAQHWREDFASN 120
Qy 121 EVVYNKADLLDPEKNDSEPSQRIKPFVIEDANFGROISYQHAHVHTPTDIYEGSTIVL 180
Db 121 EVVYNKADLLDPEKNDSEPSQRIKPFVIEDANFGROISYQHAHVHTPTDIYEGSTIVL 180
Qy 181 NELNWTSSALDEVFKKREEDPSLQWFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240
Db 181 NELNWTSSALDEVFKKREEDPSLQWFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240
Qy 241 RPWYIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASNSNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTGLKIRTSVSEMLETSLDDDFVNVASNSNAQD 300
Qy 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEQLLNNVSRANCKIIML 360
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEQLLNNVSRANCKIIML 360
Qy 361 FTDGGEERAQEIFNKNYKDKKVRFRFSVGQHNVERGPIONMACENKGYIYEIPSIGAIR 420
Db 361 FTDGGEERAQEIFNKNYKDKKVRFTESVGQHNVDGRPIQMACENKGYIYEIPSIGAIR 420
Qy 421 INTQEYLDVLRPMVLAGDKAKQVQWTVNYLDALGLVITGTLPVFNITQGFENKTNLK 480
Db 421 INTQEYLDVLRPMVLAGDKAKQVQWTVNYLDALGLVITGTLPVFNITQGFENKTNLK 480
Qy 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLOPK----- 530
Db 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLOPKIGVIGIPTIN 540
Qy 531 -----NPKSQBPVTLDFDALENDIKVEIRNKMIDGESGKPTLVKQSDERYI 581
Db 541 LKRKRPNIONPKSQBPVTLDFDALENDIKVEIRNKMIDGESGKPTLVKQSDERYI 600
Qy 582 DKGNTYTWTPVNGDYSLALVLPITYSYIYAKLEETITQARSKGKWKDSEITLKPNF 641
Db 601 DKGNTYTWTPVNGDYSLALVLPITYSYIYAKLEETITQARSKGKWKDSEITLKPNF 660
Qy 642 EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 701
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```
Db 661 EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 720
Qy 702 ELVQNYWSKOKNIKGVKARFVVDGGITRVYPKAGENWQENPETYEDSFYKRSLDNDNY 761
Db 721 ELVQNYWSKOKNIKGVKARFVVDGGITRVYPKAGENWQENPETYEDSFYKRSLDNDNY 780
Qy 762 VFTAPYENKSGPGAYESGIMYSKAVEIYIQGLKLPKPAVVGKIDVNSWIENTFTKTSIRDP 821
Db 781 VFTAPYENKSGPGAYESGIMYSKAVEIYIQGLKLPKPAVVGKIDVNSWIENTFTKTSIRDP 840
Qy 822 CAGVPCDCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGREFFEIDPSLMRHLNYSIYA 881
Db 841 CAGVPCDCKRNSDVMDCVILDDGGFLLMANHDDYTNOIGREFFEIDPSLMRHLNYSIYA 900
Qy 882 FNKSYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSLQOFLSLTFPR 941
Db 901 FNKSYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSLQOFLSLTFPR 960
Qy 942 LLEAVEMEDDDFTASLSKQSCITQTOYFFONDSPSGVLDGCGNSRIFHGEKLMNTNL 1001
Db 961 LLEAVEMEDDDFTASLSKQSCITQTOYFFONDSPSGVLDGCGNSRIFHGEKLMNTNL 1020
Qy 1002 IFIMVESKGTCPCTRLIIQAEQTSIDGPNPCDMVKQPRYKGPDPVCFDNNVLEDTDCGG 1061
Db 1021 IFIMVESKGTCPCTRLIIQAEQTSIDGPNPCDMVKQPRYKGPDPVCFDNNVLEDTDCGG 1080
Qy 1062 VS 1063
Db 1081 VS 1082

RESULT 2
O77773 PRELIMINARY; PRT; 1091 AA.
AC O77773;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2 DELTA SUBUNIT PRECURSOR.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel
subunit from porcine cerebral cortex. Expression of a soluble form of
the protein that retains [3H]gabapentin binding activity.";
RL J. Biol. Chem. 273:25458-25465(1998).
DR EMBL; AF077665; AAC36289.1; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 1091 VOLTAGE-DEPENDENT CALCIUM CHANNEL
ALPHA-2 DELTA SUBUNIT.
FT SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9E60E CRC64;

Query Match          98.8%; Score 5532; DB 6; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MAAGCLLATLTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSGYNQLVDI 60
Db 1 MAAGCLLATLTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSGYNQLVDI 60
Qy 61 YEKYQDLYTVPNNARQLVEIAARDIEKLLNSRKALYSLEAEKVAQAQHWREDFASN 120
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Db 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAQHWREDFASN 120
QY 121 EYVYNAKDDLPENKNDSPGSGRIKPVIEDANFRQISYOHAAVHIPTDIYEGSTIVL 180
Db 121 EYVYNAKDDLPENKNDSPGSGRIKPVIEDANFRQISYOHAAVHIPTDIYEGSTIVL 180
QY 181 NELNWTSALEDFVFNKREDDPSLLQWVFGSATGLARYYPASPWVDSNRPKNKIDLYDVR 240
Db 181 NELNWTSALEDFVFNKREDDPSLLQWVFGSATGLARYYPASPWVDSNRPKNKIDLYDVR 240
QY 241 RPYWIGQASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPYWIGQASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFQOLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEPSIGAIR 420
Db 361 FTDGGEERAQEIFNKNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEPSIGAIR 420
QY 421 INTQEYLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPBGVYLHPNLPKNPKSQBPVTL 540
Db 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPBGVYLHPNLPKNPKSQBPVTL 540
QY 541 DFLDALENDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDALENDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYSFYIYKAKIEETITQARSKKGMKDSKSETLKPDPNFESGYTFFIAPDYCNDLKI 660
Db 601 ALVLPYSFYIYKAKIEETITQARSKKGMKDSKSETLKPDPNFESGYTFFIAPDYCNDLKI 660
QY 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNIKGVAR 720
Db 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNIKGVAR 720
QY 721 FVYTDGGITRVPYKEAGENQWENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVPYKEAGENQWENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSNIENFTKTSIRDPACGVCDCRNSDVMDCVI 840
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSNIENFTKTSIRDPACGVCDCRNSDVMDCVI 840
QY 841 LDDGGLMANHDDYTNQIGRFFGEIDPSLMRLHVNISYAFNKSVDYOSVCEPGAAPQ 900
Db 841 LDDGGLMANHDDYTNQIGRFFGEIDPSLMRLHVNISYAFNKSVDYOSVCEPGAAPQ 900
QY 901 GAGHRSAYVPSVADIQIOWATAAWSILQFLLSLTPRLLLEAVEMEDDDFTASLSQ 960
Db 901 GAGHRSAYVPSVADIQIOWATAAWSILQFLLSLTPRLLLEAVEMEDDDFTASLSQ 960
QY 961 SCITEOTOFFNDKSFSGVLDGNCRSIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
Db 961 SCITEOTOFFNDKSFSGVLDGNCRSIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020
QY 1021 QABQTSIDGPNCDMWQKPYRKGPDVCFNNVLEDYTDGCGVS 1063
Db 1021 QABQTSIDGPNCDMWQKPYRKGPDVCFNNVLEDYTDGCGVS 1063
```

RESULT 3

Q9ERS3

ID Q9ERS3 PRELIMINARY; PRT; 1091 AA.

AC Q9ERS3;

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

```
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VOLTAGE-GATED CALCIUM CHANNEL ALPHA2/DELTA-1 SUBUNIT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;
RL Lin Y., Lipscombe D.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286448; AAG28164.1;
FT VARIANT 209 212 GSAT -> AADR.
FT VARIANT 338 338 S -> T.
FT VARIANT 599 600 SL -> RY.
FT VARIANT 869 869 S -> R.
SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;
```

Query Match 97.3%; Score 5447; DB 11; Length 1091;

Best Local Similarity 96.5%; Pred. No. 0;

Matches 1026; Conservative 22; Mismatches 15; Indels 0; Gaps 0;

```
QY 1 MAAGCLLALTTLFQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGNOLVDI 60
Db 1 MAAGCLLALTTLFQSLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGNOLVDI 60
QY 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAQHWREDFASN 120
Db 61 YEKYQDLYTVEPNNAQRLVEIAARDIEKLLSNRSKALVRLALEAEKVAQAQHWREDFASN 120
QY 121 EYVYNAKDDLPENKNDSPGSGRIKPVIEDANFRQISYOHAAVHIPTDIYEGSTIVL 180
Db 121 EYVYNAKDDLPENKNDSPGSGRIKPVIEDANFRQISYOHAAVHIPTDIYEGSTIVL 180
QY 181 NELNWTSALEDFVFNKREDDPSLLQWVFGSATGLARYYPASPWVDSNRPKNKIDLYDVR 240
Db 181 NELNWTSALEDFVFNKREDDPSLLQWVFGSATGLARYYPASPWVDSNRPKNKIDLYDVR 240
QY 241 RPYWIGQASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPYWIGQASPKDMLILVDVSGVSLTLKLRISVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFQOLLNYSRANCNKIIML 360
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKITDYKKGFSFAFQOLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFNKNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEPSIGAIR 420
Db 361 FTDGGEERAQEIFNKNKDKKVRFRFSVGOHNYERGPQIOWMACENKGYIYEPSIGAIR 420
QY 421 INTQEYLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITGQFENKTNLK 480
QY 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPBGVYLHPNLPKNPKSQBPVTL 540
Db 481 NQILGVMGVDSLEDIKRLTPRFTLCPNGYIFAIDPBGVYLHPNLPKNPKSQBPVTL 540
QY 541 DFLDALENDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
Db 541 DFLDALENDIKVEIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
QY 601 ALVLPYSFYIYKAKIEETITQARSKKGMKDSKSETLKPDPNFESGYTFFIAPDYCNDLKI 660
Db 601 ALVLPYSFYIYKAKIEETITQARSKKGMKDSKSETLKPDPNFESGYTFFIAPDYCNDLKI 660
QY 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNIKGVAR 720
Db 661 SDNTEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNIKGVAR 720
QY 721 FVYTDGGITRVPYKEAGENQWENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
Db 721 FVYTDGGITRVPYKEAGENQWENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780
```

Db 721 FVVTGGITRVPKKEAGENWQENPETYEDSFYKRSLDNDNVYFTAPYKNSGPGAYESGI 780

Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVCDCKRNSVDVCVI 840

Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVCDCKRNSVDVCVI 840

Qy 841 LDGGFLLMANHDDYTNQIGRFEGEIDPSLRHLNVSIAFNKSYDYQSVCEPGAAPQ 900

Db 841 LDGGFLLMANHDDYTNQIGRFEGEIDPSLRHLNVSIAFNKSYDYQSVCEPGAAPQ 900

Qy 901 GAGHSAVPSVADILQIGWATAAAMSILQFLLSFPRLLEAVEMDDFTASLSKQ 960

Db 901 GAGHSAVPSVADILQIGWATAAAMSILQFLLSFPRLLEAVEMDDFTASLSKQ 960

Qy 961 SCITEQTYFFNDKSFSGVLDCGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020

Db 961 SCITEQTYFFNDKSFSGVLDCGNCGRIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020

Qy 1021 QAEQTSQDPNCDMVQKPYRKGPDVCFNNVLEDYTDGCGVS 1063

Db 1021 QAEQTSQDPNCDMVQKPYRKGPDVCFNNVLEDYTDGCGVS 1063

RESULT 4

O08532 PRELIMINARY; PRT: 1103 AA.

AC O08532; O08533; O08534; O08535; O08536;

DT 01-JUN-1998 (Tremblrel. 06, Created)

DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)

DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)

DE DIHYDROPIRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA

DE SUBUNITS PRECURSOR.

GN CACNA2D1 OR CACNA2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi.

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE=97113514; PubMed=8955374;

RA Angelotti T. Hofmann F.;

RL FEBS Lett. 397:331-337(1996).

CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING.

CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-1, ALPHA-2, BETA AND GAMMA.

CC -1- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-LINKED.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.

CC -1- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE CARDIOVASCULAR SYSTEM.

CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM A PRECURSOR FORM.

CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

DR EMBL; U73484; AAB50139.1; -

DR EMBL; U73485; AAB50140.1; -

DR EMBL; U73483; AAB50138.1; -

DR EMBL; U73486; AAB50141.1; -

DR EMBL; U73487; AAB50142.1; -

DR MGD; MG1:88295; Caca2d1.

DR InterPro; IPR002035; -

DR Pfam; PF00092; vwa; 1.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KW Calcium channel; Glycoprotein; Phosphorylation; Signal;

KW Alternative splicing.

FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 957

FT CHAIN 958 1103

FT TRANSMEM 446 469

FT TRANSMEM 918 942

FT TRANSMEM 1079 1098

FT MOD\_RES 501 501

FT MOD\_RES 845 845

FT CARBOHYD 92 92

FT CARBOHYD 136 136

FT CARBOHYD 184 184

FT CARBOHYD 324 324

FT CARBOHYD 348 348

FT CARBOHYD 475 475

FT CARBOHYD 604 604

FT CARBOHYD 613 613

FT CARBOHYD 675 675

FT CARBOHYD 781 781

FT CARBOHYD 824 824

FT CARBOHYD 888 888

FT CARBOHYD 895 895

FT CARBOHYD 985 985

FT CARBOHYD 998 998

FT VARSPLIC 531 531

FT VARSPLIC 554 554

FT VARSPLIC 644 644

FT SEQUENCE 1103 AA; 124629 MW; 103773BA735120D4 CRC64;

Qy 1 MAAGCLLALTLFQSLILGPSSEEPSPSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60

Db 1 MAAGCLLALTLFQSLILGPSSEEPSPVTIKSWDKMQEDLVTLAKTASGVTLADI 60

Qy 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREFASN 120

Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREFASN 120

Qy 121 EYVYNAKDDLPEDKNDSEPGSQRIKPVFTEDANFGRQISYQAAHVHIPTDIEGSTIVL 180

Db 121 EYVYNAKDDLPEDKNDSEPGSQRIKPVFTEDANFGRQISYQAAHVHIPTDIEGSTIVL 180

Qy 181 NELNWTISALDEVEKKNREEDPSLLQVFGSATGLARYYPASPDVNSRTNPKIDLYDVR 240

Db 181 NELNWTISALDEVEKKNREEDPTLLQVFGSATGLARYYPASPDVNSRTNPKIDLYDVR 240

Qy 241 RPYVIOGAASPKDMLILVDYSGVSGTLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300

Db 241 RPYVIOGAASPKDMLILVDYSGVSGTLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300

Qy 301 VSCFQHLVQAVNRNKKVLDKAVNNITAKGIDYKKGFSFAPEQLLNTNVSANCNKIIML 360

Db 301 VSCFQHLVQAVNRNKKVLDKAVNNITAKGIDYKKGFSFAPEQLLNTNVSANCNKIIML 360

Qy 361 FTGGEERAQEIFKNYKNDKRVFRSVGQHNVERGPIQWACENKGYEIPISGAIR 420

Db 361 FTGGEERAQEIFAKYKNDKRVFTFSVQHNVDPRPIQWACENKGYEIPISGAIR 420

Qy 421 INTQEYLDVLRPMVLAGDKAKOVQWNTNVLDALEGLVITGTLTPVENITQGFENKTNLK 480

Db 421 INTQEYLDVLRPMVLAGDKAKOVQWNTNVLDALEGLVITGTLTPVENITQGFENKTNLK 480

Qy 481 NQLILGVMGVDVSLIEDIKRLTPREFTLCPNGYFAIDPNGYVLLHPNLPQK----- 530

Db 481 NQLILGVMGVDVSLIEDIKRLTPREFTLCPNGYFAIDPNGYVLLHPNLPQKPGVGIPTIN 540

Qy 531 -----NPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYI 581

Db 541 LRKRPNVQPKSQEPVTLDFDLAELENEIKVEIRNKMIDGESGEKTFRTLVKSQDERYI 600

Query Match 96.1%; Score 5379; DB 11; Length 1103;

Best Local Similarity 94.3%; Pred. No. 0;

Matches 1020; Conservative 22; Mismatches 14; Indels 26; Gaps 2;

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QY 582 DKGNTYTWTPVNGTDYSLALVLPYSPYIKAKLEETITQARSKKGMKDSKSETLKPNDF 641
DB 601 DKGNTYTWTPVNGTDYSLALVLPYSPYIKAKLEETITQARY-----SETLKPNDF 653
QY 642 EESGTYTAPDYCNLDKISDNNTFLLNFNEFIDRKTPNPNNSCNADLINRVLLDAGFTN 701
DB 654 EESGTYTAPDYCNLDKISDNNTFLLNFNEFIDRKTPNPNNSCNADLINRVLLDAGFTN 713
QY 702 ELVQYWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETEYDFYKRSLDNDNY 761
DB 714 ELVQYWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETEYDFYKRSLDNDNY 773
QY 762 VETAPYFNKSGGAYESGIMVSKAVEIYIOGKLLPAPVVGKIDVNSMTENFTKTSIRDP 821
DB 774 VETAPYFNKSGGAYESGIMVSKAVEIYIOGKLLPAPVVGKIDVNSMTENFTKTSIRDP 833
QY 822 CAGPVCDCKRNSDVMDCVTLDDGGFLMANHDDYTQIGRFFGEIDPSPMLRHLVNI SYVA 881
DB 834 CAGPVCDCKRNSDVMDCVTLDDGGFLMANHDDYTQIGRFFGEIDPSPMLRHLVNI SYVA 893
QY 882 FNKSYDYOSVCEPAGKOGAGHRSAYVPSVADIIQIGMWATAAASIIQQFLLSLTFFPR 941
DB 894 FNKSYDYOSVCEPAGKOGAGHRSAYVPSVADIIQIGMWATAAASIIQQFLLSLTFFPR 953
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRSRIFHGEKLMNTNL 1001
DB 954 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRSRIFHGEKLMNTNL 1013
QY 1002 IFIMVESKGTCPDTRLLQAQTSQSDGPNPCDMVKQPRYKGPVDFCNVLEDTDCGG 1061
DB 1014 IFIMVESKGTCPDTRLLQAQTSQSDGPNPCDMVKQPRYKGPVDFCNVLEDTDCGG 1073
QY 1062 VS 1063
DB 1074 VS 1075

RESULT 5
ID Q9UDQ3 PRELIMINARY; PRT; 745 AA.
AC Q9UDQ3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE WUGSC:H_DJ0560014.1 PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Mead K., Bauer C.;
RT "The sequence of Homo sapiens PAC clone RP4-560014.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006145; AAD20938.1;
DR InterPro; IPR002035;
FT NON_TER 1
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71E4A CRC64;
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Query Match 68.3%; Score 3823; DB 4; Length 745;
Best Local Similarity 99.7%; Pred. No. 1.le-236;
Matches 715; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 347 YNVS RANCKIIIMLTDDGGEERAQEIFNKYKDKKVRVFRFVSGQHN YERGFIQWMACSN 406
DB 1 YNVS RANCKIIIMLTDDGGEERAQEIFNKYKDKKVRVFRFVSGQHN YERGFIQWMACSN 60
QY 407 KGYEYIPEISGAIRINTQBYLDVLRPMVLAGDKAKQVQWNTWYLDALBELGLVITGLTV 466
DB 61 KGYEYIPEISGAIRINTQBYLDVLRPMVLAGDKAKQVQWNTWYLDALBELGLVITGLTV 120
QY 467 FNITQGFENKTNLKNQILGVMGVDVSLDIKRLTPRFTLCPNGYFFAIDPNGYVLLHN 526
DB 121 FNITQGFENKTNLKNQILGVMGVDVSLDIKRLTPRFTLCPNGYFFAIDPNGYVLLHN 180
QY 527 LQPKNPKSQEPVTLDFDAELENDIKVEIRNKWIDGESGEKTFRLVKSQDERYIDKGNR 586
DB 181 LQPKNPKSQEPVTLDFDAELENDIKVEIRNKWIDGESGEKTFRLVKSQDERYIDKGNR 240
QY 587 TYTWTVPVNGTDYSLALVLPYSPYIKAKLEETITQARSKKGMKDSKSETLKPNFEESY 646
DB 241 TYTWTVPVNGTDYSLALVLPYSPYIKAKLEETITQARSKKGMKDSKSETLKPNFEESY 300
QY 647 TFIAPRDYCNLDKISDNNTFLLNFNEFIDRKTPNPNNSCNADLINRVLLDAGFTNELVN 706
DB 301 TFIAPRDYCNLDKISDNNTFLLNFNEFIDRKTPNPNNSCNADLINRVLLDAGFTNELVN 360
QY 707 YNSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETEYDFYKRSLDNDNYVFTAP 766
DB 361 YNSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETEYDFYKRSLDNDNYVFTAP 420
QY 767 YFNKSGPGAYESGIMVSKAVEIYIOGKLLPAPVVGKIDVNSMTENFTKTSIRDPGAGPV 826
DB 421 YFNKSGPGAYESGIMVSKAVEIYIOGKLLPAPVVGKIDVNSMTENFTKTSIRDPGAGPV 480
QY 827 CDCKRNSDVMDCVTLDDGGFLMANHDDYTQIGRFFGEIDPSPMLRHLVNI SYVA FNKSY 886
DB 481 CDCKRNSDVMDCVTLDDGGFLMANHDDYTQIGRFFGEIDPSPMLRHLVNI SYVA FNKSY 540
QY 887 DYQSVCEPAGKOGAGHRSAYVPSVADIIQIGMWATAAASIIQQFLLSLTFFPRLEAV 946
DB 541 DYQSVCEPAGKOGAGHRSAYVPSVADIIQIGMWATAAASIIQQFLLSLTFFPRLEAV 600
QY 947 EMEDDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRSRIFHGEKLMNTNLIFIMV 1006
DB 601 EMEDDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRSRIFHGEKLMNTNLIFIMV 660
QY 1007 ESKGTCPCDTRLLQAQTSQSDGPNPCDMVKQPRYKGPVDFCNVLEDTDCGGVS 1063
DB 661 ESKGTCPCDTRLLQAQTSQSDGPNPCDMVKQPRYKGPVDFCNVLEDTDCGGVS 717

RESULT 6
ID Q9NY47 PRELIMINARY; PRT; 1150 AA.
AC Q9NY47;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RA Klugbauer N.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
```

RP	SEQUENCE FROM N.A.	
RC	TISSUE=THYROID;	
RA	Hobom M.; Dai S.; Marais E.; Lacinova L.;	
RT	"Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit."	
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AJ251368; CAB86193.1; -	
DR	InterPro: IPR002035; -	
SQ	SEQUENCE 1150 AA; 129875 MW; 37B75F687AFE573C CRC64;	
	Query Match 54.4%; Score 3045; DB 4; Length 1150;	
	Best Local Similarity 54.6%; Pred. No. 1.7e-186;	
	Matches 588; Conservative 172; Mismatches 286; Indels 30; Gaps 13;	
QY	7 LAITLTLFQSLIGPSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDIYEKYD 66	
DB	44 LWLLPLLLPLLAAPGASAYSPQOQTHMOWARLEQEVDMRIFGGVQQLREYKDNRR 103	
QY	67 LYTVPPNARQLVEIARDEIKLLSNRSKALVSLALEAEKVQAAHQWREDFASNEVYYN 126	
DB	104 LFEQENEPKLEKVGADIESLLDRKQVQALKRLADAAENFQAKRWODNIKEEDIVYD 163	
QY	127 AKDDL---DPEKNDSEPSQ--RIKPVFIEDANFGROISYQHAHVHPTDIYEGSTVLN 181	
DB	164 AKADAELEDDPESEDERGSKASTLRDLDFIEDPNFKKNVNTSYAAVQIPTDIYKGSTVLN 223	
QY	182 ELNWTALDEYFKKREEDPSLLNQVFGSATGLARYYPASPVDWNSRTPNKKIDLYDVRRR 241	
DB	224 ELNWTALDENFVEMNRQDPTLLMQVFGSATGVTRYIPATPW----RAPKKIDLYDVRRR 279	
QY	242 PWYIOGAASPKDMLILVDYSGVSGSLTLKIRTSVSEMLETSDDDFVNVASFNSAQDV 301	
DB	280 PWYIOGASSPKDMLIIVDYSGVSGSLTLKMLKTSVCEMLDTSDDDDVNVASFNEKAQPV 339	
QY	302 SCFQHLVQANVRNKKYLKADAVNNITAKGTDYKKGSPFAFEQLLNYNVSRANCKIIMLF 361	
DB	340 SCFTHLVQANVRNKKVKEAVQGMVAKGTGTGKAGFEYAFDQLQNSNITRANCKNIMMF 399	
QY	421 INTQYLDVLGRPMVLADGKAKQVQWNTNVLDALEGLVITGTLFPVFNITQGFENKTLK 480	
DB	460 INTQYLDVLGRPMVLAKGAKQVQWNTNVEDALGLVITGTLFPVFNLTQ--DGPGEKK 517	
QY	481 NOLILGVMGVDVSLIEDIKRLTPRTFPCNGYFAIDPNQYVLLHPNLPKPKSQEPVTL 540	
DB	518 NOLILGVMGIDVALNDIKRLTPNTYLGANGYVFAIDLNGYVLLHPNLPKQPTNFREPVT 577	
QY	541 DFLDALENDIKVEITRNKMDIGESKEFTLTKVKSODERYIDKGNRTYTWTVPNGTDYSL 600	
DB	578 DFLDALENDIKVEITRNKMDIGESKEFTLTKVKSODERYIDVTRNTYTWPIRSTNTSL 637	
QY	601 ALVLPYTFYIKALEETITQARKKGMKQSETLKPDPNFESGYTFTAPRDYCNDLKI 660	
DB	638 GLVLPYTFYIQANLSDQILQVLRKISKLKDFEFLPSSFESEGHVFTAPREYCKOLNA 697	
QY	661 SDNTEFLNLFNEFIDRKTTPNPNSCNADLINRVLDAGFTNELVQNVWSKQK-NIKGVKA 719	
DB	698 SDNTEFLNLFNEFIDRKTTPNPNSCNADLINRVLDAGFTNELVQNVWSKQK-NIKGVKA 757	
QY	720 RFVVDGGITRVYPKKAGENMOENPTYEDSYKRSRLNDNNTVFTAPYFNK-SGPCAYES 778	
DB	758 VFAATDGGITRVYPPNKAEDTWTNPEFFNASEFYRRSLDNGHYFKFPKPHQDALLRPLELEN 817	
QY	779 ---GIWYKSAVEIYIOGKLLKPAVGIKIDVNSWIENF-----TKTSIRDP--CAGP--- 825	
DB	818 DTWGILSTAVELSLGRTRUPAVGVGKIDLEAWAEKFKVLASNRTHQDPQKC-GPNSH 876	
QY	826 -VCCKRNSDVMDCVILDDGGFLVLSNQHWQDVGREFFEVDANMLMLALYNNSTYTRKE 936	
DB	885 SYDYQSVCEPAPGAGHRSAVYPSVADILQIGWATAAASWILQOFLLSLTTPRLLE 944	
QY	937 SYDYQAAACAPPGPNLGAAPRGVFTVADFENLAWMTSAAASWLFQOQLLYGLIYHSWFQ 996	
QY	945 AVEMEDDDFTASLSKOSCITEQTFEFEDNDSKFSFGLDCGNCSTRIFHGEKLMNTNLIFI 1004	
DB	997 ADPAEAEAG-SPTRESSCVMKOTQYFSGVSNASYNAIIDCGNCSRLFHAQRLTNNTLLEF 1055	
QY	1005 MVESGTCPCDTRLTIQAEDQTSQPNPCDMVKOPRYRKGPDCVCFDNNVLEDYDCG 1060	
DB	1056 VAEKPLCSOCEAGRLQKQTHSDGPEQCELVQRPYRRGPHICFDYNATEDSDCG 1111	
RESULT	7	
QY48	PRELIMINARY; PRT; 1143 AA.	
ID	Q9NY48	
AC	Q9NY48;	
DT	01-OCT-2000 (Tremblrel. 15, Created)	
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)	
DT	01-MAR-2001 (Tremblrel. 16, Last annotation update)	
DE	CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.	
GN	CACNA2D2.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=HEART;	
RA	Hobom M.; Dai S.; Marais E.; Lacinova L.;	
RT	"Neuronal distribution and functional characterization of the calcium channel alpha2delta-2 subunit."	
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AJ251367; CAB86192.1; -	
DR	InterPro: IPR002035; -	
SQ	SEQUENCE 1143 AA; 129084 MW; 492556C9919A0CE5 CRC64;	
	Query Match 53.9%; Score 3017.5; DB 4; Length 1143;	
	Best Local Similarity 54.5%; Pred. No. 9.5e-185;	
	Matches 586; Conservative 170; Mismatches 283; Indels 37; Gaps 14;	
QY	7 LAITLTLFQSLIGPSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDIYEKYD 66	
DB	44 LWLLPLLLPLLAAPGASAYSPQOQTHMOWARLEQEVDMRIFGGVQQLREYKDNRR 103	
QY	67 LYTVPPNARQLVEIARDEIKLLSNRSKALVSLALEAEKVQAAHQWREDFASNEVYYN 126	
DB	104 LFEQENEPKLEKVGADIESLLDRKQVQALKRLADAAENFQAKRWODNIKEEDIVYD 163	
QY	127 AKDDL---DPEKNDSEPSQ--RIKPVFIEDANFGROISYQHAHVHPTDIYEGSTVLN 181	
DB	164 AKADAELEDDPESEDERGSKASTLRDLDFIEDPNFKKNVNTSYAAVQIPTDIYKGSTVLN 223	
QY	182 ELNWTALDEYFKKREEDPSLLNQVFGSATGLARYYPASPVDWNSRTPNKKIDLYDVRRR 241	
DB	224 ELNWTALDENFVEMNRQDPTLLMQVFGSATGVTRYIPATPW----RAPKKIDLYDVRRR 279	
QY	242 PWYIOGAASPKDMLILVDYSGVSGSLTLKIRTSVSEMLETSDDDFVNVASFNSAQDV 301	
DB	280 PWYIOGASSPKDMLIIVDYSGVSGSLTLKMLKTSVCEMLDTSDDDDVNVASFNEKAQPV 339	
QY	302 SCFQHLVQANVRNKKYLKADAVNNITAKGTDYKKGSPFAFEQLLNYNVSRANCKIIMLF 361	
DB	340 SCFTHLVQANVRNKKVKEAVQGMVAKGTGTGKAGFEYAFDQLQNSNITRANCKNIMMF 399	

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QY 362 TDGGERAEIENKYN-KDKKVRVRFSGQHNYERGPIONMACENKGGYIEIPSGAIR 420
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 400 TDGEDRVQDVEKYNPNRTVRVTFSGQHNYDYTPLOMACANKGYIEIPSGAIR 459
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 421 INTQEVLDVLRPMVLGAKAKOVNTNYLDALGLGLTGTPVFNFTQFENKTNLK 480
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 460 INTQEVLDVLRPMVLGAKAKOVNTNYEDALGLGLVGTGTPVFNFTQ--DGPGEKK 517
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 481 NQILGVMGVDVSLDIKRLTFRFTLPCNGYFAIDPNGYVLLHPNLPKPKSQBPVTL 540
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 518 NQILGVMGIDVALNDIKRLTPNYTLGANGYFAIDLNGYVLLHPNLPKQTTFNRPVIL 577
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 541 DFLDAELENDIKVEIRNKIMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 578 DFLDAELENDIKVEIRNKIMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDYSL 637
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 601 ALVLPYSPYITAKLEETITQARSKKGKMDSETLKPONFESEGYTFAPRDYCNLDKI 660
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 638 GLVLPYSPYITQANLSDIQLQ-----VKYFEFLPSPSESEGHVFTAPREYCKDLNA 690
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 661 SDNTEFLNFEIDRKTPNNPNSCNADLINRVLLDAGFTNELVQYNSKQK-NIRGVKA 719
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 691 SDNTEFLNFEIDRKTPNNPNSCNADLINRVLLDAGFTNELVQYNSKQK-NIRGVKA 750
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 720 RFWVDGGITRVYPRKAGNENPETYEDSYKRSLDNDNVFTAPYFNK-SGPGAYES 778
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 751 VFAATDGGITRVYPRKAGNENPETYEDSYKRSLDNDNVFTAPYFNK-SGPGAYES 810
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 779 --GIWVSKAVELYIOGKLLPAVGIKIDVNSWIENF-----TKTSIRDP--CAGP--- 825
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 811 DTVGILVSTAVELSGRTRLRPAVGVKLDLEAWAEKFKVLASNRTHQDQPKC-CPNSH 869
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 826 -VDCCKRNSDMVDCVILDGGFLMANHDDYTNQIGRFFGEIDPDLMLHNLNYSYAFNK 884
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 870 CEMDCVNNEDLLCVLIDDGGFLVLSNQHWQDVGREFSEVDANLMLALYNNSFYTRKE 929
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 885 SYDQSVCEPFGAPKQAGHRSAYVPSVADILQIGHWATAAAWSILQFLLSLTFPRLE 944
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 930 SYDQSVCEPFGAPKQAGHRSAYVPSVADILQIGHWATAAAWSILQFLLSLTFPRLE 989
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 945 AVEMEDDDFTASLSKOSCTEQTOQFFDNDKSKFSGLVDCGNCSEFHFGEKLMNTNLI 1004
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 990 ADPAEAG-SPETRESSCVMKQTOYIFGVSNASYNAINIIDCGNCSRLFAHRLTNLLE 1048
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1005 MVESKTCPCDTRLLTIAQBTSDGNPCDMVQPRYKGPDPVCFDNNVLEDYDCG 1060
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1049 VAEKPLCSQCEAGRLQKETHSDGPEQCELVQPRYRGRPHICFDYNATEDSDCG 1104
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 8
Q9EOG2 PRELIMINARY; PRT; 1156 AA.
AC Q9EOG2;
DT 01-WAR-2001 (TReMBLrel. 16, Created)
DT 01-WAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-WAR-2001 (TReMBLrel. 16, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2-DELTA-2 SUBUNIT.
GN CACNA2D2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TKDU;
RX MEDLINE=21015416; PubMed=11130987;
RA Barclay J., Rees M.;
RT "genomic organization of the mouse and human alpha2delta2 voltage-
RT dependent calcium channel subunit genes.";
RL Mamm. Genome 11:1142-1144(2000).
DR EMBL; AF247139; RAG47846.1; --
SQ SEQUENCE 1156 AA; 130611 MW; A732545A2B302A52 CRC64;
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```
Query Match 53.9%; Score 3015.5; DB 11; Length 1156;
Best Local Similarity 54.0%; Pred. No. 1.3e-184;
Matches 583; Conservative 177; Mismatches 287; Indels 33; Gaps 15;

QY 6 LIALTLTLFQSLILGP-SSEPPPSAVTITKSWVDKQEDLVTLAKTASGVNQLVDIYEKY 64
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 45 LLLLPPELLLPPLTAPGASAYSFPQHTQHWARRLEQEDGYMRIFGGVQOQUREIYKDN 104
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 65 QDLTYTEPNNAOLVIAAARDIEKLLSNRSKALVSLALAEKVAQAARHWRQEDPASNEVY 124
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 105 RNLFEVQENEPQKLVKAGDIESLLDRKQALKRLADAAENFQKARHWRQDNKEEDIMY 164
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 125 YNAKODL---DPEKNDSEPSQ--RIKPVFIEDANFGRIISYQHAHAVHTDIEGSTIV 179
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 165 YDAKADAELEDDPESEDWERSKTSALRLDIEDPNFKNVSYTAVQIPTDIKYGSTVI 224
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 180 LNELNWTLSALDEVFKKRNREDESLMQVFGSATGLARYYPASPWVDNSRTPNPKIDLYDVR 239
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 225 LNELNWTLEALENVFIENRRQDPTLLQWVFGSATGVTRYYPATFW---RAPKKIDLYDVR 280
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 240 RRPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDDFVNVASFNQAQ 299
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 281 RRPWYIQGASSPKDMLIIVDVSGSVGLTKLTKMTSCVCEMLDLSDDDDYVNVASFNEKAQ 340
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 300 DVSCEFHLVQANVRNKKVLKADVNNTAKITDIDYKKGFSFAFQOLLNVNVSRANCKIIM 359
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 341 PVSCEFHLVQANVRNKKVFEKAVQGVKAGTGTGKAGFEYAFDQLQNSNITRANCKIM 400
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 360 LMTDGEERAQETFNKYN-KDKKVRVRFSGQHNYERGPIONMACENKGGYIEIPSGA 418
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 401 MFTDGEDRVQDVEKYNPNRTVRVTFSGQHNYDYTPLOMACNKGYIEIPSGA 460
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 419 IRTNTEYLDVLRPMVLGAKAKOVNTNYLDALGLGLTGTPVFNFTQFENKTN 478
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 461 IRTNTEYLDVLRPMVLGAKAKOVNTNYEDALGLGLVGTGTPVFNFTQ--DGPGE 518
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 479 LKNQLILGVMGVDVSLDIKRLTFRFTLPCNGYFAIDPNGYVLLHPNLPKPKSQBPV 538
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 519 KKNQLILGVMGIDVALNDIKRLTPNYTLGANGYFAIDLNGYVLLHPNLPKQTTFNRPV 578
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 539 TLDLDAELENDIKVEIRNKIMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDY 598
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 579 TLDLDAELENDIKVEIRNKIMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGTDY 638
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 599 SLALVLPYSPYITAKLEETITQARSKKGKMDSETLKPONFESEGYTFIAPRDYCNLD 658
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 639 SLGLVLPYSPYITQANLSDIQLQVLPKLSKLDFFLLPSSFESEGHVFIAPREYCKDL 698
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 659 KISDNNTEFLNFEIDRKTPNNPNSCNADLINRVLLDAGFTNELVQYNSKQK-NIRGV 717
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 699 NASDNNTEFLNFEIDRKTPNNPNSCNADLINRVLLDAGFTNELVQYNSKQK-NIRGV 758
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 718 KARFVVDGGITRVYPRKAGNENPETYEDSYKRSLDNDNVFTAPYFNK-SGPGAY 776
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 759 LAVFAATDGGITRVYPRKAGNENPETYEDSYKRSLDNDNVFTAPYFNK-SGPGAY 818
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 777 ES--GIWVSKAVELYIOGKLLPAVGIKIDVNSWIENF-----TKTSIRDP--CAGP- 825
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 819 ENDTGVGLVSTAVELSGRTRLRPAVGVKLDLEAWAEKFKVLASNRTHQDQPKC-GPS 877
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 826 ---VDCCKRNSDMVDCVILDGGFLMANHDDYTNQIGRFFGEIDPDLMLHNLNYSYAF 882
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 878 SHCEMDCEVNNEDLLCVLIDDGGFLVLSNQHWQDVGREFSEVDANLMLALYNNSFYTR 937
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 883 NKSYDQSVCEPFGAPKQAGHRSAYVPSVADILQIGHWATAAAWSILQFLLSLTFPR 942
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 938 KESYDQSVCEPFGAPKQAGHRSAYVPSVADILQIGHWATAAAWSILQFLLSLTFPR 997
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 943 LEAVEMEDDDFTASLSKOSCTEQTOQFFDNDKSKFSGLVDCGNCSEFHFGEKLMNTNLI 1002
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 998 FOADPAEAG-SPETRESSCVMKQTOYIFGVSNASYNAINIIDCGNCSRLFAHRLTNL 1056
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF042793; AAB96914.1; -  
DR InterPro; IPR002035; -  
SQ SEQUENCE 1076 AA; 122116 MW; EBC474836B7EDA85 CRC64;

Query Match 53.3%; Score 2983.5; DB 4; Length 1076;  
Best Local Similarity 54.8%; Pred. No. 1.3e-182;  
Matches 576; Conservative 170; Mismatches 267; Indels 39; Gaps 15;

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QY 33 IKSHVDRKQEDLVTLAKTASGVNQLVDIYEKYQDLTYVEPNNAQLVEIAARDIEKLLSN 92
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MOHWARLEQEVGVIRIFGVQVQLRIYKDRNMLFEVQENEPQKIVKVGAGDIESLLDR 60

QY 93 RSKALVSLALEAKVQAAHQWREDFASNVYVYNAKDDL---DPEKNDSEPGSQ--RIKP 147
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 KVOALKRLADAENFQKAHRWQDNKEEDIVYDADAKADAELDDPSESDVERGSKASTLRL 120

QY 148 VFIEDANFGQISYQHAHVHPTDIYEGSTIVLNELNWTSAIDRVFKKNREEDPSLLQV 207
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 DFIEDPNFKNVSYAAVQIPTDIYKGVSTVILNENWTALENVFMENRRQDPTLLQV 180

QY 208 FGSATGLARYPPASPPVNDNRTNPKIDLYVRRRPWTIOGAASPKMDLILVDVSGSYGL 267
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 FGSATGVTRYYPATPW---RAPKKIDLYVRRRPWTIOGAASPKMDVILVDVSGSYGL 236

QY 268 TLKLIRTSVSEMLETLSDDDDFVNVASFNSNAQDVSFQHLVQANVRNKKVYLKDAVNNTA 327
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 TLKLMKTSVCEMLDTSDDDDVNVASFNEKAQPVSCFTHLVQANVRNKKVFEKAVQGVMA 296

QY 328 KGITDYKKGFSFAFEQLLNVSANCNKIIMLTDDGGERAQEIFNKYN-KDKKVRVFR 386
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 KGITGYKAGFEYAFDQLQNSNITRANCNKIMMFTDGGEDRVQDVFKEYNPNTRVFT 356

QY 387 FSVGQHNRYERGPQIOWACENKGYIYEIPSGAINTQEVLDVLRPMVLADGAKOVQW 446
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 357 FSVGQHNRYVTPLOWMACANKGYIFEPSIGAINTQEVLDVLRPMVLADGAKOVQW 416

QY 447 TNYVLDALGLVITGLTPVFNITGQENKTNLKNQILGVMGVDVLEDKRTPFTL 506
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 417 TNYVEDALGLVITGLTPVFNLTQ---DGPGEKKNQILGVMGIDVALNDIKRTPNLT 474

QY 507 CPNGYFAIDPQGVLLHLPNLPKASQBPVTLDFDLDAELENDIKVIRKMKIDGESGE 566
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 475 GANGYFAIDPQGVLLHLPNLPKQPTTFNREPVTLDFAELENDIKVIRKMSIDGNKGH 534

QY 567 KTFRTLVKSDERYIDKGNRTYTTPVNGTDYSIALVLPYSFYIRAKLEETITQARSK 626
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 535 KQIRTLVKSLDERYIDVTRNYTWPIRSTNSYGLVLPYSTYIQLQANLSDQILQ---- 590

QY 627 KGMKQDSETLKPDNFBESGYTFTIAPRYCNDLKTSDNNTFLLNFNFIIDRKTNNPSCN 686
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 591 ---VKYFEFLPSSEGHVFTIAPREYCKDLNASDNNTEFLKFNIELMEKVTDPDSKCN 647

QY 687 ADLNRVLLDAGFTNELVQVWSKQ-NIKGVKARFVVTDDGITRVYPKEAGENQWENPE 745
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 NFLHNLILDTGTITQQLVVRVWRDQDNTYSLAVFAATDGGITRVFPNKAEDWTNPE 707

QY 746 TYEDSFYKRSILDNNYVFTAPYFNK-SGPGAYES---GIMVSKAVEYIYQGLKKPAVVG 801
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 708 PFNASFVRSILDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRTRLPVAVG 767

QY 802 IKIDVNSWIENF-----TKTSIRDP---CAGP---VDCCKRNSDVMPCVILDDGGFLLMA 850
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 768 VKLDLEAWAEKFKVLASNRTHQDQPKC-GPNSHCEMDCEVNNEDLLCVLIDDGGFVLVS 826

QY 851 NHDDYTNQIGREFGEIDPSLMRHLVNTSVYAFNKSYYQSVCEPGAAPKQAGHRSAYVP 910
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 827 NONHOWQVGRFSEVDANLMLALNNYSFYTRKESYDYQACAPOPPCNGLGAAPRGFVP 886

QY 911 SVADILQIGWATAAASLIQOQLLSLTFPRLLAEVEMEDDDFTFASLSKOSCIQEQYF 970
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 887 TVADFNLAWWTSAANWSLQQLLYGLIYHSWQADPAEAG-SPEFRESSCVMKQIQY 945
```

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QY 971 FDNDKSFSGVLDCGNCRIHFHGEKLMNTNLIFFIMVSKGTGCPDTRLLIOAQE--TSDG 1028
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 946 FGSYNASYNALIDCGNCRLFHAQRLTNTNLLFVYAPLCSQCEAGRLQKETHCPADG 1005

QY 1029 PNPCDMVKOPRYRKGPVDFVFNNDVLEDTDCG 1060
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1006 PEQELVQRPYRGRPHICFDYNATEDTSDCG 1037
```

```
RESULT 11
Q9NSA6 PRELIMINARY; PRT; 975 AA.
ID Q9NSA6 AC Q9NSA6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE LUAC11.1 (CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 2D SUBUNIT
DE (K1AA0558)) (FRAGMENT).
GN LUAC11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z84492; CAB41767.2; -
DR InterPro; IPR002035; -
FT NON_TER 1
SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;
```

Query Match 50.3%; Score 2814; DB 4; Length 975;  
Best Local Similarity 56.9%; Pred. No. 8.1e-172;  
Matches 541; Conservative 143; Mismatches 230; Indels 36; Gaps 14;

```
QY 132 DPEKNDESPGSG--RIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVLNELNWTSA 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 DPESEDVERGSKASTLRDLDFIEDPNFKNVSYAAVQIPTDIYKGVSTVILNELNWTAL 61

QY 190 DEVFKKREEDPSLLQVFGSATGLARYPPASPPVNDNRTNPKIDLYVRRRPWTIOGAA 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 ENVFENRNKQPTLLQVFGSATGVTRYYPATPW---RAPKKIDLYVRRRPWTIOGAS 117

QY 250 SPKQMLILVDVSGSYGLTLKLIRTSVSEMLETLSDDDDFVNVASFNSNAQDVSFQHLVQ 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 SPKQMLILVDVSGSYGLTLKLIRTSVCEMLDTSDDDDVNVASFNEKAQPVSCFTHLVQ 177

QY 310 ANVRNKKVLKDAVNNTAKGTTDYKKGFSFAFEQLLNVSANCNKIIMLTDDGGERA 369
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 ANVRNKKVFEKAVQGVMAKGTGYKAGFEYAFDQLQNSNITRANCNKIMMFTDGGEDRV 237

QY 370 QEIFNKYN-KDKKVRVFRFSGVGOHNYERGPQIOWACENKGYIYEIPSGAINTQEVLD 428
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 QDVEFKNWPNRTYVFTFSVGQHNRYDVTPLQWACANKGYIFEPSIGAINTQEVLD 297

QY 429 VLGRPMVLADGAKOVQWNTNYLDALGLVITGTPVFNITGQENKTNLKNQILGVMA 488
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 298 VLGRPMVLADGAKOVQWNTNYVEDALGLVITGTPVFNLTQ---DGPGEKKNQILGVMA 355

QY 489 GVDVLEDKRTPFTLCPNGYIFAIDPQGVLLHLPNLPKASQBPVTLDFDLDAELE 548
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 GIDVALNDIKRTPNLTGANGYVFAIDPQGVLLHLPNLPKQPTTFNREPVTLDFAELE 415

QY 549 NDIKVEIRNKMIDGESGEKTFRTLVKSDERYIDKGNRTYTTPVNGTDYSIALVLPYS 608
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 416 DENKEEIRRSIDGNKHKQIRTLVKSLDERYIDVTRNYTWPIRSTNSYGLVLPYS 475

QY 609 FYYIKALEETITQARSKKGMKQDSETLKPDNFBESGYTFTIAPRYCNDLKTSDNNTFLL 668
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 476 TFYIQLANLSDQILQ-----VKYFEFLPSSEGHVFTIAPREYCKDLNASDNNTEFL 528
```



QY	669	LNFEFIDRKTNNPNSCNADLINRVLDAGFTNKLQVYNSKOK-NIKGVKARFVVTDDG	727
Db	529	KNFTELMEKVTSPDSKQCNFFLNHLNLDITGITQOLVERVWRDQDLNTYSLLAVFAATDGG	588
QY	728	ITRVYPKEAGENQENPETEYDFYKBSLNDNDVYFAPYFNK-SGPGAYES--GTWVS	783
Db	589	ITRVFPNKAADMTENPEFPNPFYRSLNDNHGTVFPPHQDALLRPLENDTVGLVLS	648
QY	784	KAVEIYTOGKLLKPAVGIKIDVNSWTFN-----TKTSIRDP--CAGP-----VCDCRN	832
Db	649	TAVELSGLRRTLRPAVGVKLDLEAWAEKFKVLASNTHODQPKC-GPNSHCEMDCEVN	707
QY	833	SDVMDCVILDDGGFLMANHDDYNTQIGRFEIDPSLMRHLVNISYAFNKSVDYQSV	892
Db	708	NEDLLCVILDDGGFLVSLNQNHQWQVGRFSEVDANLMLALYNNSFYRKESDYQAA	767
QY	893	EPGAAPKQAGHRSAYVPSVADILQICGWATAAAWSILQOFLLSLTPRLLAEVEMEDDD	952
Db	768	APQPPGNLGAAPRGVFTVADFLNLAWTSAAAWSLQOFLLYGLIYHSFQADPAEAG	827
QY	953	FTASLSKQSCITEQTYFFDNDSKFSGVLDGCGNCSRIFFHGEKLMNTNLIFIMVESKGT	1012
Db	828	-SPETRESSCVAKOTQYFGSVNAYNAIDCGNCSRLFHAQRLTNLFLVVAEKPLCS	886
QY	1013	PCDFRLLIQAEQ--TSDGPNPCDMVKQPRYKRGPDVCFDNNVLEDDYDCG	1060
Db	887	QCEAGRLQKETHCPADGPEQCELVQRPRYRGPCHICFDYNATEDTSDCG	936
RESULT 12			
ID	Q921L5	PRELIMINARY; PRT; 1091 AA.	
AC	Q921L5;		
DT	01-MAY-1999 (TREMBlrel. 10, Created)		
DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)		
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)		
DE	CALCIUM CHANNEL ALPHA-2-DELTA-C SUBUNIT.		
GN	CACNA2D3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRIN;		
RX	MEDLINE=99098955; PubMed=9880589;		
RA	Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;		
RT	"Molecular diversity of the calcium channel alpha2delta subunit.";		
RL	J. Neurosci. 19:648-691(1999).		
DR	EMBL; AJ010949; CAA09423.1; .		
DR	MGI; MGI:1338890; CACNA2D3.		
DR	InterPro; IPR002035; .		
SQ	SEQUENCE 1091 AA; 122777 MW; 7AE2BDAl0077A0A CRC64;		
Query Match			
Best Local Similarity 20.0%; Score 1119.5; DB 11; Length 1091;			
Matches 321; Conservative 230; Mismatches 443; Indels 131; Gaps 41;			
QY	3	AGCLALATLTFOSLLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGSVNLVDIYE	62
Db	14	ASALLA-TALLYAALGDVVRSEQOIPLSV-VKLWASAFGEIKSAAYSGSOLLQKKYK	71
QY	63	KYQDLTVFPNNARQLVEAARDIEKLLSNRSKALVSLALEAEKVAQAAHROWEDFASNEV	122
Db	72	EYKQVAIEIDGLQVLVKLAKIMEEFHKKSEAVRRLVEAAEEAHLKHEFDADL---QY	128
QY	123	VYVNAK--DLDPEKNDSPGSGRIKPVFIEDANFR-QISYQAAVHIPTDIYEGSTV	179
Db	129	EYFNAVLIINERKDGNGFLGKEFI---LAPDNHFNFLPNVLSLDVQVPTNMYNKDPAI	185
QY	180	LNELNWTSLDVEYFKKNREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR	239

Db	186	VNGVYWSLSNKFVVDNEDRDPSLIQYFGSAKGFQYPIKWEPDE---NGVIAFDCR	242
QY	240	RRPWYTOGAASPKDMLILVDVSSVSGLTILKLTSTVSSEMLETSDDDDFNVASSENQAQ	299
Db	243	NRKWIQAATSPKDVVILVDVSGSMKGLRTIAKQTVSSITDLTGDDDDFFNIITYNEELH	302
QY	300	DVS-CFQ-HLVQANVRNKKVLDKAVANNITAKGITDYKKGFSAFEQQLNNTVNSRAN--CN	355
Db	303	YVEPCLNGLTVQADRTNKEHREHLDFKFAKGIGMDIALNEAFNILDNFHTGGSGICS	362
QY	356	KIIMLETFDGGEEARAEIIFNKYN-KDKKVRVFRFSVGQHNTERGPIQMACENKGIYYEIP	414
Db	363	QAIMLITDGAVDYDTIFAKYNWPDVKRVIIFTYILIGREAAAFADNLKWMACANKGFFQIS	422
QY	415	SIGAIRINTOEYLDVLRGPMVLADKAKQVQWNVYLD-----ALEGLVI--TGT	463
Db	423	TLADVQENVMHEYLHVSRLPKVI--DQSHDVVWTEAYIDSTLPQAKLADDOGLVMTVA	480
QY	464	LPVFNITGQFENKTNLKNQILGVGVDSLEIDIKRLTPRTFLCPNGIYFAIDPNGYVLL	523
Db	481	MPVFS---KONETRSG-ILLGVGTDVPVKELKTIPIKYLGIHGYAPAITNNGYILT	535
QY	524	HPNLQP---KNPKSQEP--VTDLFDAELENDIKVEIRNKMIDGESGEKTRTLVKSGDE	578
Db	536	HPELRPLYEBGKKRRKPNYSVDLSEVEDRDDV-LRNAMVNRKTKG--FSMEVK----	588
QY	579	RYIDKGNRT-----YTWTPVNGTDYSIALVLPY-YSEFYIKAKLEETITQARSKGKMK	631
Db	589	KTVDKGRVLVMTNDYITDIKTPFSLGVALSRGHGKIYF-----RGWNT	634
QY	632	DSETLKPDNPEESGYTFIAPRDYCN-DLKISDNNTEFLLNNEFIDRKTNNPNSCNADLI	690
Db	635	IEEGL--HDEHPDVSLEDESYCNTDLHPEHLSQLEAIKLYLKGEK-LLQCDKELI	691
QY	691	NRVLDAAGFTNELVQNYWS-----KOKNIKGVARFVVTGGITRVYP-----	733
Db	692	QEVLFDA--VVSAPIEAYWTSLALNKSSENSDKGVEAFGLTRTGLSRINLNVGAEQLTNQD	750
QY	734	-KENGKQENPETYEDSFYKRSLDN--DNVFTAPY----FNKSGPGAYESGIMVSKAV	786
Db	751	FLKAGDKENIFADHFPFLMYRRAEQIAGSFVSIPTGTGVNKS-----NVVTASTSI	804
QY	787	EIYTOGKLLKPAVGIKIDVNSWTFNFKTSIRDPGAGVCDCKRNSDMDCVILDDGGF	846
Db	805	QLDERKSPVVAAGVGIQMKLEFFQKFWTASQCSLQKCSICDDTVNCLIDNNGF	864
QY	847	LLMANHDDYTNQIGRFFGEIDPPLMRHLVNISYAFNKSVDYQSVCEPGAAPKQAGHRS	906
Db	865	ILVS--EDYT-QTGDFFGEVEGAVNKLTTMGSPKRITLYDYQAMCR---ANKSSDSA	918
QY	907	AYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLAEVEMEDDDFTASLSK-----	961
Db	919	GLLDPYKAFI-----SAAKWTMTLVLFVEF----NLCSSWHSDMTAKAOKLQTLPE	968
QY	962	CITEQTYFFDNDSKFSGVLDGCGNCSRIFFHGEKLMNTNLIFIMVESKGTCPDTRLLIQ	1021
Db	969	CDTEYPAFVSEFTIKETGNACEDCSKSFVIOQIPSSNLFMVVDS--SCLCESVAPIT	1026
QY	1022	ABQTSQGNP---PCDMVKQPRYKRGPDVCFDNNVLEDDYDCGGVS	1063
Db	1027	MAPIEIRYNESLKCERLKAQKIRRRPESCHGPHPENARECGGAS	1071
RESULT 13			
ID	Q9NY16	PRELIMINARY; PRT; 997 AA.	
AC	Q9NY16;		
DT	01-OCT-2000 (TREMBlrel. 15, Created)		
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)		
DT	01-MAR-2001 (TREMBlrel. 16, Last annotation update)		
DE	CALCIUM CHANNEL ALPHA2-DELTA3 SUBUNIT.		
OS	Homo sapiens (Human).		

```

Query Match      16.7%: Score 337; DB 5; Length 2190;
Best Local Similarity 24.9%: Pred. No. 5.8e-51;
Matches 289; Conservative 222; Mismatches 410; Indels 238; Gaps 47;

29 SAVTIKSWDKMQEDLVLTAKTAGVNLVDIYEKYQDLYTVEPNARQLVEIARADIEK 88
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
13 SKATVGVKATQFGDLEALFAAKITKSQBEIKYKEYN--ARVELKNGFTLIIKSTIKNVGR 70

89 LLSNRSKALVSLALEAEKGVQAHHQWREDFASNEVVY-----NAKDDLDPEKNDSE 139

```



QY 89 LLSNRKALVSLALBAEKVQAQHQREDFA--SNEWVYNKADDDLDPEKNDSEPG-----S 142  
 Db 71 ML-----ARKMDAVRCIQEFTYFSSKYSTFNCSSELEFNEAEFAWYRN 117  
 QY 143 QRIKPVFIEDANF-GROISYOHAAHPTDIIYEGSTIVLNLNWTALDEVEFKKNEEDP 201  
 Db 118 MELNP-----DTHFYNTVPDTHSSVHVSNWDRSERVLKTIWSEHLDVEFRQYQSDP 173  
 QY 202 SLLWQVFGSATGLARIYPASPWVDNSRTPNKIDLYDVRRRPWIQGAAPKMDMLILVDVS 261  
 Db 174 ALSWOYFGSDTGILRHYPAAQWTDTPNRDDADTYDCRKRSWYIETATCSKDIVILLDS 233  
 QY 262 GSVSGTLTKLIRTSVSEMLETSLDDDFNVASFNSAQD-VSCFQ-HLVQANVRNKKVLK 319  
 Db 234 GSWTGRHVRHAKFTIRSIDLTSNDDFTILRYSSEVNDIIFCFNGALVQATPENIEVEN 293  
 QY 320 DAVNNI-TAKGTDYKKGFSFAFOLLNYSNR---ANCKNIIMLFTDGGEEAQAEIF 373  
 Db 294 QOIEQLDDEPGYANITLAYETAFQLLRKYDSRHCVTSTCNOAIMLVTDGVAGNTTEVF 353  
 QY 374 NKYN-----KDKKRVRFESVGOHNYERGIQWMAKNGYIYIPIGAIIRINTOE 425  
 Db 354 QXNNGNGENGTSQMDTRVFTYLLGKEVTKVREIQWMAKNGYIYIPIGAIIRINTOE 413  
 QY 426 YLDVLGRPMVLADKAKQVQWNTNYLDAL-----ELGLVITGTLVPFNITGOFENK 476  
 Db 414 YVDVATPLVLQNEQHPT-WTHAFTDKTYDKTSNEKRPRMLISVGPAPDFRYRHANS 472  
 QY 477 TNLKQOLIIGVNGVDVSLERIKRLPREFTLCPNGYVFAIDPNGYVLLHNPLOP-----K 530  
 Db 473 TNPRL-LGVAGTDVPVEDIDKLLPYKLGNGYSFVVSNNGYVLLHNPLOP-----K 531  
 QY 531 NPKSOEPTVLDLAE-LENDIK-----VEIRNKMIDGESGE-KTPRTLKVSQDERY 580  
 Db 532 NPNYN---SIDTVEHLEFEDQSPREPGEISILHIRNAMYHEANEFKSISVFKYDKMR 588  
 QY 581 IDKGNRTYTWPNGDYSLALVLT-TSFYIKAKLEETIQAQSKKGMKDSKTLKPD 639  
 Db 589 VSEERQDYFAPLPTFTGLVMPSEYKTKWIRKVEEYD---KNKHKINISOFFIGE 644  
 QY 640 NFE-----SGYTFIAP-----RDYC---NDLKISDNNTEFLNNEFID--- 676  
 Db 645 NKKVHPDWWYKYHLEGHEFTPEALREFLAKWQNDKWEQAEDESDDDDKDLNC 704  
 QY 677 -RRTPNPS--CNADLINRVLDAFTNELVQNYW-----SKQNKIKVKA--RFVYTDG 726  
 Db 705 GRKTLGDDAYCNKELVNLIFDAKVNS-SYGVWRFESDEERQLIERFRADLRFRVATMS 763  
 QY 727 GTRVYPKAGENWQ-----ENPEYEDSFYKRSL-----DNDNYVFT 764  
 Db 764 GLTR-----WOFIFGEVVDTRDFGDYHTTAIDETWYKSAILOHEDRAESFYVS 814  
 QY 765 APVENKSGPGAYESGIMVSKAVEIYIQLKLPVAVGVIKIDVNSWIENFTKTSIRDPCAG 824  
 Db 815 VKYD-----DPMEDSEVKCNHCL 833  
 QY 825 PVCDCRNSDVMDCVILDGGLMANHDDYTNQIGRFFGEIDPDSLMRHLNYSYVAFNK 884  
 Db 834 PIC-----TDDVDVCCVVIDNNAYIVIGN--INTTKFFGEFGHDVMTAMVERGIFLSIE 886  
 QY 885 STDYQSVQ--EPGAPKQAGHRSAYVPSVAD-ILQIGWATAAWSILQQFLLSITFPR 941  
 Db 887 VDYQKQCKEPEKAVNE-----YTDEIEDEYVAVGDKGSSA----- 923  
 QY 942 LLEAVEMEDDDFTASLSK-----QSCITEQYQFFDNDKSKSFGVLDC--GNCRSRIF 992  
 Db 924 --SKPKDDSDDENAMPEDEPEPDYKACDKRSTLYAL--OPSALVGINDVFEAPSTRPFL 979  
 QY 993 GEKLMNTNLIIFIVE-----SKGTCPCDTRLLIQAEOTS-DGPNPCDMVKOPRY-RKGPDV 1046  
 Db 980 VKKIPNSNLVNVVNVLMPSR-----SVRLTTEPQRMEDKEFPCKLWMSFYERRIEE 1034  
 QY 1047 CFDDNNLYEDTD 1058

Db 1035 C1--TVHEDLSD 1044

Search completed: July 23, 2001, 07:47:50  
 Job time: 636 sec

us-09-397-548-17.rspt

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Mon Jul 23 08:36:44 2001

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 07:28:39 ; Search time 92.97 Seconds

(without alignments)

711.421 Million cell updates/sec

Title: US-09-397-548-14

Perfect score: 5748

Sequence: 1 MAACLLALTLTFLQSLIG.....IIGIQFLLMLVSGSTRLL 1091

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgnl\_9/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /cgnl\_9/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
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5: /cgnl\_9/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
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22: /cgnl\_9/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5748	100.0	1091	16 AAR71011	Human neuronal cal
2	5748	100.0	1091	19 AAW63145	Human calcium chan
3	5748	100.0	1091	21 AAB10576	Human calcium chan
4	5744	99.9	1091	19 AAW37879	Human calcium chan
5	5742	99.9	1091	14 AAR33553	Sequence of the al
6	5728.5	99.7	1110	19 AAW63148	Human neuronal cal
7	5708.5	99.3	1086	16 AAR71013	Human calcium chan
8	5708.5	99.3	1086	21 AAW63153	Human calcium chan
9	5708.5	99.3	1086	21 AAB10587	Human calcium chan
10	5691.5	99.0	1084	16 AAR71015	Human neuronal cal
11	5691.5	99.0	1084	19 AAW63155	Human calcium chan

12	5691.5	99.0	1084	21 AAB10589	Human calcium chan
13	5672	98.7	1103	16 AAR71012	Human neuronal cal
14	5672	98.7	1103	19 AAW63151	Human calcium chan
15	5672	98.7	1103	21 AAB10586	Human calcium chan
16	5652	98.3	1079	19 AAW63154	Human calcium chan
17	5652	98.3	1079	21 AAB10588	Human calcium chan
18	5646	98.2	1079	16 AAR71014	Human neuronal cal
19	5508.5	95.8	1106	18 AAW37712	Rabbit skeletal ca
20	5508.5	95.8	1106	18 AAW18389	Rabbit calcium cha
21	5508.5	95.8	1106	21 AAR77545	Rabbit skeletal ca
22	5487.5	95.5	1106	16 AAR73056	Rabbit skeletal ca
23	5364.5	93.3	1100	10 AAP95644	Rabbit skeletal mus
24	5034.5	52.8	1145	21 AAY92322	Human alpha-2-delt
25	5081.5	44.9	508	19 AAW42032	(Alpha)-2 subunit
26	5081.5	44.9	508	21 AAY77546	Human skeletal cal
27	1122.5	19.5	1085	21 AAY92320	Human alpha-2-delt
28	1118	19.5	1120	21 AAY92321	Human alpha-2-delt
29	1088	18.9	1096	21 AAY92324	Human alpha-2-delt
30	992.5	17.3	1096	21 AAY92323	Human alpha-2-delt
31	733.5	12.8	519	21 AAY70460	Human membrane cha
32	161	2.8	1829	18 AAW29322	DNA polymerase wit
33	158.5	2.8	894	20 AAY00133	Enterococcus faeca
34	158.5	2.8	962	20 AAY00244	Enterococcus faeca
35	158.5	2.8	962	20 AAY00246	Enterococcus faeca
36	158.5	2.8	962	20 AAY00248	Enterococcus faeca
37	158.5	2.8	962	20 AAY00132	Enterococcus faeca
38	158.5	2.8	962	20 AAY00134	Enterococcus faeca
39	158.5	2.8	962	20 AAY00136	Enterococcus faeca
40	155	2.7	1516	21 AAB18195	Plasmodium falcipa
41	154.5	2.7	946	21 AAB29100	Human inter-alpha-
42	154.5	2.7	1315	20 AAY08642	S. aureus SdrD pro
43	154	2.7	903	15 AAR60183	PA(1-725)-----Huma
44	152.5	2.7	789	17 AAR91244	B. thuringiensis V
45	152.5	2.7	789	18 AAW19515	B. cereus VIP3A(b)

#### ALIGNMENTS

#### RESULT 1

AAR71011  
ID AAR71011 standard; Protein; 1091 AA.  
XX  
AC AAR71011;  
XX  
DT 01-DEC-1995 (first entry)  
XX  
DE Human neuronal calcium channel subunit alpha 2b.  
XX  
KW Calcium channel subunit; antagonist; agonist; diagnosis;  
KW Lambert Eaton Syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO9504822-A.  
XX  
PD 16-FEB-1995.  
XX  
PF 11-AUG-1994; 94WO-US09230.  
XX  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
XX  
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
XX  
DR WPI; 1995-090900/12.  
XX  
DR N-PSDB; AAQ84664.  
XX  
PT DNA encoding human calcium channel sub-unit(s) - used for  
PT developing prods. for studying calcium channels, e.g. for  
PT obtaining agonists and antagonists





XX PS Claim 4; Columns 283-288; 166pp; English.

CC The present sequence represents the alpha-2 subunit of a human calcium channel. Calcium channels are membrane-spanning, multi-subunit proteins CC that allow controlled entry of calcium ions into cells. This leads CC to depolarisation events required for muscle contraction. The recombinant CC subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of CC compounds that modulate the channel. The DNA encoding the subunits can CC be alternatively spliced when transcribed, giving more than one form of CC the protein from the same transcript, each having slightly different CC properties. In addition, the reactivity of the alpha 1 subunit with IgG CC molecules from the serum of an individual with Lambert Eaton Syndrome CC (LES) can be used as a diagnostic for the disease.

XX SQ Sequence 1091 AA;

Query Match 100.0%; Score 5748; DB 19; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGCLLALTLTFLQSLILIGPSSSEPPPSAVTIKSWDKMOEDLVTLAKTAGSYNQLVDI 60  
 Db 1 maagcllaltltlflqslilgsssepppsavtlkswdkmqedlvtlaktasgvnqlvdi 60

Qy 61 YEKYQDLYTEPNNAQLVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120  
 Db 61 yekyqdytvepnnaqlveiaardieklksnrskalvslaleaeqvaaahqwredfasn 120

Qy 121 EWTYNAKDDLDPEKNSEPGSQRIKPVIEDANFGROISYQHAHVHPTDIYEGSTVL 180  
 Db 121 evwtynakddldpeknsepgsqrikpviefednfgroisyoahavhptdiyegstvl 180

Qy 181 NELNWTSLDVEFKKNEEDPSLLQVPGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240  
 Db 181 nelnwtlsldvefkkneedpsllqvfgsatglaryypaspvvdnsrtpnkidlydvr 240

Qy 241 RPWYIQGAASPKDMLILVDVSGVSGLTKLIRTSVSEMLETSLDDDFNVNASFNSNAQD 300  
 Db 241 rpwyiqgaaspkdmlilvdvsgvsgltklirtsvsemlletlsdddfnvvasfnsnaqd 300

Qy 301 VSCFQHLVQANRNKVLKDAVNITAKGIDYKKGFSFAFEOILLNYSRANCNKIIML 360  
 Db 301 vscfqhlvqanrnkvldavnitakgidtykkgfsfafeoillnysrancnkiiiml 360

Qy 361 FTDGGEERAQEIFNKYKDKVRVFRPSVGOHNYERGPIONMACENKGYEYIPEISGAIR 420  
 Db 361 ftdggeeeraqelfnkdkdkvrfrpsvgohnyergpionmacenkgyeyieipsigair 420

Qy 421 INTQBYLDVLRPMVLGAKRQVQWNTVYLDALGLVITGTLFVFNITQGFENKTNLK 480  
 Db 421 intqbyldvlrpmvlgakrkqvntvnyldalglvigtltlfpvfnitqgfentnlnk 480

Qy 481 NQLILGVMGVDSLEDIKRLPRTLCPNGYFPAIDPNYVLLHPNLQPKPKSQEPVTL 540  
 Db 481 nqlilgvmgvdsledikrlprtlcpngyfpaidpnyvllhpnlpkpkpsqepvltl 540

Qy 541 DFLDALENDLKVEIRNKMIDGSEKFRITLVKSQDERYTDKGNRTYTWTVPNGTDYSL 600  
 Db 541 dfldaelendlkveirnkmidgsegekfrilvksqderytldkgnrtytwtvpngtdysl 600

Qy 601 ALVLFYFYIKALEETITQAKSKGKMDSETLPKDPNFEEGYTFIAPRDYCNLDKI 660  
 Db 601 alvlfyfyikaleetiqakskgkmdsetlpkdpnfesgytfiaprdycndlki 660

Qy 661 SDNTEFLLNFEIDRTPNPNPCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVAR 720  
 Db 661 sdntefllnfeidrtpnnpncnadlinrvlldagftnelvqnywskoknikgvvar 720

Qy 721 FVVTGGITRVYPKRAGENMOENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI 780  
 Db 721 fvvtggitrvyprkragenmoenpetyedsfykrslndndnvftapyfnkspgpayesgi 780

Db 721 fvvtggitrvyprkeagenqenpetyedsfykrslndndnyvftapyfnkspgpayesgi 780

Qy 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKSTRPCAGVPCDCKRNSDVMDCVI 840  
 Db 781 mvskaveiyyiogkllkpaavgikidvnswieenftkstrpcagvpcdckrnsdvmdcvi 840

Qy 841 LDGGFLMAHNDHYTNOIGRFFGFEIDPSLMRHLVNIISVYAFNKSIDYQSVCEPAAAPKQ 900  
 Db 841 ldggflmahnddytnoigrffgfeidpslmrhlvniisvafnksdyqsvcepaapakq 900

Qy 901 GAGHRSAYVPSVADILQIGWATAAANSILOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
 Db 901 gaghrsayvpsvadilqigwataaawsilqflsltfprlleavemeddftaslskq 960

Qy 961 SCITEQTOYFFDNDKSKSPSGVLDGNCRSRIFHGEKLMNTNLIIFIMVESKGTCPCTRLLI 1020  
 Db 961 sciteqtqoyffndsksfsgvldcgnrcsrifhgeklmntnlifimveskgtpcptrlli 1020

Qy 1021 QAEQTSQGNPCDMVKQPRYRKGPVCFDNNVLEDYTDGCGVSGNLPSLIWYIIGIQFLLL 1080  
 Db 1021 qaeqtsdgnpcdmvkprryrgkpvdcfdnnvledytdcggvsgnlpsliwyiigiqflll 1080

Qy 1081 WLVSNGTHRL 1091  
 Db 1081 wlvsngthrll 1091

RESULT 3  
 AAB10576  
 ID AAB10576 standard; Protein; 1091 AA.  
 AC AAB10576;  
 XX 22-DEC-2000 (first entry)  
 XX Human calcium channel alpha-2 subunit protein.  
 KW Human; calcium channel; calcium channel subunit; diagnosis;  
 KW Lambert Eaton Syndrome; calcium channel subunit alpha-2.  
 OS Homo sapiens.  
 PN US6096514-A.  
 PD 01-AUG-2000.  
 XX 25-MAY-1995; 95US-0450562.  
 PR 04-APR-1988; 88US-0176899.  
 PR 02-FEB-1990; 90US-0482384.  
 PR 08-NOV-1990; 90US-0603751.  
 PR 30-NOV-1990; 90US-0620250.  
 PR 15-AUG-1991; 91US-0745206.  
 PR 10-APR-1992; 92US-0868354.  
 PR 13-JUL-1992; 92US-0914231.  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 PR 07-FEB-1994; 94US-0193078.  
 PR 04-APR-1994; 94US-0223305.  
 PR 11-AUG-1994; 94US-0290012.  
 PR 23-SEP-1994; 94US-0311363.  
 PR 28-SEP-1994; 94US-0314083.  
 PR 07-NOV-1994; 94US-0336257.  
 PR 13-MAR-1995; 95US-0404950.  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX Ellis SB, Williams ME, McCue AF, Harpold MM;  
 XX WPI; 2000-548230/50.  
 DR N-PSDB; AAA71707.  
 XX Human calcium channel beta subunit polynucleotides, useful for  
 PT

PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
PS Syndrome

XX Example IV; Column 135-144; 153pp; English.

XX This invention describes a novel isolated DNA molecule (I) comprising a  
CC sequence encoding a beta3-1 subunit of a human calcium channel.  
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
CC beta3 subunit encoding DNA are useful for isolation and cloning of  
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
CC express heterologous calcium channel are useful for identifying compounds  
CC that modulate calcium channel activity and in assays for identifying  
CC agonists and antagonists of calcium channel activity in humans. Human  
CC calcium channel subunit or eukaryotic cells expressing the channel are  
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
CC sequence represents the human calcium channel alpha-2 subunit which is  
CC described in the method of the invention.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5748; DB 21; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAAGCLLALTTLTQSLILIGSPSEPPPSATVTKSWDKMQEDLVTLAKTAGVYNQLVDI	60
Db	1	maagcillaaltltlqsliligspssepppsavtikswdkmqedlvtlaktasgvnqlvdi	60
Qy	61	YEKYQDLTYVEPNARQLVEIAARDIEKLLSNRSKALVSLALEKVOAAHQWREDFASN	120
Db	61	yekyqdltyvepnarqvlveiaardieklslsrskalvslalesekvaahqwrdfasn	120
Qy	121	EVVYNKADLDPEKNDESPQSRIKPVFIEDANFGROISYOHAAVHIPTDIYEGSTIVL	180
Db	121	evvynakddldpekndepsqrlkpvfiedanfrqisvghaavhiptdiyegstivl	180
Qy	181	NELNWTSSALDEVKKNREEDSLWQVFGSGATGLARYYPASPFWVDSNRTPNKIDLYVR	240
Db	181	nelnwtssaldevekknreedslwqvfsgsatglaryypaspfwvdsnrtpnkidyvrr	240
Qy	241	RPWYIQGAASPKDMLILVDVSGVSLGLTKLIRTSVSMLETLSDDDFVNVASFNNAQD	300
Db	241	rpwyiqgaaspkdmlilvdvsgvsglklirtsvsmletlsdddfvnavasfnnaqd	300
Qy	301	VSCFOHLYQVANNRNKKVLKDAVNNTAKGIDYKKGFSAFEQLNLYNVRANCKIIML	360
Db	301	vscfqlhlyqanvrnkvlkdavnnitakgitydkkgfsafeqlnlynvrancnkiiiml	360
Qy	361	FTDGEERAQELFNKYNKDKVRFRFSVGOHNYERGPIONMACENKGYEIPSGAIR	420
Db	361	ftdgggeeraqeifnkynkdkvrfrfsvgqhnryergpionmacenkgyyieipsigair	420
Qy	421	INTQBYLDVLRPMVLADKAKQVWNTVYLDALGLVITGTLVPVNTIGOFENKTLK	480
Db	421	intqeyldvlgprpmvladkkaqvwnvtyldaleglvitgtlvpvntigofenktlk	480
Qy	481	NOLILGVMGVDVSLIEDIKRLTPRTFLCPNGYFYAIDPNGYVLLHPNLQPKPKSQEPVTL	540
Db	481	nqililgvmgvdslesdikrltptrfclcpngyfyaidpnyvllhpnlpkpkpsqepvtl	540
Qy	541	DFLDAELENDIKVEIRNKMIDGSEKGFRLVKSQDERYIDKGNRTYTWTPVNGTDYSL	600
Db	541	dflaelendikveirnmidgesektfrtlvksqderydkgnrtytwtpvngtdysl	600
Qy	601	ALVLPYSPYYIKAKLEETITQARSKCKMKDSEFLKPDNFEESGYTFIAPRVCNDLKI	660
Db	601	alvlpysyiyakaleecitqarsskckmkdseclpdkpndfeesgytfiaprvcndliki	660
Qy	661	SDNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYWSKOKNKGKVKAR	720
Db	661	sdnteflnfnfedrkttpnpnpncnadlinrvlldagftnelvqywsqknkgkvikar	720

Qy	721	FVVTGGITRVYKPEAGENQENPETVEDSFYKRLSDNDNVFTAPYFNKSGPGAYESGI	780
Db	721	fvvtggitrvypkeagenqenpetyedsfyrslndndnyvftapynfksppayesgi	780
Qy	781	MVSKAVIYIQQKLLKPAVVGIKIDVNSWIEZNFKTTSIRDPACGVPDCCKRNSDVMDCVI	840
Db	781	mvskaiveiyqgkllkpavvgikidvnswiezntfkttsirdpcagvpdcckrnsdvmcvi	840
Qy	841	LDGGGFLMANHDDYTNQIGRFGCEIDPDSLMRHLVNI SVAFNKSVDYQSVCEPGAAPKQ	900
Db	841	lddggflmanhddytngirffgeidpslmrhlvni svafnksydyqsvcepgaapkq	900
Qy	901	GAGHRSAYVPSVADILQIGWATAAASIIQQFTLSLTFPRLLEAVEMEDDDFTASLSKQ	960
Db	901	gaghrsayvpsvadilqgwataaasliqqfllstfprlleavemdddfstaslskq	960
Qy	961	SCITEQYQYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGPCCDTRLLI	1020
Db	961	sciteqtqyffndksfsgvldcgncsrifhgeklmntnlifimveskgtpcdtrlli	1020
Qy	1021	QAETSQGNPCDMVKOPRYRKGPDCVCFDNNVLEDYTDGCGVSGNLPSLWIIIGIQFILL	1080
Db	1021	qaetsdgnpcdmvkvpryrgpdcvcdnnvledytdcgvgslpnlswyilgqflll	1080
Qy	1081	WLVSGSTHRL 1091	
Db	1081	wlvsgsthrll 1091	
RESULT 4			
AAW37879			
ID	AAW37879	standard; Protein; 1091 AA.	
AC	AAW37879;		
XX	28-AUG-1998	(first entry)	
DE	Human calcium channel a2d subunit.		
XX	Calcium channel; human; central nervous system disorder;		
KW	Lambert-Eaton syndrome; diagnosis; therapy.		
OS	Homo sapiens.		
PN	W09811131-A2.		
XX	19-MAR-1998.		
PF	11-SEP-1997; 97WO-US16146.		
PR	16-SEP-1996; 96US-0713118.		
XX	(AMHP ) AMERICAN HOME PROD CORP.		
PI	Chen ARS, Franco R, Shuey DJ;		
DR	WPI; 1998-207325/18.		
XX	N-PSDB; AAV29060.		
PT	DNA encoding human neuronal calcium channel subunit(s) - useful for		
PT	diagnosis of and treatment of central nervous system disorders, e.g.		
PT	Lambert-Eaton syndrome		
XX	Disclosure; Fig 2; 89pp; English.		
XX	This polypeptide comprises the a2d subunit of the human neuronal		
CC	calcium channel. cDNA clones (see AAV29059-61) encoding the a1b		
CC	subunit (see AAW37878), the a2d subunit and a b3 subunit (see AAW37880)		
CC	have been isolated. These have been inserted into expression		
CC	vectors and are stably expressed in transfected cell lines. The		
CC	transformed cells show omega-conotoxin GVIA binding activity,		
CC	and omega-conotoxin GVIA toxin sensitive potassium-stimulated		
CC	calcium uptake, indicating that the proteins expressed by the		

CC clones are capable of forming a functioning calcium channel.  
 CC Nucleic acids encoding the 3 subunits, as well as vectors, host  
 CC cells and methods of isolating nucleic acids encoding related  
 CC calcium channels are disclosed. Fusion proteins incorporating the  
 CC subunit proteins, antibodies, and assays for identifying agents  
 CC that modulate calcium channel activity are also provided. Such  
 CC agents can be used to treat certain central nervous system  
 CC disorders by altering calcium channel activity. Methods of  
 CC diagnosing diseases associated with particular calcium channels,  
 CC such as Lambert-Eaton syndrome, are disclosed.  
 XX  
 SQ Sequence 1091 AA;

Query Match 99.9%; Score 5744; DB 19; Length 1091;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1090; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAGCLLALTTLFQSLIGPSSEEPFSAVTIKSWDKMQEDLYTLAKTASGVNQLVDI 60  
 DB 1 maagcillaltitlqslilgspseepfsavtikswdkmqedlytlaktasgvnqlvdi 60

QY 61 YEKYODLVTPNNARQVETAEADIEKLLSNRSKALVSLAEAEKVOAAHQRDFASN 120  
 DB 61 yekyodlvtpennarqvelaeadielkllsnrskalvslaleaeekvooahqrdfasn 120

QY 121 EYVYNNAKDDLDPEKNDESPGSRQIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180  
 DB 121 evvynnakddldpekndeespqsrqikpvfiedanfgroisqyhaavhptdiyegstivl 180

QY 181 NELNWTSSALDEVFKNREDEPSLLMQVGSATGLARYPASPDWNSRTPNKIDLYDVR 240  
 DB 181 nelnwtssaldevfknredepsllmqvgsatglarypaspdwnsrtpnkidlydvr 240

QY 241 RPWYIOGAASPKDMLILVDVSGVSLGLKILRTSVSEMLETLSDDDFVNVAFSNSAQD 300  
 DB 241 rpwyiogaaspkdmlilvdvsgvsglklilrtsvseMLETLSDDDFVNVAFSNSAQD 300

QY 301 VSCFQHLVQANRNKVLKDAVNNTAKGIDTYKGFSAFQOLLNRYNVRANCNKIIML 360  
 DB 301 vscfqlvqanrnkvkldavnnitakgidtykgsfafqollnrynvrancnkiiiml 360

QY 361 FTDGGEERAQEIFNKNYKDKVPRFVSQHNVERGPIQMACENKGYIYIPISGAIR 420  
 DB 361 ftdggeeraqelfnknkdkvprfvsqhnvergpiqmacenkgyiyeipsair 420

QY 421 INTQEVLDVLRPMVLADKAKOVQWTVNYLDALBELGVITGTLFVNTGOFENKTNLK 480  
 DB 421 intqevldvgrpmvlagdkakovqwtvnyldalbelgvitgtlfpvntgofenktnlk 480

QY 481 NQLILGVNGVDVSLDILKRLTPRFLCPNGYFFAIDPNGYVLLHPLNLPKPKSQEPVTL 540  
 DB 481 nqlilgvngvdsledikrltpfrflcpngyffaidpngyvallhplnlpkpkseqvptl 540

QY 541 DFLDAELNDIKVETRNKMDIGSEKFERLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
 DB 541 dflaelendikveirnkmdigesekferlvksqderiydkgnrtytwtpvngtdysl 600

QY 601 ALVLPYTFYFKALEETITQARKKGMKDSFTLKPDPNPEESGYTFIAPRDYCNLDKI 660  
 DB 601 alvlptytfyfkaleetitqarkkgmkdsetlkdnpnpeesgytftiaprdocndlki 660

QY 661 SDNNTEFLNNEFIDRTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKVAKR 720  
 DB 661 sdnnTEflnnEFidrtpnpnpCNADlinrvllDAGftnelvqynskqknkvakar 720

QY 721 FVVTGGITRVPKAGENQWENPETYEDSFYKRSILDNDNYFTAPYFNKSPGAYESGI 780  
 DB 721 fvvtggitrvpkagenqwenpetyedsfykrsildndnyftapyfnkspgayesgi 780

QY 781 MYSKAVEYIYQGLKLPVAVGFIKDVNSWENFTTSTRDCAGPVCDCKRNSDVMDCVI 840  
 DB 781 mvsKaveyiyqglklpavvgfikdvnsWenfttstrdcagpvcdckrnsdvmdcvi 840

QY 841 LDDGSELLMANHDDTYNQIGRFFGEIDPSLMRHLVNI SYAFNKSYDYOSVCEPGAAPKQ 900  
 DB 841 lddgsellmanhddtyngirffgeidpslmrhlvnisvaynkSYdyosvcepgaapkq 900

QY 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTPRLLEAVEMEDDDFTASLSKQ 960  
 DB 901 gaghsayvpsvadilqigwataaawsilqflsltprrlleavemedddftaslskq 960

QY 961 SCITEQTQYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNLI FIMVYESKGTGCPDTRLLI 1020  
 DB 961 sciteqtqyffndksksgvldcgncsrfhgekmlntnlifimveskgtgcpdtrlll 1020

QY 1021 QAEQTSQSDGNPCDMVKQPRYRKGPVCFDNNVLEDTDCGVSGLNPSLWYIIGIOFLLL 1080  
 DB 1021 qaeqtsdgnpncdmvkqpryrkgpvcfdnnvledtdcgvgsglnpslwyiigiflll 1080

QY 1081 WLVSNGTHRL 1091  
 DB 1081 wlvsngthrll 1091

RESULT 5  
 AAR33553  
 ID AAR33553 standard; Protein; 1091 AA.  
 XX  
 AC AAR33553;  
 XX  
 DT 30-JUN-1993 (first entry)  
 XX  
 DE Sequence of the alpha 2 human calcium channel subunit.  
 XX  
 KW Human calcium channel subunit; diagnosis; agonist; antagonist;  
 KW Lambert Eaton syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9304083-A.  
 XX  
 PD 04-MAR-1993.  
 XX  
 PF 14-AUG-1992; 92WO-US06903.  
 XX  
 PR 15-AUG-1991; 91US-0745206.  
 PR 10-APR-1992; 92US-0868354.  
 XX  
 PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 XX  
 PI Brenner R, Ellis SB, Feldman DH, Harpold MM, Mccue AF;  
 PI Williams ME;  
 XX  
 DR WPI; 1993-093936/11.  
 DR N-PSDB; AAQ37821.  
 XX  
 PT DNA encoding specific human calcium channel sub-units - used for  
 PT identifying calcium channel agonists and antagonists and  
 PT diagnosing Lambert Eaton syndrome  
 XX  
 PS Disclosure; Page 134-138; 150pp; English.  
 XX  
 CC DNA encoding a human neuronal calcium channel alpha 2 subunit was  
 CC isolated from a human genomic DNA library probed under low and high  
 CC stringency conditions with a fragment of DNA encoding the rabbit  
 CC skeletal muscle calcium channel alpha 2 subunit. The fragment  
 CC included nucleotides having a sequence corresponding to the  
 CC nucleotide sequence between nucleotides 43 and 272 inclusive of  
 CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA.  
 CC PCR analysis identified splice variants of the human calcium alpha  
 CC 2 subunit transcript. In particularly preferred embodiments, the  
 CC DNA encoding the alpha 2 subunit is produced by alternative  
 CC processing of a primary transcript that includes DNA encoding the  
 CC amino acids set forth in AAR33553 and the DNA of AAQ37823 inserted  
 CC between nucleotides 1624 and 1625 of AAQ37821.

XX	Sequence	1091 AA;
QY	Query Match	99.9%; Score 5742; DB 14; Length 1091;
QY	Best Local Similarity	99.9%; Pred. No. 0;
QY	Matches 1090; Conservative	0; Mismatches 1; Indels 0; Gaps
QY	1 MAAGCCLLALTLTLFOSLIGTSPSEPPFPASVYIKSWDKMQEDLVTTLAKTASGVNQLVDI	60
QY	1 maagccllaltltlfgsligspseepfpasvtikswdkmqedlvtlaktasgvnqlvdi	60
QY	61 YEKYQDLTYVPENNAQQLVEIAARDIEKLNSRKALVSLALEAEKVQAAHQWREDFASN	120
QY	61 yekyqdltyvpennarqlveiaardieklslsrkalvslawesekvgaahqwrefasn	120
QY	121 EVVYVNAKDOLPEKNDEPSSGSRITKPVIEDANFGROIYSQHAHVHIPTDIEYGSTIVL	180
QY	121 evvyvnakdoldpekndepssgrrtkpviedanfgroisvqhaavhiptdieygstivl	180
QY	181 NELNWTLSALDEVFKKNREBPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYXVRR	240
QY	181 nelnwtlsaldevfkknreepslmqvfgsatglaryypasppwvdsrtpnkidlydvrr	240
QY	241 RPWYIOGAASPDKMLILVDVSGSVSGLTILKLIRTSVSMLTETLSDDDFVNVAFSNSAQD	300
QY	241 rpwyiggaaspdkmlilvdsvsgsgltlklirtsvsmltelsdddfvnvafsnasqd	300
QY	301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDTYKKGFSFAFEQLLNLYNVRANCNKIIML	360
QY	301 vscfqlhlganvrnkvkldavnnitakgidtykkgfsfafeqlnlynvrancnkiml	360
QY	361 FTDGGEERAQEIFPNKYNDKKVRFVRFVSGOHNRYBERGPIONMACENKGYEYIETPSIGAIR	420
QY	361 ftdggeeraqeifpnknyndkkvrvfsvgohnybergpionmacenkgyeypsigaair	420
QY	421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALBELGLVITGTLTPVFNITQGFENKTNLK	480
QY	421 intqeyldvlgrpmvladgkakqvqwnvtyldalbelglvltgtltpvfnitqgfekcnlk	480
QY	481 NQLTLGVMGVDVLSLEDIKRLTFRFTLCRPNGYVFAIDPNGYVLLHPNLPKNPKSQEPVTL	540
QY	481 nqltlgvmgvdvlsledikrltfrftlcrpnngyvfaidpngyvllhpnlpknpkseqpvtl	540
QY	541 DFLDAELENDIKYEIRNKMIDGESKEFTTLVKQSODERYIDKGNRTYTWTVPNGTDSL	600
QY	541 dfldaelendikyeirnkmidgeskefttlvkqsoderyidkgnrtytwtvpngtDSL	600
QY	601 ALVLPTYSFYIIKAKLEETITQARSKKKGMKQSEITLKPDPNFEESGYTIIAPRDCVNDLKI	660
QY	601 alvlptysfyikakleetitqarskkgmkselitkpdnfeesgyttiaprdocvndlki	660
QY	661 SDNNTPELLNFEFIDRKPNNPNSCNADILNVLDDAGFTNELVQNWYSKOKNLKGVKAR	720
QY	661 sdnntellnfeefidrknppnpscnadilnvlldagftnelvqnwyskknlgvkar	720
QY	721 FVVTDDGITRVYKEAGENQENPETYEDSFYKRSILDNDNVYFTAPYFNKSGPGAYESGI	780
QY	721 fvtddgitrvykeagenqenpetyedsfykrslndndnyvftapyfnkspgpaysesi	780
QY	781 MYSKAVEIYIOGKLLPAAVVGIKIDVNSWIENTFTKTSIRDPCAGVCDCKRNSDVMDCVI	840
QY	781 mvskaveyiogkllpavvgikidvnswientftktsirdpcagvcdckrnsdvmdevi	840
QY	841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSYDYOSVCEGCAAPKQ	900
QY	841 lddggfllmanhddytngirfgeidpsimrhlvnlsvyafnksydyosvcegpapqk	900
QY	901 GAGHRSAYVPSVADILQIGWATAAASWILQOFLSLTLPRLLEAVEDEDDDFASLSKQ	960
QY	901 gaghrsayspsvadilqigwataaaswllqqlsltlprlleavededddftaslskq	960
QY	961 SCITEQTQYTFPDNDKSFSGVLDCGNCSTRIFHGEKLMNTNLIFIMVSEKSGPCDTRLLI	1020

Query Match 99.7%; Score 5728.5; DB 19; Length 1110;

AA	Sequence	1110 AA;
SO		

Disclosure: Columns 131-138: 166pp: English.

DNA encoding human calcium channel alpha 1B sub:unit protein -  
useful for recombinant production of the channel for screening of  
its modulators and diagnosis of Lambert Eaton Syndrome

xx The present sequence represents the alpha-2 subunit of a human calcium  
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
CC that allow controlled entry of calcium ions into cells. This leads  
CC to depolarisation events required for muscle contraction. The recombinant  
CC subunit, when expressed with nucleic acids encoding the complete calcium  
CC channel, can be used in assays for the detection and characterisation of  
CC compounds that modulate the channel. The DNA encoding the subunits can  
CC be alternatively spliced when transcribed, giving more than one form of  
CC the protein from the same transcript, each having slightly different  
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
CC molecules from the serum of an individual with Lambert Eaton Syndrome  
CC (LES) can be used as a diagnostic for the disease.

Best Local Similarity 98.3%; Pred. No. 0; Matches 1091; Conservative 0; Mismatches 0; Indels 19; Gaps 1;			
QY	1	MAAGCLLALTTLFQSLIGSPSEPPFPSPATIKSWDKMQEDLVTLAKTAGSVNQLVDI	60
Db	1	maagcllaltltlfgslilgspseepfssavtikswdkmqedlvtlaktasgvnqlvdi	60
QY	61	YEKQDLYTFEPNARQIVETAARDIEKLLNSRKALVSLAEAEKVQAAHQWREDFASN	120
Db	61	yekyqdytvepennargivelaardieklslnsrkalsvslaeakvqaahqwredfasn	120
QY	121	EVVYNNAKDDLDPEKNDSEPGSQRKPFVIEDANFGRQISYQHAHVHPTDIYEGSTIVL	180
Db	121	evvynnakddlpeknndsepgsrkpfviedanfgrqisvqhaavhptdiyegstivi	180
QY	181	NELNWTSALEDVFKKREEDPSLLQVFGSATGLARYYPASPDWNSRTPNKIDLYDVR	240
Db	181	nelnwtalsedvfkknreedpsllqvfgsatglaryypaspdwdsrtpnkidlydvr	240
QY	241	RPWTIQGAASPKMLILVDVSGVSGGLTKLIRTSVSEMLETSLDDDFNVVASFNSAQD	300
Db	241	rpwyiqgaaspkmlilvdvsgsvgltklirtsvsemlletlsdddfnvvasfnasqd	300
QY	301	VSCFQHLVQANVRNKKVLDKAVNITAKGIDYKGFSAFEQOLLNYSRANCNKIIML	360
Db	301	vscfghlvqanvrnkvlkdavnitakgidykghsfafeqllnynsvrancnkilml	360
QY	361	FTDGEERAQEIFNKYKDKKVRFRFSGQHNTERGPIQWACENKGYVEIPISGAIR	420
Db	361	ftdgeeraqeifnkynkdkkvrfrfsgvghnvergpiqmacenkgyveipeisga	420
QY	421	INTQBYDLVGRPMVLGAKKAKQVQWNTNYLDALGLVITGTLPVFNITGOFENKTNL	480
Db	421	intqeyldvlgrpmvlgakakqvwnvnyldaleglvitgtlpvfnitgfgfentnlk	480
QY	481	NQLILGVMGVDVSLIEDIKLTPRETLCPNGYFFALDPNGYVLLHPNLOPK	540
Db	481	nqlilgvmgvdvsliedikltpretlcpngyffaldpngyvvllhpnlpkpgvgiptin	540
QY	531	-----NPKSQBPVTLDFDAELENDEIKVEIRNKMIDGESGKTEPTLVKSODERYI	581
Db	541	lkrkrrpnlpnkpsepvtdlfdlaelendikvelrnmkmdgesgkctfttlvksqeryi	600
QY	582	DGNRTYTWTPVNGTDYSLALVPTYFYIYKALEETITQARSKKGKMKDSETLKPDNF	641
Db	601	dkgnrtvtpvngtdyslalvptysfyikaleetitqarskkgmkdsetlkpdnf	660
QY	642	EESGYTFIAPRDYCNDLKISDNNTFELLNFNEFDRTKTPNPNPCNADLINRVLLDAGFTN	701
Db	661	eesgytfiaprdydcndlkisdnntefllnfnefdrtktpnnpncnadlinrvlldagftn	720
QY	702	ELVQNYWSKQKNIKVKARFVVTDGGITRVYPKBAENQWQENPETYEDSFYKRSILDNDNY	761
Db	721	elvqnywskqnikvgarfvttdggitrvypkeagewqenpetyedsfykrslndndny	780
QY	762	VFTAPYFNKSGPGAYESGIMVSKAVEYIYQGLKLPAVVGKIDVNSWIENFTKTSIRDP	821
Db	781	vftapyfnksgpgayesgimvskaveiyiqgklklpavvgikidvnswieftktsirdp	840
QY	822	CAGPVCCKRNSVDMCVILDDGGFLMANHDDYTNQIGRFFGEIDSLMRHLNIVSYA	881
Db	841	cagpvcckrnsdvmcviiddggflmanhddytngirffgeidpslmrhlvnisyva	900
QY	882	FNKSYDYQSVCEPAAKQAGHSAVPSVADILQIGWATAAASWTLQOFLSLTFFPR	941
Db	901	fnksydyqsvcepaaqkqaghsavpsvadllqigwataaaswllqqlflslitfpr	960
QY	942	LLEAVEMEDDDFTASLSKQSCITEQTOYFFDNDSKFSVGLDCGNCGRIFHGEKIMNTNL	1001
Db	961	lleavemedddftaslskqsciteqtoyffdnksksfsgvldcncgrifhgeklmntnl	1020
QY	1002	IFIMVESKGCPCDTRILLIAQEQTSQDGNPCDMYQKPRYKGPVDCFDNNVLEDTDCGG	1061
Db			

Db	1021	ifimveskgtcpcdtrlllqaeqtsdgnpcdmvqprykrkgpdcfdnnvledytdcgg	1080
QY	1062	VSGNLPSLWYIIGIOFLLLWLVSSTHRL	1091
Db	1081	vsglnpslwyiigiqflllwlvsgsthrll	1110
RESULT 7			
AA71013			
ID	AA71013	standard; Protein; 1086 AA.	
AC	AA71013;		
XX			
DT	01-DEC-1995	(first entry)	
XX			
DE		Human neuronal calcium channel subunit alpha 2c.	
XX			
KW		Calcium channel subunit; antagonist; agonist; diagnosis;	
XX		Lambert Eaton Syndrome.	
OS		Homo sapiens.	
XX			
PN	W0504822-A.		
XX			
PD	16-FEB-1995.		
XX			
PF	11-AUG-1994;	94WO-US09230.	
XX			
PR	11-AUG-1993;	93US-0105536.	
PR	05-NOV-1993;	93US-0149097.	
XX			
PA		(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.	
XX			
PI	Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;		
XX			
DR	WPI; 1995-090900/12.		
DR	N-PSDB; AAQ84667.		
XX			
PT	DNA encoding human calcium channel sub-unit(s) - used for		
PT	developing prods. for studying calcium channels, e.g. for		
XX	obtaining agonists and antagonists		
PS	Disclosure; Page 237-242; 285pp; English.		
XX			
CC	Human neuronal alpha 2 coding sequence (AAQ84664) transcript is		
CC	differentially processed in skeletal muscle, aorta, and CNS in		
CC	the region corresp. to nt 1595-1942 of AAQ84664 in each of the		
CC	tissues. Five alternatively spliced variant transcripts that differ		
CC	in the presence or absence of one to three different portions of		
CC	this region. There are three sequences involved (see AAQ84664 FT		
CC	and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five		
CC	alpha 2 encoding transcripts from the different tissues include		
CC	different combinations of the three sequences, except for one of		
CC	the alpha 2 transcripts expressed in aorta which lacks all three		
CC	sequences. The five alpha 2 forms identified are (1) a form that		
CC	lacks sequence 3 called alpha 2a, expressed in skeletal muscle		
CC	(2) one that lacks sequence 1 called alpha 2b, expressed in CNS		
CC	(3) one that lacks sequences 1 and 2 called alpha 2c, expressed in		
CC	aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,		
CC	expressed in aorta and (5) one that lacks sequences 1 and 3		
CC	called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e		
CC	are set forth in AAQ84666-Q84669 and AA71012-R71015 respectively.		
XX			
SQ	Sequence 1086 AA;		

Query Match 99.3%; Score 5708.5; DB 16; Length 1086;			
Best Local Similarity 99.5%; Pred. No. 0;			
Matches 1086; Conservative 0; Mismatches 0; Indels 5; Gaps 1;			
QY	1	MAAGCLLALTTLFQSLIGSPSEPPFPSPATIKSWDKMQEDLVTLAKTAGSVNQLVDI	60
Db	1	maagcllaltltlfgslilgspseepfssavtikswdkmqedlvtlaktasgvnqlvdi	60

QY 61 YEKYQDLYTVEPNNAQOLVETAAEDIEKLLNSRSKALVSLAEAEKVQAAHQRWEDFASN 120  
Db 61 yekyqdylytvepnnarqlveaardieklennrskalvslaeakvqaahqrwefasn 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 evvynakddldpekdndsepgsqrikpvfiedanfgrqisyqhaavhiptdiyegstivl 180  
QY 181 NELNWTSSALDEVFKKNEEDPSLLWQVFGSATGLARIYPASPWVDNSRTPNKKIDLYDVR 240  
Db 181 nelnwtssaldevfkknreedpsllwqvfgsatglariypaspwvdnsrtpnkidlydvr 240  
QY 241 RPWYIQAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETLSDDDFVNVSFNSNAQD 300  
Db 241 rpwyiqaaspkdmlilvdvsgvsgitlklirtsvsemlletlstdddfvnvsfnnaqd 300  
QY 301 VSCFOHLVQANVRNKKVYLKDAVNNTAKGITYDKGFSFAFEQLLNYNVSRANCKIIML 360  
Db 301 vscfghlvqanvrnkvlkdavnntakgitdykkgfsafeqllnynvsranckiiiml 360  
QY 361 FTDGEERAQELFNKYNKDKKVRFRSVGQHNRYERGPQIMACENKGYIYEISGAIR 420  
Db 361 ftdgeeraqelfnkynkdkkvrfrsvgqhnryergpqimacenkgyyiyeisga 420  
QY 421 INTQBYDLVGRPMVLADGKAKQVQWTVNYLDALGLVITGTLVPFNITGQFENKTNLK 480  
Db 421 intqbydlvgrpmvladgkakqvqwtvnyldaleglvigtltlpfnitgqfenktnlk 480  
QY 481 NOLILGVMGVDSVLEIDKRLPRFTCLPNGYFYFAIDPNGYVLLHPNLPKNPKSQEPVTL 540  
Db 481 nqililgvmgvdsvedikrlprftclpngyfyfaidpngyvvllhpnlpknlpk 540  
QY 541 DFLDAELNDKVEIRNKMIDGESKTRFLVKSDERYIDKGNRYITWTVPNGTDYSL 600  
Db 541 dfldaelndkveirnkmidgesektrflvksderyidkgnryitwtvpngtdysl 600  
QY 601 ALVLPYFYIKAKLEETIQAKSKGKMDSETLKPDPNEESGYTFIAPDRCNDLKI 660  
Db 601 alvlpysfyikakleetiqarskkgkmdsetlkdndnyvftapyfnsksgpaysgi 660  
QY 661 SDNTEFLNFEIDRTPNPNCSNADLNRLVLDAGFTNRLVQVNSKQKNGVKAR 720  
Db 661 sdntefilnfeidrtppnpscnadlnrllvldagftnelvqnywskqkngvkar 720  
QY 721 FVWTDGGITRYPRKAGENQENETEDSYKSLDNDNVFTAPYFNKSGPCAYESGI 780  
Db 721 fvttdggitryprkagenqenetyedsykrslndndnvftapyfnsksgpaysgi 780  
QY 781 MVSKAVEIYIOGKLLKPAVGIKIDVNSWENFTKTSIRDPGAPVCDCKRNSDVMDCVI 840  
Db 781 mvskaveiyiogkllkpaavgikidvnsweenftktsirdpcagpvcckrnsdvm 840  
QY 841 LDGGFLLMANHDDYTNIGRFFGEIDPSLMRHLNVSIVYAFNKSVDYQVCEPAAPKQ 900  
Db 841 ldggfllmanhddytngirffgeidpslmrhlvnsvyafnksydyqvceppaapk 900  
QY 901 GAGHSASVPSVADILQIGWATAAASILQOFLSLTFPRLLEAVENEDDDFTASLSKQ 960  
Db 901 gaghsasvpsvadilqigwataaasilqofllsltfprlleavenedddftaslsk 960  
QY 961 SCITBQTOYFFDNDKSFSGVLDGNCNRSIFHGEKLMNTNIFTMVESKGTCPDTRLLI 1020  
Db 961 scitebtqoyffdnksfsgvldgncnrsifhgeklmntniftmveskgtpcdtrll 1020  
QY 1021 QAEQTSQDGNPCDMVQPRYRKGPVDCPDNNVLEDYTDGCGVSGNLPSLWYIIGIQFLL 1080  
Db 1021 qaeqtsqdgndpncdmvqpryrkpgvdcpdnnvledytdcgvgsgnlpslwyliqf 1080  
QY 1081 WLVSQSTHRL 1091  
Db 1081 wlvsgsthrll 1086

RESULT 8  
AAW63153  
ID AAW63153 standard; Protein; 1086 AA.  
XX  
AC AAW63153;  
XX  
DT 12-OCT-1998 (first entry)  
XX  
DE Human calcium channel alpha-2c subunit.  
XX  
KW Alpha-2 subunit; human; calcium channel; assay; detection;  
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
XX  
OS Homo sapiens.  
PN US5792846-A.  
XX  
PD 11-AUG-1998.  
XX  
PF 31-MAY-1995; 95US-04555543.  
XX  
PR 04-APR-1994; 94US-0223305.  
PR 04-APR-1988; 88US-0176899.  
PR 04-APR-1989; 89US-0603751.  
PR 04-APR-1989; 89WO-US01408.  
PR 20-FEB-1990; 90US-0482384.  
PR 30-NOV-1990; 90US-0620250.  
PR 15-AUG-1991; 91US-0745206.  
PR 31-MAY-1995; 95US-04555543.  
XX  
PA (SIBI-) SIBIA NEUROSCIENCES INC.  
XX  
PI Brenner R, Ellis SB, Feldman DR, Harpold MM, McCue AF;  
PI Williams ME;  
XX  
DR WPI; 1998-456192/39.  
DR N-PSDB; AAV42702.  
XX  
PT DNA encoding human calcium channel alpha 1B subunit protein -  
PT useful for recombinant production of the channel for screening of  
PT its modulators, and diagnosis of Lambert Eaton Syndrome  
XX  
PS Claim 3; Columns 293-300; 166pp; English.  
XX

The present sequence represents the alpha-2c subunit of a human calcium channel. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha 1 subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.

XX Sequence 1086 AA;

Query Match 99.3%; Score 5708.5; DB 19; Length 1086;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1086; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAACGLIALTLTLOSLLIGPSSEPPSPVATIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
Db 1 maagclialtltlfqslligpsseepfpavtikswdqmgedlvtlaktasgvnqlvdi 60  
QY 61 YEKYQDLYTVEPNNAQOLVETAAEDIEKLLNSRSKALVSLAEAEKVQAAHQRWEDFASN 120  
Db 61 yekyqdylytvepnnarqlveaardieklennrskalvslaeakvqaahqrwefasn 120

QY 121 EVYYNAKDDLDPEKNDSEGGQRIKPVFIEDANFORQISYOHAAVHIPTDIYEGSTIVL 180  
Db 121 evyyynakddldpekndsepgsqrlkpvfiedanfrqisqyhaavhiptdiyegstivl 180  
QY 181 NELNWTSAIDVEFKKREDEPSSLLWQVCSAGCLARYYPASPWVDSRTPNPKIDLDVRR 240  
Db 181 nelnwtসাঈদেফকক্রেদেপসল্লবকসাগকলার্য্যপসবদসরত্পনকিডব্র 240  
QY 241 RPYWIGAAAPKDMILLVDVSGVSLTTLKLRITSVSEMLETSLDDDFNVASFNSNAQD 300  
Db 241 rpywigaaapkdmiilvdvsgvsltlklritsvsemlletlstddfnvafnsnagd 300  
QY 301 VSCFOHLVQANVRNKKVLKADANNITAKGIDYKKGFSFAFEOQLNLYNSRANCNKIIML 360  
Db 301 vscfqlhvdqanvrnkvlkadannitakgidykkgfsfafeoqlnlynvrancnkiml 360  
QY 361 FTDGGERAEIENKYNKDKVVRVFSVGOHNERGPTOWMACENKGYIYEPSTIGAIR 420  
Db 361 ftdggeeraeifnkynkdkvrvfsvgohnyergptowmacenkgyyiepsigair 420  
QY 421 INTQEYLDVLRPMVLGAKQVQNTVYLDALGLVITGTLPVFNITGQENKTNLK 480  
Db 421 intqeyldvlrpmvlgakqvqntvnyldaleglvitgtlvpfnitgqfentnlk 480  
QY 481 NQILGVMGVDSLEDIKRLTPRTLCNPGYYPFADPNGLVYLLHPNLPKNPKSQEPVTL 540  
Db 481 nqilgvmgvdsledikrltprtlcpngyyypfadpnglvylhpnlpknpksepvtl 540  
QY 541 DFLDAELENDIKVEIRNKNMDGESGKERTLVKSDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 dfldaelendikveirnkmdgesgkertlvksderyidkgnrtytwtvpngtdysl 600  
QY 595 DFLDAELENDIKVEIRNKNMDGESGKERTLVKSDERYIDKGNRTYTWTPVNGTDYSL 595  
QY 601 ALVLPYSFYIKAKLEETITQARSKKGMKDSSETLKPONFESGYTFIAPRDCNDLKI 660  
Db 596 alvlpysfyyikaleetitqarskkgmkdssetlkpdnfeesgytfiaprdcndlki 655  
QY 661 SONTEFLNFEIDRKPNNPSCNADINRVLLDAGFTNELVQYWSKQNIKGVKAR 720  
Db 656 sdntefllnfeidrktppnpscndlinrvlldagftnelvqywsqkniqvkgr 715  
QY 721 FVVTGGITRVYPKEAGENWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPAYESGI 780  
Db 716 fvtvggitrvypkeagenwenpetyedsfykrsildndnyvftapyfnksgpayesgi 775  
QY 781 MYSKAVEIYIQGLKLPVAVGVIKIDVNSNIENFTKTSIRDPACAGPVCDCKRNSDVMDCVI 840  
Db 776 mvskaaveiyiqglklpavvgvikidvnsnienfktksirdpcagpvcdckrnsdvmdcvi 835  
QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSXYDYOSVCEPGAAPKQ 900  
Db 836 ldggfllmanhddytngigrffgeidpslmrhlvnsyafnksydyosvcepgaapkq 895  
QY 901 GAGHSAYVPSVADILQGWATAAASILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960  
Db 896 gaghsayvpsvadilqgwataaasilqflsltprlleavemedddftaslskq 955  
QY 961 SCITEQYFFNDKDSFSGVLDGNCRSRIFHGKELMNTNLIFIMVESKGTCPCDTRLII 1020  
Db 956 sciteqyffndkdsfsgvldgncrsrifhgeklnmtnlifimveskgtcpcdrlll 1015  
QY 1021 QAEQTSQGNPCDMVKQPKRYRGPVCFNNVLEDYTDGCGVSGGLNPSLWYIIGIQLLL 1080  
Db 1016 qaeqtsdgnpcdmvkpkrgrgpcvfcfnvledytdcgvgsgglnpsslwyiigiqlll 1075  
QY 1081 WLVSQSTHRL 1091  
Db 1076 wlvsgsthrll 1086

RESULT 9

AAB10587

ID AAB10587 standard; Protein; 1086 AA.

XX

AC AAB10587;  
XX 22-DEC-2000 (first entry)  
DT Human calcium channel alpha-2c subunit protein.  
XX  
DE Human; calcium channel; calcium channel subunit; diagnosis;  
XX Lambert Eaton Syndrome; calcium channel subunit alpha-2c.  
KW Homo sapiens.  
OS  
XX US6096514-A.  
PN  
XX 01-AUG-2000.  
PD  
XX 25-MAY-1995; 95US-0450562.  
PF  
XX 04-APR-1988; 88US-0176899.  
PR 02-FEB-1990; 90US-0482384.  
PR 08-NOV-1990; 90US-0603751.  
PR 30-NOV-1990; 90US-0620250.  
PR 15-AUG-1991; 91US-0745206.  
PR 10-APR-1992; 92US-0868354.  
PR 13-JUL-1992; 92US-0914231.  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
PR 07-FEB-1994; 94US-0193078.  
PR 04-APR-1994; 94US-0223305.  
PR 11-AUG-1994; 94US-0290012.  
PR 23-SEP-1994; 94US-0311363.  
PR 28-SEP-1994; 94US-0314083.  
PR 07-NOV-1994; 94US-0336257.  
PR 13-MAR-1995; 95US-0404950.  
XX  
XX (SIBI-) SIBIA NEUROSCIENCES INC.  
XX  
PI Ellis SB, Williams ME, McCue AF, Harpold MM;  
XX WPI; 2000-548230/50.  
DR N-PSDB; AAA71725.  
XX  
PT Human calcium channel beta subunit polynucleotides, useful for  
PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
PT Syndrome  
XX  
XX Disclosure; Column 237-244; 153pp; English.  
XX  
CC This invention describes a novel isolated DNA molecule (I) comprising a  
CC sequence encoding a beta3-1 subunit of a human calcium channel.  
CC Nucleic acid probes comprising 14-30 contiguous nucleotides of  
CC beta.3 subunit encoding DNA are useful for isolation and cloning of  
CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
CC express heterologous calcium channel are useful for identifying compounds  
CC that modulate calcium channel activity and in assays for identifying  
CC agonists and antagonists of calcium channel activity in humans. Human  
CC calcium channel subunit or eukaryotic cells expressing the channel are  
CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
CC sequence represents the human calcium channel alpha-2c subunit which is  
CC described in the method of the invention.  
XX  
XX Sequence 1086 AA;  
SQ  
Query Match 99.3%; Score 5708.5; DB 21; Length 1086;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1086; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
QY 1 MAAGCLALTLTLFQSLIGPSSSEFPSPSAVTIKSWVDKMQEDLVTLAKTAGSYGNQLVDI 60  
Db 1 maagclaltltlflqslilgppsseefpsavtikswvdkmqedlvtlaktasgynqlvdi 60  
QY 61 YEKYQDLYTVFEPNNARQLVEIAARDTEKLLSNRSKALVSLALEAEKVQAAHQHREDPASN 120  
XX



Db 61 yekyqdltyvepnarqlveiaardieklslsrskalsvlsaleaeakvqaahqwrefasn 120  
QY 121 EVVYNKADLDPEKNDSEPGSQRIKPVFTEDANFGQISQYHAAVHIPTDIYEGSTIVL 180  
Db 121 evvynakddlpekdndsepgsgrikpvfiedanfgqisqyhaavhiptdiyegstivl 180  
QY 181 NEUNWTSALDEVKKNREEDPSLLMQVFGSATGLARYYPASPVWDSNRTPKNKIDLDVRR 240  
Db 181 neunwtsaldevkknreedsllwqfsgatglaryypaspvwdsnrtpknkidldvrr 240  
QY 241 RPYWIOGAASPDKMLILVDVSGVSGLTGLKIRTSVSEMLETLSDDDFVNVASFENNAQD 300  
Db 241 rpywiggaaspdkmlilvdvsgvsgltlklirtsvsemletlssdddfvnvasfnsnaqd 300  
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGTTDYKGFSPAFEOILLNYSRANCNKIIML 360  
Db 301 vscfqlhvanvrnkvlkdavnnitakgttdykkgfafaefqllnynsrancnkliml 360  
QY 361 FTGGEERAQEIFKNYKOKKVRFRFSVQGHNYERGPIQWACENKGYEIPSIGAIR 420  
Db 361 ftggeeraqeifknynkdkkvrfrfsvqghnyergpiqwmacenkgyyeipsigair 420  
QY 421 INTQEVLDVLRPMVLADGAKQOVQWNTNYLDALGLVITGLPVFNITGQFENKTNLK 480  
Db 421 intqeyldvlgpmvladgkakqvntnyldalelglvltglpvnitgqfentknlk 480  
QY 481 NOLILGVMGVDSLEDKRLTRPFTLCPNGYFAIDPNGVLLHLPNLOPKNPKSQBPVIL 540  
Db 481 nqilgvmgvdsleedkrltrpftlcpngyfaidpngvllhlpnlqpk-----epvll 535  
QY 541 DFLDAELNDIKYIRNKMIDGESGKTRTLVKSDERYIDKGNRTYTWTPVNGDYSL 600  
Db 536 dfldaelndikveirnkmidgesgktrtlvksderyidkgnrtytwtvpvngtdysl 595  
QY 601 ALVLPYFYIYAKLEETITQARSKGKMKDSETLKPNFESGYTFIAPRDYCNLDKI 660  
Db 596 alvlpysfyiakaleetitqarskgkmdsetlkdndfseesgytfiaprdycondkll 655  
QY 661 SDNNTFELNFEIDRKTPNPNPCNADLNRLVLLDAGFTNELVQWYKQKNIKGVKAR 720  
Db 656 sdntfelnfnefidrktpnpncnadlnrvlldagftnelvqwykqknikgvkar 715  
QY 721 FVYTDGGITRVYKPEAGENQENPETYEDSFYKRSILDNDNYFTAPYFNKSGPGAYESGI 780  
Db 716 fvtydggitrvypkeagenqenpetyedsfykrsldndnyftapfynksgpgayesgi 775  
QY 781 MYSKAVEIIOGKLLPNAVVGKIDVNSWENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840  
Db 776 mvsakaveiioqkllpnavvgikidvnswnftktsirdpcagpvcdckrnsdvmdevi 835  
QY 841 LDGPGFLLMANHDDYTNQIGRPFGEITDPSLMRLHVNISYVAFNKSYDYOSVCEPGRAPKQ 900  
Db 836 ldgpgfllmanhdycnqigrfgeitdpslmrlhvnlsyvatnksydyosvcepgsarpkq 895  
QY 901 GAGHSAYVPSVADILQIGWATAAWSILQOFLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
Db 896 gaghsayvpsvadilqgwataawsilqlfsltfprlleavemedddftaslskq 955  
QY 961 SCITEOTQFFDNDKSFSGVLDCGNCSEIFHGEKLMNTNLIIFIMVESKGTCPDPRLLI 1020  
Db 956 scitedtqyffndksfsfgvldcgcncsrfhgeklmntnlifimveskgtcpdtrlll 1015  
QY 1021 QABOTSQGNPCDMVKQPRYRKGPVCFDNNVLEDYTDGCGVSGLNPSLWYIIGTQFLLL 1080  
Db 1016 qaeqtsdgnpcdmvkqpryrkgpvcfdnnvledytdcgvgsglnpslwyiigiqflll 1075  
QY 1081 WLVSQSTHRL 1091  
Db 1076 wlvsqsthrll 1086

RESULT 10  
AAR71015

ID AAR71015 standard; Protein; 1084 AA.  
XX  
AC AAR71015;  
XX  
DT 01-DEC-1995 (first entry)  
XX  
DE Human neuronal calcium channel subunit alpha 2e.  
XX  
KW Calcium channel subunit; antagonist; agonist; diagnosis;  
KW Lambert Eaton Syndrome.  
OS Homo sapiens.  
XX  
PN W09504822-A.  
XX  
PD 16-FEB-1995.  
XX  
PF 11-AUG-1994; 94WO-US09230.  
XX  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
XX  
PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX  
PI Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
XX  
DR WPI; 1995-090900/12.  
DR N-PSDB; AAQ84669.  
XX  
PT DNA encoding human calcium channel sub-unit(s) - used for  
PT developing prods. for studying calcium channels, e.g. for  
PT obtaining agonists and antagonists  
XX  
PS Disclosure; Page 248-253; 285pp; English.  
XX  
CC Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
CC differentially processed in skeletal muscle, aorta, and CNS in  
CC the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
CC tissues. Five alternatively spliced variant transcripts that differ  
CC in the presence or absence of one to three different portions of  
CC this region. There are three sequences involved (see AAQ84664 FT  
CC and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
CC alpha 2 encoding transcripts from the different tissues include  
CC different combinations of the three sequences, except for one of  
CC the alpha 2 transcripts expressed in aorta which lacks all three  
CC sequences. The five alpha 2 forms identified are (1) a form that  
CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
CC expressed in aorta and (5) one that lacks sequences 1 and 3  
CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
CC are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.  
XX  
SQ Sequence 1084 AA;  
  
Query Match 99.0%; Score 5691.5; DB 16; Length 1084;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;  
  
QY 1 MAAGCLLATLTLFQSLIGPSSSEFPFSAVVIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 maagcllatltlftqsligpsseepfpaavtiksvdkmqedlvtlaktasgvnqlvdi 60  
QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLSNRSKALVLSALEAEKVAQAAHQRWFASN 120  
Db 61 yekyqdltyvepnarqlveiaardieklslsrskalsvlsaleaeakvqaahqwrefasn 120  
QY 121 EVVYNKADLDPEKNDSEPGSQRIKPVFTEDANFGQISQYHAAVHIPTDIYEGSTIVL 180  
Db 121 evvynakddlpekdndsepgsgrikpvfiedanfgqisqyhaavhiptdiyegstivl 180

QY 181 NELNWT SALDEVFKKNEEDPSLLQVFGSATGLARYYPASPMWNSRTPNKNIDLYDVR 240  
Db 181 nelnwt saldevfkknredpsllqvfgsatglaryypaspmwvnsrtpnknidlydvrr 240  
QY 241 RPWYIQAASPKDMLILVDVSGVSGLTTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 rpwyiqgaaspkdmlilvdvsgvsglttlkirtsvesmletlsdddfvnvasfnsnaqd 300  
QY 301 VSCFOHLVQANVKNKVLDAVNNTAKGTDYKKGFSFAPEQOLLNYSRANCNIIML 360  
Db 301 vscfqlhvanvknkvlkdaannicakgtdykkgsfafeqllnynsrancnkilm 360  
QY 361 FTDGGERAQEIFKNYKDKKRVFRFSVQGNHYERGPIQWMACENKGYEIPSGAIR 420  
Db 361 ftdggeersaqeifknkdkkrrvfrfsvqgnhyergpiqwmacenkgyyelpsgair 420  
QY 421 INTQEYLDVLRPMVLGAKAKOVQNTNYYLDALGLVITGTLPVFNITGQFENKTNLK 480  
Db 421 intqeyldvlgrpmvlgakakqvntnyldaleglvitgtlvpfnitgqfenktnlk 480  
QY 481 NQLILGVMGVDSLEDIKRLTRFTLCPNGYFAIDPNGYVLLHPNLQPNKSKQEPVIL 540  
Db 481 nqlilgvmgvdsledikrltrftlcpngyfaidpngyvilhpnlgpknpsqepvli 540  
QY 541 DELDAELNDIKVEIRKNMIDGESGKTFRTLVKSODERYIDKGNRTYTTPVNGTDYSL 600  
Db 541 deldaelndikveirknmidgesgktrftlvksoderyidkgnrtyttpvngtdysl 600  
QY 601 ALVLPYSFYIKAKLEETITOQSKKKMKDSETLKPDNFEESGYTFIAPRDYCNLDKI 660  
Db 601 alvlpysfyikakleetitqary-----setlkdndfeesgytfiaprdycndkli 660  
QY 661 SDNNTFELNFEFIDRTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720  
Db 654 sdnteflfnfdrktpnpnpscnadlinrvlldagftnelvqnywskqknikgvkar 713  
QY 721 FVVTGGITRVYPKKAGENQENPEYEDSFYKRSIDNDNYYFTAPYFNKSGPGAYESGI 780  
Db 714 fvtvggitrvypkagenqenpetyedsfyrslndndnyftapyfnkspggaysgi 773  
QY 781 MYSKAVEIYIOGKLKPAVVGIKIDVNSNIENFTKTSIRDPCAGPVCDCKRNSDMDCVI 840  
Db 774 mvskaveiyoqklkpaavgikidvnsnienftktsirdpcagpvcckrnsdmdcvi 833  
QY 841 LDGGFLLMANHDDTNGIRFGEIDPSLMRHLVNSIVAFNKSVDYOSVCEPGAAPKQ 900  
Db 834 ldggfllmanhddytngirfgeidpslmrhlvnsivafnksydyosvcepgaapkq 893  
QY 901 GAGHRSAYVPSVADILQIGWATAAASWTLQOFLLSLTPRLEAVEMEDDDFTASLSKQ 960  
Db 894 gaghrsayvpsvadllqigwataaawslqoqlslstprlleavemedddftaslskq 953  
QY 961 SCITEQTOYFFDNDSKFSGLVDCGNCSEIFHGEKLMNTNLIFIMVESKGTCPCTRLLI 1020  
Db 954 sciteqtqoyffndsksfvgldcncseifhgeklmntnlifimveskgtcpcdtrlli 1013  
QY 1021 QAEQSDGNPCDMVKQPRYKRGDPDVCENNVLDEYDCGGVSGNLNPSLWYIIGIOFLLL 1080  
Db 1014 qaeqsdgnpcdmvkqpryrkgdpdvcennvleaydcggvsgnlpslwyiigioflll 1073  
QY 1081 WLVSGSTHRL 1091  
Db 1074 wlvsgsthrll 1084

RESULT 11  
ID AAW63155  
XX AAW63155 standard; Protein; 1084 AA.  
AC AAW63155;  
XX  
DT 12-OCT-1998 (first entry)  
XX

DE Human calcium channel alpha-2e subunit.  
XX Alpha-2 subunit; human; calcium channel; assay; detection;  
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
XX Homo sapiens.  
XX US5792846-A.  
XX 11-AUG-1998.  
XX 31-MAY-1995; 95US-0455543.  
XX 04-APR-1994; 94US-0223305.  
XX 04-APR-1988; 88US-0178899.  
XX 04-APR-1989; 89US-0603751.  
XX 04-APR-1989; 89WO-US01408.  
XX 20-FEB-1990; 90US-0482384.  
XX 30-NOV-1990; 90US-0620250.  
XX 15-AUG-1991; 91US-0745206.  
XX 31-MAY-1995; 95US-0455543.  
XX (SIBI-) SIBIA NEUROSCIENCES INC.  
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
PI Williams ME;  
XX WPI; 1998-456192/39.  
XX N-PSDB; AAV42704.  
XX DNA encoding human calcium channel alpha 1B sub-unit protein -  
PT useful for recombinant production of the channel for screening of  
PT its modulators, and diagnosis of Lambert Eaton Syndrome  
XX Claim 3; Columns 305-310; 166pp; English.  
XX The present sequence represents the alpha-2e subunit of a human calcium  
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
CC that allow controlled entry of calcium ions into cells. This leads  
CC to depolarisation events required for muscle contraction. The recombinant  
CC subunit, when expressed with nucleic acids encoding the complete calcium  
CC channel, can be used in assays for the detection and characterisation of  
CC compounds that modulate the channel. The DNA encoding the subunits can  
CC be alternatively spliced when transcribed, giving more than one form of  
CC the protein from the same transcript, each having slightly different  
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
CC molecules from the serum of an individual with Lambert Eaton Syndrome  
CC (LES) can be used as a diagnostic for the disease.  
XX Sequence 1084 AA;  
SQ

Query Match 99.0%; Score 5691.5; DB 19; Length 1084;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTLTFLSLLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60  
Db 1 maagcllaltltlfgsliligpsseepfsavtikswdkmqedlvtlaktasvngqlvdi 60  
QY 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHQWREDFASN 120  
Db 61 yekyqdltyvepnnarqlveiaardiekllsnrskalvslaleaeqvahqhwredfasn 120  
QY 121 EVVYVNAKDDLPKNDSEPGSQRKPFVEDANFQRQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 evvyynakddlpkndsepgsqrikpvfiedanfgrqisyqhaavhiptdiyegstivl 180  
QY 181 NELNWT SALDEVFKKNEEDPSLLQVFGSATGLARYYPASPMWNSRTPNKNIDLYDVR 240  
Db 181 nelnwt saldevfkknredpsllqvfgsatglaryypaspmwvnsrtpnknidlydvrr 240  
QY 241 RPWYIQAASPKDMLILVDVSGVSGLTTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300

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Db 241 rpwyigaaapdkmlllvdsvsvgltklirtsvemletisdddfvnvasfnsnagd 300
QY 301 VSCFQHLVQANVRNKKVKZKADANNITAKGIDYKKGFSAFQELLNYSRANCNKIIML 360
Db 301 vscfghlvqanvrnkvlkdavnnitakgidykkgfafaeqllynvnsrancnkiml 360
QY 361 FVDGGEERAQETFNKYNKDKKVRFRFSVQGHNYRGPIQWMACENKGYEYIPIGAI 420
Db 361 fcdggeeraqeifnkynkdckvrvfrfsvqghnyergplqwmacenkgyyeipsaigair 420
QY 421 INTQYLDVLGRPMVLADGKAKOVWNTVYLDALSELGVITGTLVPVNTIGQFNKTNLK 480
Db 421 intqeyldvlgrpmlvadgkakqvgtwnvyldealeiglvitgtlvpvntigqfentlk 480
QY 481 NOLILGVGVDSLEIDIKRLTPRTCLPCNGYFEAIDPNGYVLLHPNLPKPKSOEPTVL 540
Db 481 nqlilgvmgvdslesidkrltpfclpcngyfeaidpnyvllhpnlpkpkseqeptvl 540
QY 541 DFLDALENDIKVEIRNMIDGEGSEKTRFRLVKSQDRIYDKGNRTYTWTPVNGTDYSL 600
Db 541 dfldaelendikvelrnmidgesektrftrlvksqderyldkgnrtytwtpvngtdysl 600
QY 601 ALVLPYFYFYKAKLEETITQAKSKGKMKDSETLKPDNFEESGYTFIAPRDYCNDLKI 660
Db 601 alvlpysfyfyykakleetitqary-----sellkpdnfeesgytfiaprdydcndlki 653
QY 661 SDNTEFLNFEIDRTPNPNPCNADLINRVLLDAGFTNELVQYWSKOKIKGVKAR 720
Db 654 sdnntefllnfeidrtkpnpcnadmllnrvllldagftnelvqywsqknkkgvkar 713
QY 721 FVVDGGITRYPKAEAGENWQENPETYEDSYKRSNDONVYFTAPYFNKSGPGAYESGI 780
Db 714 fvtvdggitrrypkaegenwqenpetyedsfyrslndnvyftapyfnksgpgayesgl 773
QY 781 MYSKAVELYIGKLLKPAVVGKIDVNSWIENTFKTSIRDPACGVPDCCKRNSDVMDCVI 840
Db 774 mvskavelyigkllkpaavgikidvnswnientfktksirpcagvpdcckrnsdvmdcv1 833
QY 841 LDDGGFLMANHDDYTQIGRFFGEIDPISLMRHLVNTSVYAFNKSVDYQSVCEPGAAPKQ 900
Db 834 ldggflmanhddytqigrffgeidpslmrhlvntsvyafnksydyqsvcepgaapkq 893
QY 901 GAGHRSYVPSVADIIGWMTAAAWSILQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
Db 894 gaghrsavpsvadilqgwmtaawsilqfllsltfprlleavemedddftaslskq 953
QY 961 SCITEQYQFEFNDKSFSGVLDCGNCSTRIPHGEKLMNTNLIIFIMVESKTCPCDTRLLI 1020
Db 954 sciteqtqyifndksfsgvlcgcncsrifhgeklmntnlifimveskctpcdtrlli 1013
QY 1021 QAEQTSQPNPCDMVKOPRYRKGPVDFCFDNNVLEDYTDGGSGLNPSLWYIIGIFLL 1080
Db 1014 qaeqtsqpnpcdmvkqpryrgkpdvcfdnnvledytdcggsvglpslwyiigifll 1073
QY 1081 WLVSNGTHRL 1091
Db 1074 wlvsngthrll 1084
```

## RESULT 12

AAB10589

ID AAB10589 standard; Protein; 1084 AA.

XX AC AAB10589;

XX DT 22-DEC-2000 (first entry)

XX DE Human calcium channel alpha-2e subunit protein.

XX DE Human calcium channel; calcium channel subunit; diagnosis;

XX KW Lambert Eaton Syndrome; calcium channel subunit alpha-2e.

XX

OS Homo sapiens.

XX US6096514-A.

XX PD 01-AUG-2000.

XX XX

XX 25-MAY-1995; 95US-0450562.

XX XX

XX 04-APR-1988; 88US-0176899.

XX PR 02-FEB-1990; 90US-0482384.

XX PR 08-NOV-1990; 90US-0603751.

XX PR 30-NOV-1990; 90US-0620250.

XX PR 15-AUG-1991; 91US-0745206.

XX PR 10-APR-1992; 92US-0868354.

XX PR 13-JUL-1992; 92US-0914231.

XX PR 11-AUG-1993; 93US-0105536.

XX PR 05-NOV-1993; 93US-0149097.

XX PR 07-FEB-1994; 94US-0193078.

XX PR 04-APR-1994; 94US-0223305.

XX PR 11-AUG-1994; 94US-0290012.

XX PR 23-SEP-1994; 94US-0311363.

XX PR 28-SEP-1994; 94US-0314083.

XX PR 07-NOV-1994; 94US-0336257.

XX PR 13-MAR-1995; 95US-0404950.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX XX

XX Ellis SB, Williams ME, McCue AF, Harpold MW;

PI WPI; 2000-548230/50.

XX DR N-PSDB; AAA71727.

XX XX

XX Human calcium channel beta subunit polynucleotides, useful for

XX PT producing recombinant eukaryotic cells and for diagnosing Lambert Eaton

XX PT Syndrome

XX XX

XX Disclosure; Column 253-260; 153pp; English.

XX XX

XX This invention describes a novel isolated DNA molecule (I) comprising a

XX CC sequence encoding a beta3-1 subunit of a human calcium channel.

XX CC Nucleic acid probes comprising 14-30 contiguous nucleotides of

XX CC beta.3 subunit encoding DNA are useful for isolation and cloning of

XX CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that

XX CC express heterologous calcium channel are useful for identifying compounds

XX CC that modulate calcium channel activity and in assays for identifying

XX CC agonists and antagonists of calcium channel activity in humans. Human

XX CC calcium channel subunit or eukaryotic cells expressing the channel are

XX CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This

XX CC sequence represents the human calcium channel alpha-2e subunit which is

XX CC described in the method of the invention.

XX XX

XX Sequence 1084 AA;

XX SQ

Query Match 99.0%; Score 5691.5; DB 21; Length 1084;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTTLTFLQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSNOLVDI 60

Db 1 maagcllaltltlfgsligpssepppsavtikswdkmqedlvtlaktasgvnqlvdi 60

QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLLSNRSKALVSALAEAEKVAQAHQWREDFASN 120

Db 61 yekyqdltyvepnnarqlveiaardieklslrskalvsalaeaeakvqahqwfedfasn 120

QY 121 EVVYVYNAKDDLPEKNDSEPGSORIKPVIEDANFGRQISYOHAAVHIPTDIYEGSTIVL 180

Db 121 evvyvynakddlpeknndsepgsqrikpviedanfgrqisyqhaavhiptdiyegstivi 180

QY 181 NELNNTSALDEYFVKKNREDDPSLLQVFGSATGLARYYPASVPWNSRTPNKIDYDVR 240

Db 181 nelnntsaldevfknreedpsllqvfgsatglaryypasvpwvnsrtpnkidydvrr 240

QY 241 RPWYIQAASPKDMLILVDVSGSVGLTLKLRISVSEMLETISDDDFVNVASFNSNAQD 300  
Db 241 rpwyiqaaspkdmlilvdsvsgsltlklrtsvsemletisdddfvnnvasfnasqd 300  
QY 301 VSCFQHLVQANVRNKKVLDANNITAKITDYKKGFSFAFEOLLNINVSANRNCNKLIML 360  
Db 301 vscfghlvqanvrnkkvldavnnitakitdykkgfsfafegllnynvsanrncnkilm 360  
QY 361 FTDGGEERAQEIFNKNYKDKKVRFRFSVGOHNYERGPIONMACENKGGYYPISGAIR 420  
Db 361 ftdggeeraqeifnknkdkkvrfrfsvgghnyergpionmacenkgyypisgaair 420  
QY 421 INTQEVLDVLRPMVLGADKAKOVQWNTVYLDALLEGVLITGLPVFNITGOFENKTNLK 480  
Db 421 intqevldvlgprmvlgadkakovqwnvtyldalelgvlitgltpvfnitgofenktnlk 480  
QY 481 NQILGVMGVDSLEIDIKRLTFRFLPCPNNGYFAIDPNGYVLLHNPLOPKNPKSOEPVTL 540  
Db 481 nqilgvmgvdvsleidikrltfrflpcpnngyfaidpnyvllhnploqknpksoepvtl 540  
QY 541 DFLDAELENDIKVEIRNKMIDGSEKFTRLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
Db 541 dfldaelendikveirnkmidgesektftlrvksqderydkgnttytwtpvngtdysl 600  
QY 601 ALVLTYSFYIYKALEETITQARSKKGMKDSFELKPDNFEESGYTFIAPRDYCNLDKI 660  
Db 601 alvltysfyiykaleetitary-----setlkpdnfeesgytfiaprdydcndiki 660  
QY 661 SDNNTEFLNFEIDRTKPNPNSCNADLINRVLLDAGFTNELVONYSKOKNIKGVKAR 720  
Db 661 sdnnTEFLNFEIDRTKPNPNSCNADLINRVLLDAGFTNELVONYSKOKNIKGVKAR 720  
QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKSLDNDNYYFTAPYFNKSGPGAYESGI 780  
Db 721 fvtvgtgtrvypkeagenwqenpetyedsfyrslndndnyftapyfnksgpgayesgi 780  
QY 781 MYSKAVEYIYQGLKLPVAVGKIDVNSWENFTYSTRDPCAGVCDCKRNSDVMDCVI 840  
Db 781 mvskaveyiyqglklpvavgkidvnswnftystdrpcagvcdckrnsdvmdcvi 840  
QY 841 LDGCGFLMANHDDYTNOIGRFEGIDPSLMRHLNYSVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 ldggfllmanhddytngirfegidpslmrhlvnsyvafrnksvdyqsvcepgaapkq 900  
QY 901 GAGHRSAVPSVADILQIGWATAAASWILQOFLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
Db 901 gaghrsavpsvadilqigwataaawilqoqlsltfprlleavemedddftaslskq 960  
QY 961 SCITQTOYFFDNDKSGSVLDCGNCRIHFHGEKLMNTNLFIMVESKGTGCPDTRLLI 1020  
Db 961 sciteqtgyffndksksvgldegncsrifhgeklmntnlifimveskgtpcdtrlli 1020  
QY 1021 QAEQTSQGNPCDMYKQPRYRKGPVCDNDNVLEDTYDCGGVSGNLNPSLWYIIGTQFLIL 1080  
Db 1021 qaeqtsdgnpcdmkykpryrkpgvcdndnvledtydcggvsgnlpslwyiigtqflll 1080  
QY 1081 WLVSQSTHRL 1091  
Db 1081 wlvsqsthrll 1091  
QY 1091 WLVSQSTHRL 1094  
Db 1091 wlvsqsthrll 1094

RESULT 13  
AAR71012  
ID AAR71012 standard; Protein: 1103 AA.  
XX  
AC AAR71012;  
XX  
DF 01-DEC-1995 (first entry)  
XX Human neuronal calcium channel subunit alpha 2a.  
XX  
XX Calcium channel subunit; antagonist; agonist; diagnosis;  
KW

Lambert Eaton Syndrome.  
XX Homo sapiens.  
XX W09504822-A.  
XX 16-FEB-1995.  
XX 11-AUG-1994; 94WO-US09230.  
XX 11-AUG-1993; 93US-0105536.  
XX 05-NOV-1993; 93US-0149097.  
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX Ellis SB, Gillespie A, Harpold MM, McCue AF, Williams ME;  
XX WPI; 1995-090900/12.  
XX N-PSDB; AAQ84666.  
XX DNA encoding human calcium channel sub-unit(s) - used for  
XX developing prods. for studying calcium channels, e.g. for  
XX obtaining agonists and antagonists  
XX Disclosure; Page 231-236; 285pp; English.  
XX Human neuronal alpha 2 coding sequence (AAQ84664) transcript is  
XX differentially processed in skeletal muscle, aorta, and CNS in  
XX the region corresp. to nt 1595-1942 of AAQ84664 in each of the  
XX tissues. Five alternatively spliced variant transcripts that differ  
XX in the presence or absence of one to three different portions of  
XX this region. There are three sequences involved (see AAQ84664 FT  
XX and AAQ84665 FT), sequence 1, sequence 2 and sequence 3. The five  
XX alpha 2 encoding transcripts from the different tissues include  
XX different combinations of the three sequences, except for one of  
XX the alpha 2 transcripts expressed in aorta which lacks all three  
XX sequences. The five alpha 2 forms identified are (1) a form that  
XX lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
XX (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
XX (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
XX aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
XX expressed in aorta and (5) one that lacks sequences 1 and 3  
XX called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
XX are set forth in AAQ84666-Q84669 and AAR71012-R71015 respectively.  
XX Sequence 1103 AA;

Query Match 98.7%; Score 5672; DB 16; Length 1103;  
Best Local Similarity 97.6%; Pred. No. 0;  
Matches 1083; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
Db 1 maagcllalttlfqlsligpsseppfsavtikswdkmqedlvtlaktaagvgnqlvdi 60  
QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
Db 61 yekyqdytvepnnarqlveiaardieklslrskalvslaleaekvqaahqrdfasn 120  
QY 121 EVVYNNAKDDLDPKNDSEPGSQRIKPVFIEDANRGRQISYOHAAVHIPTDIYEGSTVL 180  
Db 121 evvynnakddldekndsepgsqrikpvfiedanrgrqisyohaaahiptdiyegstvl 180  
QY 181 NELNWTSALEDFVKKNRREDPSLLWQVFGSATGLARYYPASVPWNSRTPNKRIDLYDVR 240  
Db 181 nelnwtaldefvkknreedpsllwqvfgsatglaryypasvpwnsrtpnkridlydvr 240  
QY 241 RPWYIQAASPKDMLILVDVSGSVGLTLKLRISVSEMLETISDDDFVNVASFNSNAQD 300  
Db 241 rpwyiqaaspkdmlilvdsvsgsltlklrtsvsemletisdddfvnnvasfnasqd 300  
QY 301 VSCFQHLVQANVRNKKVLDANNITAKITDYKKGFSFAFEOLLNINVSANRNCNKLIML 360  
Db 301 vscfghlvqanvrnkkvldavnnitakitdykkgfsfafegllnynvsanrncnkilm 360

Db 301 vscfqlhvanvknkvlkdavnnitakgtdykgkfsfafeqllnynvsrancnkiml 360  
QY 361 FTGGEERAQEIENKYNKKKRVFRFSVGQHNHYERGPIOMMACENKGYIYEIPSGAIR 420  
Db 361 ftdggeeraqeifnkynkdkkvrfrfsvgqhnhyergpiqwmacenkgyyeipsgair 420  
QY 421 INTQEVLDVLRGPNVLADGAKAQOVQNTNYLDALGLVITGTPVFNITGQEPENTNLK 480  
Db 421 intqeyldvlgpnmvlagdkakqvgntnyldalelgltgtpvfnitgqfenktnlk 480  
QY 481 NQILGVMGVDSLEDEKRTPTFTLCPNGYFAIDPBGVLLVLPNLPKQ-----530  
Db 481 nqilgvmgvdsledkrltptftlcpngyfaidpbgvllvlpnlpkq-----530  
QY 531 -----NPKSQEPVTLDFLDAELNDIKVEIRNMKIDGESGERTFPLVKSQDERYI 581  
Db 541 lrkrrpnqpksgqevtlldfaelndikveirnmkldgesgektfrtlvksqderyl 600  
QY 582 DKGNTVTWTPVNGTDYSLALVLPYTFYVYKAKLEETITQABSKGKMKDSETLKPDNF 641  
Db 601 dkgntvtwtpvngtdyslalvlpftyfyvyykakeetitqary-----setlkpdnf 653  
QY 642 EESGYTFIAPRDYCNLDIKISDNNTEFLLNNEFIDRTPNPNPSCNADLINRVLLDAGFTN 701  
Db 654 eesgytfiaprdycndlikisdntefllnnfnefidrktppnpscnadlinrvlldagftn 713  
QY 702 ELVONYSKKNKTKGVKARVVTGGITRVYPREAGENWOENPETTEDSYKRSLONDNY 761  
Db 714 elvqnywskqknkvgkavrtvtdggitrvypkeagenwdenpetyedsykrslndny 773  
QY 762 VFTAPYENKSGPAGAYESGIMVSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKSTRDP 821  
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QY 822 CAGVPCDKRNSDMVCVILDDGFLLMANHDDYTNOIGRFFGEIDPISLMRHLVNTSVYA 881  
Db 834 cagpvcdkrsndmvdvildggfllmanhddytngirffgeidpslmrhlvntsvya 893  
QY 882 FNKSVDYQSVCEGAPKQAGHRSAYVPSVADILQGWATAAAWSILOQFLSLTFPR 941  
Db 894 fnksydyqsvcepgaapkgaghrrsayvpsvadilqgwataaawsilqgflsltfpr 953  
QY 942 LLEAVEMEDDDFTASLSKQSCITEOTOTYFFDNDKSKFSGLDCGNCRIHFHGEKLMNTNL 1001  
Db 954 lleavemedddftaslskqsciteqtgyffondsksfsgvldcncsrifhgeklmntnl 1013  
QY 1002 IFIMVESKGTCPCDTRLIIQAETS DSGPNPCDMVKOPRYRKGPDPVCFDNNVLEDYTDGCG 1061  
Db 1014 ifimveskgtpcdtrliiqaetsdsgpnpcdmvkopryrkgpdcfdnnvledytdcgg 1073  
QY 1062 VSGUNPSLWYIIQIQLLWLVSGSTHRL 1091  
Db 1074 vsgunpslwyligqillwlvsgsthrll 1103

RESULT 14  
AAW63151  
ID AAW63151 standard; Protein; 1103 AA.  
XX  
AC AAW63151;  
XX  
XX 12-OCT-1998 (first entry)  
DT Human calcium channel alpha-2a subunit.  
DE  
DE Alpha-2 subunit; human; calcium channel; assay; detection;  
KW characterisation; Lambert Eaton Syndrome; LES; diagnosis.  
KW  
XX Homo sapiens.  
XX  
XX US5792846-A.  
PN  
XX

PD 11-AUG-1998.  
XX 31-MAY-1995; 950S-0455543.  
PR 04-APR-1994; 940S-0223305.  
PR 04-APR-1988; 880S-0176899.  
PR 04-APR-1989; 890S-0603751.  
PR 04-APR-1989; 89WO-US01408.  
PR 20-FEB-1990; 900S-0482384.  
PR 30-NOV-1990; 900S-0620250.  
PR 15-AUG-1991; 910S-0745206.  
PR 31-MAY-1995; 950S-0455543.  
XX (SIBI-) SIBIA NEUROSCIENCES INC.  
XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;  
PI Williams ME;  
XX WPI; 1998-456192/39.  
DR N-PSDB; AAV42700.  
XX.  
PT DNA encoding human calcium channel alpha 1B subunit protein -  
PT useful for recombinant production of the channel for screening of  
PT its modulators, and diagnosis of Lambert Eaton Syndrome  
XX  
XX Claim 3; Columns 287-294; 166pp; English.  
XX  
CC The present sequence represents the alpha-2a subunit of a human calcium  
CC channel. Calcium channels are membrane-spanning, multi-subunit proteins  
CC that allow controlled entry of calcium ions into cells. This leads  
CC to depolarisation events required for muscle contraction. The recombinant  
CC subunit, when expressed with nucleic acids encoding the complete calcium  
CC channel, can be used in assays for the detection and characterisation of  
CC compounds that modulate the channel. The DNA encoding the subunits can  
CC be alternatively spliced when transcribed, giving more than one form of  
CC the protein from the same transcript, each having slightly different  
CC properties. In addition, the reactivity of the alpha 1 subunit with IgG  
CC molecules from the serum of an individual with Lambert Eaton Syndrome  
CC (LES) can be used as a diagnostic for the disease.  
XX Sequence 1103 AA;  
XX  
QY Query Match 98.7%; Score 5672; DB 19; Length 1103;  
Best Local Similarity 97.6%; Pred. No. 0;  
Matches 1083; Conservative 0; Mismatches 1; Indels 26; Gaps 2;  
QY 1 MAAGCLLALTLTLFQSLILIGPSSSEPPPSAVTTKSWVDKMQEDLVTAKTAGVGNQLVDI 60  
Db 1 maagcallaltltlfigslilgssseepfapsavtikswvdkmqedlvtlaktasgvnqlvdi 60  
QY 61 YEKYODLYTVEPNNAQOLVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHOWREDFASN 120  
Db 61 yekyodlytvepnnaqlvelaardiekllsnrskalvslaleaekvqaahqwredfasn 120  
QY 121 EVVYNAKDDLDPEKNDSEPCSQRIKPVFIEDANFRQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 evvyynakddldpekndsepgsqrikpvyfiedanfrqisyqhaavhiptdiyegstivl 180  
QY 181 NELNWTSSALDEVFKKNEEDPSLLVQVFGSGATGLARYYPASPWVDNSRTPNKIDLYDVR 240  
Db 181 nelnwtssaldevfkknreedpsllvqvfgsatglaryypaspwvdsnrtpnkidlydvr 240  
QY 241 RPWYIOGAASPDKMLILVDYVSGSVSGITLKLIRTSVSEMLETLSDDDFVNVSNSNAQD 300  
Db 241 rpwyiogaaspdkmllilvdysvsgsvsgitlklirtsvsemlletlsdddfvnvsnnaqd 300  
QY 301 VSCFOHLVQANVRNKKVYLKDAVNNITAKGTDYKKGFSFAFEQLLNYNVSRANCNKIIML 360  
Db 301 vscfqlhvanvrnkkyvlkdavnnitakgtdykgkfsfafeqllnynvsrancnkiml 360  
QY 361 FTGGEERAQEIENKYNKKKRVFRFSVGQHNHYERGPIOMMACENKGYIYEIPSGAIR 420  
Db 361 ftdggeeraqeifnkynkdkkvrfrfsvgqhnhyergpiqwmacenkgyyeipsgair 420

Db 361 ftdggeeraqelfnkynkdkkvrfrfsvqghnyergpiqmacenkgyyveipsgair 420  
QY 421 INTQBYDLVGRPMVLGAKAKQVQWNTWYLDALBELGLVITGTLVFNITGOFENKTNLK 480  
Db 421 Intqeyldvlgprpmvlagdkakqvqtnvyldalelgivitgtlpvfnitgqfenktnlk 480  
QY 481 NQLILGVGVGVSLIEDIKRLPRFTLPCNGYFFADPNQYVLLHNPLOPK-----530  
Db 481 nqlilgvmgvdsvedikrlprftlpcngyffadpnqyvilhnpkplgvipntin 540  
QY 531 -----NPKSQPVTLDFDALENDIKVEIRNMKIDGESGKTFRTLVKSODERYI 581  
Db 541 lrrkrrpnlnqpkseqvltldfdaelendikveirnmkidgesgkftlrvksqderyl 600  
QY 582 DKGNTYTWTPVNGDYSLALVPLYSFYIKAKLEETITQARSKGKMKDSETLKPDNF 641  
Db 601 dkgnrtwtvpngtdyslalvplysfyikakleetitqary-----setlkpdnf 653  
QY 642 EESGYTFIAPRDCYNDLKISDNTFELNFEFIDRKTNPNSCNADLINRVLLDAGFTN 701  
Db 654 eesgytfiaprdcndlkisdnteflnfnefidrktnpnpscnadlinrvlldagftn 713  
QY 702 ELVQNWSKQKNIKGVKARFVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 761  
Db 714 elvqywnskqknikgvkarfvvtggitrvypkeagenqenpetyedsfykrsldndny 773  
QY 762 VFTAPYFNKSGPAYESGIMSKAVEIYIYQGLKLPVAVVIGIKIDVNSWTENKTSIRDP 821  
Db 774 vftapyfnksgpayesgimskaveiyiqgkllkpavvgikidvnswnlenfkttsirp 833  
QY 822 CAGPVCDCRNSDNDVCDVLDGGFLMANHDDYTNQIGRFFGETDPSLMRHLVNLISVA 881  
Db 834 cagpvcdcrcnsdndvcdvldggflmanhddytnqigrffgetdpslmrhlvnlisva 893  
QY 882 FNKSYDYQVCPGAPKOGAGHRSAVPSVADIIQIGWATAAAMSIIQQFLLSLTFFR 941  
Db 894 fnskdyqsvcepapagaghrsaavpsvadliqgwataaawsiiqqflslstftr 953  
QY 942 LLEAVEMEDDDFTASLSKSCITEQTQYFFDNDKSFSGVLDCGNCSTRIFHGEKLMNTNL 1001  
Db 954 lleavemedddftaslsksciteqtqyffndksksfsgvlcdgncsrifhgeklmntnl 1013  
QY 1002 IFTWVESKTCPCDTELLTQAEQTSQGNPCDMVQPRYRKGPVCFDNNVLEDYDTCGG 1061  
Db 1014 iftwvesktpcdtrlltqaeqtsqgnpcdmvqpryrkpgpdcvcdhvnviedydcgg 1073  
QY 1062 VSGLPNLSLWYIIGIQLLWLVSGSTHRL 1091  
Db 1074 vsglpnslwyiigiqlllwlsvgsthrll 1103

RESULT 15

AAB10586  
ID AAB10586 standard; Protein; 1103 AA.  
XX AC AAB10586;  
XX DT 22-DEC-2000 (first entry)  
XX DE Human calcium channel alpha-2a subunit protein.  
XX KW Human; calcium channel; calcium channel subunit; diagnosis;  
XX LW Lambert Eaton Syndrome; calcium channel subunit alpha-2a.  
XX OS Homo sapiens.  
XX PN US6096514-A.  
XX PD 01-AUG-2000.  
XX PF 25-MAY-1995; 95US-0450562.  
XX PR 04-APR-1988; 88US-0176899.

PR 02-FEB-1990; 90US-0482384.-  
PR 08-NOV-1990; 90US-0603751.  
PR 30-NOV-1990; 90US-0620250.  
PR 15-AUG-1991; 91US-0745206.  
PR 10-APR-1992; 92US-0868354.  
PR 13-JUL-1992; 92US-0914231.  
PR 11-AUG-1993; 93US-0105536.  
PR 05-NOV-1993; 93US-0149097.  
PR 07-FEB-1994; 94US-0193078.  
PR 04-APR-1994; 94US-0223305.  
PR 11-AUG-1994; 94US-0290012.  
PR 23-SEP-1994; 94US-0311363.  
PR 28-SEP-1994; 94US-0314083.  
PR 07-NOV-1994; 94US-0336257.  
PR 13-MAR-1995; 95US-0404950.  
XX (SIBI-) SIBIA NEUROSCIENCES INC.  
XX Ellis SB, Williams ME, McCue AF, Harpold MM;  
XX WPI; 2000-548230/50.  
XX N-PSDB; AAA711724.  
XX Human calcium channel beta subunit polynucleotides, useful for  
XX producing recombinant eukaryotic cells and for diagnosing Lambert Eaton  
XX Syndrome -  
XX Disclosure: Column 229-236; 153pp; English.  
XX This invention describes a novel isolated DNA molecule (I) comprising a  
XX nucleic acid encoding a beta3-1 subunit of a human calcium channel.  
XX Nucleic acid probes comprising 14-30 contiguous nucleotides of  
XX beta3 subunit encoding DNA are useful for isolation and cloning of  
XX calcium channel subunit-encoding DNA. Recombinant eukaryotic cells that  
XX express heterologous calcium channel are useful for identifying compounds  
XX that modulate calcium channel activity and in assays for identifying  
XX agonists and antagonists of calcium channel activity in humans. Human  
XX calcium channel subunit or eukaryotic cells expressing the channel are  
XX useful for diagnosing Lambert Eaton Syndrome (LES) in a human. This  
XX sequence represents the human calcium channel alpha-2a subunit which is  
XX described in the method of the invention.  
XX Sequence 1103 AA;

Query Match 98.7%; Score 5672; DB 21; Length 1103;  
Best Local Similarity 97.6%; Pred. No. 0;  
Matches 1083; Conservative 0; Mismatches 1; Indels 26; Gaps 2;

QY 1 MAAGCILLALTTLTFLQSLIGPSSEEPFSAVTTIKSVKMOEDLVTLAKTAGVGNOLVDI 60  
Db 1 maagcillaltltlflqsligpsseepfsavttiksvkmoedlvtlaktasgvnqlvdi 60  
QY 61 YEKYODLYTVEPNARQOLVEIAARDIEKLISNRKALVSLALEAEKVAQAHOWREDFASN 120  
Db 61 yekyodlytvepnarqlveiaardieklisnrskalvslaleaekvaahqwrdfasn 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFRQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 evvynakddldpekndsepgsqrikpvfiedanfrqisyqhaavhiptdiyegstivl 180  
QY 181 NELNWTSAIDDEVFKKNEEDPSSLWQVFGSATGLARYYPASPWPVNSRTPNKIDLYDVR 240  
Db 181 nelnwtaldevfkknreedpsllwqvfgsatglaryypaspwpvnsrtpnkdilydvrr 240  
QY 241 RPWYIOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
Db 241 rpwyiggaaspkdmlilvdvsgsvsgitlklirtsvsemlletisdddfvnnvasfnnaqd 300  
QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAEQLLNYSRANCNKIIML 360  
Db 301 vscfqlhvanvrnkvlkdvannitakgitdykkgfsfafeqllnynvrancnkiiml 360

QY 361 FTDGGERAEIFNKYNKDKVVRERFSVGOHNYERGPIONMACENKGYYYEIPSIGAIR 420  
Db 361 fcdgggeeraqelfnkynkdkkvrfrfsvvgumyergpiqwmacenkgyyeipsigair 420  
QY 421 INTQEYLDVLRPMVLGAKQKQVOMTNYVLDALGLVITGTLFVFNITGQFENKTNLK 480  
Db 421 intqeyldvlgprpmvlgakqkqvomtnvyldaleglvitgtlpvfnitgqfenktnlk 480  
QY 481 NQLILGVWGVDSLEEDIKRLPRFTLCPNGYFFAIDPNGYVLLHPNLOPK----- 530  
Db 481 nqlilgvmgvdsledikrltprftlcpngyffaidpngyvllhpnlpqkpgvgiptin 540  
QY 531 -----NPKSQBPVTLDFDLDALENDIKVEIRNMIDGESGEKTFRTLVKSODERYI 581  
Db 541 lkrtrpnlqnpksqepvldfldaelendlkveirnmidgesgektfritlvksoderyi 600  
QY 582 DRGNRTYTWTPVNGTDYSLALVLPYSYIYAKALEETITQARSKKGMKDSSETLKPDNF 641  
Db 601 dkgnrtytwtpvngtdyslalvlpysyiyakaleetitqary-----setlkpdnf 653  
QY 642 EESGYTFIAPRDYCNLDKISDNTEFLNFEFIDRKTPNPNPCNADLINRVLLDAGFTN 701  
Db 654 eesgytfiaprdycndlkisdntefllnfefidrktppnpscnadlinrvlldagftn 713  
QY 702 ELVQNWSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNY 761  
Db 714 elvqnywskqknikgvkarfvvtddgtrvypkeagenwqenpetyedsfykrsldndny 773  
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Db 774 vftapyfnksgpayesgimvskaveiyiqgkllkpavvgikidvnswienvftktsirdp 833  
QY 822 CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLNYSVYA 881  
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QY 882 FNKSYDYQSVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTPPR 941  
Db 894 fnksydyqsvcepagaapkogaghrsaysvpsvadilqigwataaawsilqfllsltpfr 953  
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Db 954 lleavemedddftaslskqsciteqtqyffndnksfsgvldcncsrfhgeklmntnl 1013  
QY 1002 IFIMVESKGTCPCDTRLLIQAEQTSQDGNPCDMVKQPRYKGPDPVCFDNNVLEDYDCGG 1061  
Db 1014 ifimveskgtcpcdtrlliqaeqtsdgnpcdmvkqpryrgpdpvcfdnnvledydcgg 1073  
QY 1062 VSGLNPSLWYIIIGIOFLILWLVSNGTHRL 1091  
Db 1074 vsglnpwlwyiigioflilwlvsngthrll 1103



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:30:13 ; Search time 37.55 Seconds  
(without alignments)  
585.294 Million cell updates/sec

Title: US-09-397-548-14  
Perfect score: 5748  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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4: /cgnl\_7/ptodata/1/1aa/6B\_COMB.pap.\*  
5: /cgnl\_7/ptodata/1/1aa/PCBUS\_COMB.pap.\*  
6: /cgnl\_7/ptodata/1/1aa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5748	100.0	1091	1	US-07-745-206A-25
2	5748	100.0	1091	1	US-08-455-543A-52
3	5748	100.0	1091	2	US-08-223-305C-52
4	5748	100.0	1091	2	US-08-311-363-25
5	5744	99.9	1091	3	US-08-713-118-4
6	5744	99.9	1091	4	US-09-452-007-4
7	5708.5	99.3	1086	1	US-08-455-543A-54
8	5708.5	99.3	1086	2	US-08-223-305C-54
9	5691.5	99.0	1084	1	US-08-455-543A-56
10	5691.5	99.0	1084	2	US-08-223-305C-56
11	5672	98.7	1103	1	US-08-455-543A-53
12	5672	98.7	1103	2	US-08-223-305C-53
13	5652	98.3	1079	1	US-08-455-543A-55
14	5652	98.3	1079	2	US-08-223-305C-55
15	5508.5	95.8	1106	1	US-08-433-675B-5
16	5490.5	95.5	1106	1	US-08-336-257A-8
17	5257.5	91.5	1086	6	5386025-8
18	2581.5	44.9	508	1	US-08-435-675B-6
19	182	3.2	885	3	US-09-074-579-5
20	182	3.2	885	4	US-09-388-774-5
21	159.5	2.8	946	3	US-09-074-579-3
22	159.5	2.8	946	4	US-09-388-774-3
23	154	2.7	903	1	US-08-021-601-12
24	154	2.7	903	1	US-08-082-849B-12
25	154	2.7	903	5	PCT-US94-01624-12
26	152.5	2.7	789	1	US-08-471-033-32
27	152.5	2.7	789	2	US-08-471-044-32

28	152.5	2.7	789	2	US-08-463-483A-32	Sequence 32, Appl
29	152.5	2.7	789	2	US-08-471-046A-32	Sequence 32, Appl
30	152.5	2.7	789	2	US-08-470-566B-32	Sequence 32, Appl
31	152.5	2.7	789	2	US-08-838-219B-4	Sequence 4, Appl
32	152.5	2.7	789	2	US-08-469-334-32	Sequence 32, Appl
33	152.5	2.7	789	3	US-09-300-528-32	Sequence 32, Appl
34	152.5	2.7	789	3	US-09-233-336A-4	Sequence 4, Appl
35	152.5	2.7	789	4	US-09-233-752A-4	Sequence 4, Appl
36	150.5	2.6	789	4	US-08-960-780-6	Sequence 6, Appl
37	150.5	2.6	789	4	US-09-073-898-6	Sequence 6, Appl
38	148.5	2.6	790	4	US-08-960-780-4	Sequence 4, Appl
39	148.5	2.6	790	4	US-09-073-898-4	Sequence 4, Appl
40	147.5	2.6	746	2	US-08-838-219B-6	Sequence 6, Appl
41	147.5	2.6	746	3	US-09-233-336A-6	Sequence 6, Appl
42	147.5	2.6	746	4	US-09-233-752A-6	Sequence 6, Appl
43	145.5	2.5	790	4	US-08-960-780-8	Sequence 8, Appl
44	145.5	2.5	790	4	US-09-073-898-8	Sequence 8, Appl
45	141.5	2.5	789	1	US-08-471-033-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-07-745-206A-25  
; Sequence 25, Application US/07745206A  
; Patent No. 5429921  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: McCue, Ann  
; APPLICANT: Feldman, Daniel  
; TITLE OF INVENTION: Human Calcium Channel Compositions and  
; TITLE OF INVENTION: Methods  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fitch, Even, Tabin & Flannery  
; STREET: 135 S. LaSalle  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/745,206A  
; FILING DATE: 19910815  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Feder, Scott B  
; REFERENCE/DOCKET NUMBER: 51504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-372-7842  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-745-206A-25

Query Match 100.0%; Score 5748; DB 1; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLFQSLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60



Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MAAGCLLATLTTLFQSLIGPSSSEPPPSAVTTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
Db	1	MAAGCLLATLTTLFQSLIGPSSSEPPPSAVTTIKSWDKMQEDLVTLAKTASGVNQLVDI	60
QY	61	YERYQDLYTEPNNAHQVLEIAARDIEKLSNRSKALVSLALEAEKVQAAHQWREDFASN	120
Db	61	YERYQDLYTEPNNAHQVLEIAARDIEKLSNRSKALVSLALEAEKVQAAHQWREDFASN	120
QY	121	EVVYNAKDDLPEDKNDSEPGSRIKPIPVFIEDANFRQISYQAAHVHPIPTDIYEGSTIVL	180
Db	121	EVVYNAKDDLPEDKNDSEPGSRIKPIPVFIEDANFRQISYQAAHVHPIPTDIYEGSTIVL	180
QY	181	NELNWTSALEDEVEFKKNEEDPSLLWQVFGSATGLARYYPASPWDNSRTNPKIDLDVRR	240
Db	181	NELNWTSALEDEVEFKKNEEDPSLLWQVFGSATGLARYYPASPWDNSRTNPKIDLDVRR	240
QY	241	RPWYIOGAASPDKMLILVDVSGSVGLTLKLIIRTSVSEMLETISDDDFVNVASFNSNAQD	300
Db	241	RPWYIOGAASPDKMLILVDVSGSVGLTLKLIIRTSVSEMLETISDDDFVNVASFNSNAQD	300
QY	301	VSCFQHLVQANVNKKVLDKAVANNITAKGITDYKKGFSFAFEQLLNYSRANCNKIIML	360
Db	301	VSCFQHLVQANVNKKVLDKAVANNITAKGITDYKKGFSFAFEQLLNYSRANCNKIIML	360
QY	361	FTDGGERAQEIENKYNKDKKRVFRFSVGOHNYERGPIOWMACENKGYIIEIPSGAIR	420
Db	361	FTDGGERAQEIENKYNKDKKRVFRFSVGOHNYERGPIOWMACENKGYIIEIPSGAIR	420
QY	421	INTQEYLDVLRPMWLAGDKAKQVQNTNVDLALGLVITGTLPVFNITGQFENKTNLK	480
Db	421	INTQEYLDVLRPMWLAGDKAKQVQNTNVDLALGLVITGTLPVFNITGQFENKTNLK	480
QY	481	NQILGVMGVDVSLDIKRLTPFTICPNGYIFAIDPNGVYLHPNLOPNKPSQEPVTL	540
Db	481	NQILGVMGVDVSLDIKRLTPFTICPNGYIFAIDPNGVYLHPNLOPNKPSQEPVTL	540
QY	541	DFLDALENDIKYIENKMKIDGSGEKTFTLVKSDERYIDKGNRTYTTPVNGTDYSL	600
Db	541	DFLDALENDIKYIENKMKIDGSGEKTFTLVKSDERYIDKGNRTYTTPVNGTDYSL	600
QY	601	ALVLPYSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFFIAPRDYCNLDKI	660
Db	601	ALVLPYSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFFIAPRDYCNLDKI	660
QY	661	SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQYWSQKNIKGVKAR	720
Db	661	SDNTEFLNFEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQYWSQKNIKGVKAR	720
QY	721	FVYTDGTRVYKPEAGENQENPEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI	780
Db	721	FVYTDGTRVYKPEAGENQENPEYDSFYKRSLDNDNVFTAPYFNKSGPGAYESGI	780
QY	781	MVSKAVEIYIQGLKLPVAVGIRIDVNSWIENTFTKSIRPCAGPVCDCRNSDVMDCVI	840
Db	781	MVSKAVEIYIQGLKLPVAVGIRIDVNSWIENTFTKSIRPCAGPVCDCRNSDVMDCVI	840
QY	841	LDDGGLLMANHDYDYNQIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ	900
Db	841	LDDGGLLMANHDYDYNQIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAAPKQ	900
QY	901	GAGHRSAYVPSVADIQIGWATAAASILQOFLLSITFPRLLAEVEMEDDDFTASLSKQ	960
Db	901	GAGHRSAYVPSVADIQIGWATAAASILQOFLLSITFPRLLAEVEMEDDDFTASLSKQ	960
QY	961	SCITEQTQYFFDNDKDSFSGLVDCGNCSTRIFHGEKLMNTNLIIFIMVESKTCPCDTRLLI	1020
Db	961	SCITEQTQYFFDNDKDSFSGLVDCGNCSTRIFHGEKLMNTNLIIFIMVESKTCPCDTRLLI	1020
QY	1021	QAEQTSDBGPNPCDMVKQPRYRKGPVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIOFLLL	1080
Db	1021	QAEQTSDBGPNPCDMVKQPRYRKGPVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIOFLLL	1080

Db	1021	QAEQTSDBGPNPCDMVKQPRYRKGPVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIOFLLL	1080
QY	1081	WLVSGSTHRL 1091	
Db	1081	WLVSGSTHRL 1091	
RESULT 3			
US-08-223-305C-52			
: Sequence 52, Application US/08223305C			
: Patent No. 5851824			
: GENERAL INFORMATION:			
: APPLICANT: Harpold, Michael			
: APPLICANT: Ellis, Steven			
: APPLICANT: Williams, Mark			
: APPLICANT: Feldman, Daniel			
: APPLICANT: McCue, Ann			
: APPLICANT: Brenner, Robert			
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND			
: TITLE OF INVENTION: METHODS			
: NUMBER OF SEQUENCES: 57			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Brown, Martin, Haller & McClain			
: STREET: 1660 Union Street			
: CITY: San Diego			
: STATE: California			
: COUNTRY: USA			
: ZIP: 92101-2926			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Diskette			
: COMPUTER: IBM Compatible			
: OPERATING SYSTEM: DOS			
: SOFTWARE: FastSEQ Version 1.5			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/223,305C			
: FILING DATE: April 4, 1994			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: 07/868,354			
: FILING DATE: April 10, 1992			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/745,206			
: FILING DATE: 15-AUG-1991			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/620,250			
: FILING DATE: 30-NOV-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/482,384			
: FILING DATE: 20-FEB-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/603,751			
: FILING DATE: 04-APR-1989			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: WO PCT/US89/01408			
: FILING DATE: 04-APR-1989			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/176,899			
: FILING DATE: 04-APR-1988			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Seidman, Stephanie L.			
: REGISTRATION NUMBER: 33,779			
: REFERENCE/DOCKET NUMBER: 52516 (P519739)			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: (619)238-0999			
: TELEFAX: (619)238-0062			
: INFORMATION FOR SEQ ID NO: 52:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 1091 amino acids			
: TYPE: amino acid			
: STRANDEDNESS: single			
: TOPOLOGY: linear			
: MOLECULE TYPE: protein			
: FRAGMENT TYPE: internal			
US-08-223-305C-52			

Query Match 100.0%; Score 5748; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLFOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTLTFLFOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120  
DB 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120

QY 121 EYVYNKADLLDPKNDSEPGSORIKPVFIEDANFGRIQISYQAAHVHPTDIYEGSTIVL 180  
DB 121 EYVYNKADLLDPKNDSEPGSORIKPVFIEDANFGRIQISYQAAHVHPTDIYEGSTIVL 180

QY 181 NELNWTLSALDEVFKKNEEDPSLLQWVFGSATGLARYYPASPWWNSRTNPKIDLYDVR 240  
DB 181 NELNWTLSALDEVFKKNEEDPSLLQWVFGSATGLARYYPASPWWNSRTNPKIDLYDVR 240

QY 241 RPYWIOGAASPDKMLILVDYSGVSGLTLLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300  
DB 241 RPYWIOGAASPDKMLILVDYSGVSGLTLLKIRTSVSEMLETISDDDFVNVASFNSNAQD 300

QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKGFSPAFEQLLNYSRANCNKIIML 360  
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKGFSPAFEQLLNYSRANCNKIIML 360

QY 361 FTGGERAQEIENKYNKKVRFRFVSGQHNHYERGPIOWMACENKGYIYEIPSGAIR 420  
DB 361 FTGGERAQEIENKYNKKVRFRFVSGQHNHYERGPIOWMACENKGYIYEIPSGAIR 420

QY 421 INTQEYLDVLRPMWLAGDKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480  
DB 421 INTQEYLDVLRPMWLAGDKAKOVQNTNVLDALEGLVITGTLPVFNITGQFENKTNLK 480

QY 481 NQILGVMGVDVSLDKRLTPRTLCNPGYFAIDPNGYVLLHPNLQKNPKSQEPVTL 540  
DB 481 NQILGVMGVDVSLDKRLTPRTLCNPGYFAIDPNGYVLLHPNLQKNPKSQEPVTL 540

QY 541 DFLDAELNDIKVEINKNKIDGESGKTRFTLVKSQDERYDKGNRTYTWTPVNGTDYSL 600  
DB 541 DFLDAELNDIKVEINKNKIDGESGKTRFTLVKSQDERYDKGNRTYTWTPVNGTDYSL 600

QY 601 ALVLPYTSFYIIKALEETITQARSKKMKDSETLKPNFESGYTFTAPRDYCNDLKI 660  
DB 601 ALVLPYTSFYIIKALEETITQARSKKMKDSETLKPNFESGYTFTAPRDYCNDLKI 660

QY 661 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNKGVKAR 720  
DB 661 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNKGVKAR 720

QY 721 FVYTDGGLTRVYKEAGENQWNPETIYDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
DB 721 FVYTDGGLTRVYKEAGENQWNPETIYDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780

QY 781 MYSKAVEIYIOGKLLPAPVVGKIDVNSNIENFTKTSIRDPGAGVCCCKRNSDVMDCVI 840  
DB 781 MYSKAVEIYIOGKLLPAPVVGKIDVNSNIENFTKTSIRDPGAGVCCCKRNSDVMDCVI 840

QY 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSVDYQSVCEPGAAPQ 900  
DB 841 LDGGLFLMANHDDYTNQIGRFFGEIDPSLMRHLVNIISYAFNKSVDYQSVCEPGAAPQ 900

QY 901 GAGHSAYPSVADIIQIGWATAAANSILOQFLSLTTPRLEAVEMEDDDFTASLSQ 960  
DB 901 GAGHSAYPSVADIIQIGWATAAANSILOQFLSLTTPRLEAVEMEDDDFTASLSQ 960

QY 961 SCITEQTYFFDNDKSFSGVLDGNCNCSIRIFHGEKLMNTNLIIFIMVESKGTCPCTRLLI 1020  
DB 961 SCITEQTYFFDNDKSFSGVLDGNCNCSIRIFHGEKLMNTNLIIFIMVESKGTCPCTRLLI 1020

QY 1021 QABQTSQDPNCPDMVKQPRYRKGPVCFDNNVLEDYTDGCGVSGNLNPSLWYIIGIQFLL 1080  
DB 1021 QABQTSQDPNCPDMVKQPRYRKGPVCFDNNVLEDYTDGCGVSGNLNPSLWYIIGIQFLL 1080

QY 1081 WLYSGSTHRL 1091  
DB 1081 WLYSGSTHRL 1091

RESULT 4  
US-08-311-363-25  
; Sequence 25, Application US/08311363  
; Patent No. 5876958  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: Human Calcium Channel Compositions and  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,363  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-51506  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1091 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-311-363-25

Query Match 100.0%; Score 5748; DB 2; Length 1091;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTFLFOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTLTFLFOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120  
DB 61 YEKYODLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVAQAHHQWREDFASN 120

QY 121 EYVYNKADLLDPKNDSEPGSORIKPVFIEDANFGRIQISYQAAHVHPTDIYEGSTIVL 180  
DB 121 EYVYNKADLLDPKNDSEPGSORIKPVFIEDANFGRIQISYQAAHVHPTDIYEGSTIVL 180

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181 NELNWTSALEDEVEFKKREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLDYDVR 240
181 NELNWTSALEDEVEFKKREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLDYDVR 240
241 RPWYIOGAASPKDMLLDVDSVSGSLTKLRTSVSEMLETSDDDFVNVSFNSNAQ 300
241 RPWYIOGAASPKDMLLDVDSVSGSLTKLRTSVSEMLETSDDDFVNVSFNSNAQ 300
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLLNYSRANCNKIIML 360
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLLNYSRANCNKIIML 360
361 FTDGGEERAQEIFKNYKDKKVRFRFVSQGHNYERGPQIOWMACENKGYIYEPSIGAIR 420
361 FTDGGEERAQEIFKNYKDKKVRFRFVSQGHNYERGPQIOWMACENKGYIYEPSIGAIR 420
421 INTQEYLDVLGRPMVLADKAKOVQNTNVDLALEGLVITGTLPLVFNITGQFENKTNLK 480
421 INTQEYLDVLGRPMVLADKAKOVQNTNVDLALEGLVITGTLPLVFNITGQFENKTNLK 480
481 NQILGVMGVDSLEDIKRLTPFTLCPNGYYPADPNQVYLLHPLNLPKNPKSQEPVTL 540
481 NQILGVMGVDSLEDIKRLTPFTLCPNGYYPADPNQVYLLHPLNLPKNPKSQEPVTL 540
541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
601 ALVLPYSFYIYKAKLEETITQARSKGKMDSETLKPONFESGYTFIAPRDYCNLDKI 660
601 ALVLPYSFYIYKAKLEETITQARSKGKMDSETLKPONFESGYTFIAPRDYCNLDKI 660
661 SDNTEFLNFEFIDRKTPNPNNSCNADLNRYLLDAGFTNELVQNYWSKQNIKGVKAR 720
661 SDNTEFLNFEFIDRKTPNPNNSCNADLNRYLLDAGFTNELVQNYWSKQNIKGVKAR 720
721 FVYTDGGITRVYKPEAGENQWENPEYEDSFYKRSRLDNDNYVTAPYFNKSGPGAYESGI 780
721 FVYTDGGITRVYKPEAGENQWENPEYEDSFYKRSRLDNDNYVTAPYFNKSGPGAYESGI 780
781 MVSKAVEIYIOGKLLPAPVGVGIDVNSWTEFTKTSIRPCAGPVCDCRNSDVMDCVI 840
781 MVSKAVEIYIOGKLLPAPVGVGIDVNSWTEFTKTSIRPCAGPVCDCRNSDVMDCVI 840
841 LDGSGFLMANHDDYTNQIGRFGEIDPISLMRHLVNIISVYAFNKSXYDQSVCEPGAAPKQ 900
841 LDGSGFLMANHDDYTNQIGRFGEIDPISLMRHLVNIISVYAFNKSXYDQSVCEPGAAPKQ 900
901 GAGHRSAYVPSVADILQIGHWATAAASILQQLFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
901 GAGHRSAYVPSVADILQIGHWATAAASILQQLFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
961 SCITEQYEFDDNDKSFSGVLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCPCDTRLLI 1020
961 SCITEQYEFDDNDKSFSGVLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCPCDTRLLI 1020
1021 QAEQTSQGNPCDMVKOPRYRKGPVDCFDNNVLEDYTDGCGVSGSLNPSLWYIIGIQFLLL 1080
1021 QAEQTSQGNPCDMVKOPRYRKGPVDCFDNNVLEDYTDGCGVSGSLNPSLWYIIGIQFLLL 1080
1081 WLVSNGTHRL 1091
1081 WLVSNGTHRL 1091
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RESULT 5  
US-08-713-118-4  
; Sequence 4, Application US/08713118  
; Patent No. 6040436  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru

```
APPLICANT: Suey, David J.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/713,118  
FILING DATE: 16-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mata, Elizabeth W.  
REGISTRATION NUMBER: 38,236  
REFERENCE/DOCKET NUMBER: ACC96-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-713-118-4
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Query Match 99.9%; Score 5744; DB 3; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1090; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAAGCLIALTLTFLQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSYNQVLVDI 60
DB 1 MAAGCLIALTLTFLQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGSYNQVLVDI 60
QY 61 YEKYQDLYTVEPNARQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQHREDFASN 120
DB 61 YEKYQDLYTVEPNARQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQHREDFASN 120
QY 121 EVVYINAKDDLDPKNDSEPGSORIKPVFTEDANFGRIQISYQAAHVHPDIDYEGSTIVL 180
DB 121 EVVYINAKDDLDPKNDSEPGSORIKPVFTEDANFGRIQISYQAAHVHPDIDYEGSTIVL 180
QY 181 NELNWTSALEDEVEFKKREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLDYDVR 240
DB 181 NELNWTSALEDEVEFKKREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLDYDVR 240
QY 241 RPWYIOGAASPKDMLLDVDSVSGSLTKLRTSVSEMLETSDDDFVNVSFNSNAQ 300
DB 241 RPWYIOGAASPKDMLLDVDSVSGSLTKLRTSVSEMLETSDDDFVNVSFNSNAQ 300
QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLLNYSRANCNKIIML 360
DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQQLLNYSRANCNKIIML 360
QY 361 FTDGGEERAQEIFKNYKDKKVRFRFVSQGHNYERGPQIOWMACENKGYIYEPSIGAIR 420
DB 361 FTDGGEERAQEIFKNYKDKKVRFRFVSQGHNYERGPQIOWMACENKGYIYEPSIGAIR 420
QY 421 INTQEYLDVLGRPMVLADKAKOVQNTNVDLALEGLVITGTLPLVFNITGQFENKTNLK 480
DB 421 INTQEYLDVLGRPMVLADKAKOVQNTNVDLALEGLVITGTLPLVFNITGQFENKTNLK 480
QY 481 NQILGVMGVDSLEDIKRLTPFTLCPNGYYPADPNQVYLLHPLNLPKNPKSQEPVTL 540
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Db 481 NOLILGVMGVDSLEDIKRLTPRTLCFNGYFAIDPNGYALLHPNLPKPKSOEPTVL 540  
Qy 541 DFLDAELNDIKVEIRNMIDGESGKERTLVKSQDERYIDKGNRTYTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRNMIDGESGKERTLVKSQDERYIDKGNRTYTPVNGTDYSL 600  
Qy 601 ALVLPYTFYIYKAKLEETITQARSKKMKDSETLKPDPNFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIYKAKLEETITQARSKKMKDSETLKPDPNFEESGYTFIAPRDYCNLDKI 660  
Qy 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELYQVYWSKQKNIKVYKAR 720  
Db 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELYQVYWSKQKNIKVYKAR 720  
Qy 721 FVWTDGGITRVYKPEAGENQWENPETEDSFYKRSNDNDNVETAPYFNKSGPGAYESGI 780  
Db 721 FVWTDGGITRVYKPEAGENQWENPETEDSFYKRSNDNDNVETAPYFNKSGPGAYESGI 780  
Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAPVDCCKRNSDVMDCVI 840  
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAPVDCCKRNSDVMDCVI 840  
Qy 841 LDDGGFLLMANHHDDYTNOIGREFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGRAPKQ 900  
Db 841 LDDGGFLLMANHHDDYTNOIGREFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGRAPKQ 900  
Qy 901 GAGHRSAYVPSVADILQIGWATAAASIIQQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
Db 901 GAGHRSAYVPSVADILQIGWATAAASIIQQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
Qy 961 SCITEQYQYFFDNDKSFSGVLDCGNGSRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
Db 961 SCITEQYQYFFDNDKSFSGVLDCGNGSRIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020  
Qy 1021 QAEQTSQGNPCDMVKOPRYKGDVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIQFLLL 1080  
Db 1021 QAEQTSQGNPCDMVKOPRYKGDVCFDNNVLEDYTDGCGVSGLNPSLWYIIGIQFLLL 1080  
Qy 1081 WLVSQSGTHRL 1091  
Db 1081 WLVSQSGTHRL 1091

RESULT 6  
US-09-452-007-4  
; Sequence 4, Application US/09452007  
; Patent No. 6140485  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suey, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/452,007  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118

FILING DATE: 16-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mata, Elizabeth W.  
REGISTRATION NUMBER: 38,236  
REFERENCE/DOCKET NUMBER: ACC96-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1091 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-452-007-4  
Query Match 99.9%; Score 5744; DB 4; Length 1091;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1090; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MAAGCLLALTTLTFLQSLIGPSSSEPPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTTLTFLQSLIGPSSSEPPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60  
Qy 61 YEKYQDLYTVEPNNAQQLVEIAARDTEKLLSNRSKALVSLALEAEKVQAAHQRDEFSN 120  
Db 61 YEKYQDLYTVEPNNAQQLVEIAARDTEKLLSNRSKALVSLALEAEKVQAAHQRDEFSN 120  
Qy 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRIQISYQAAHVHPTDIYEGSTIVL 180  
Db 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRIQISYQAAHVHPTDIYEGSTIVL 180  
Qy 181 NELNWTALDEVEFKKREDEPSSLKQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240  
Db 181 NELNWTALDEVEFKKREDEPSSLKQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240  
Qy 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Qy 301 VSCFOHLVQANVRNKKVLDAVNNTAKGITDYKGFSAFQOLLNYSRANCNKIIML 360  
Db 301 VSCFOHLVQANVRNKKVLDAVNNTAKGITDYKGFSAFQOLLNYSRANCNKIIML 360  
Qy 361 FTDGGEERAQEIFNKYNKKVFRFVSQGHNYERGIQWACENKGYIYEIPSGAIR 420  
Db 361 FTDGGEERAQEIFNKYNKKVFRFVSQGHNYERGIQWACENKGYIYEIPSGAIR 420  
Qy 421 INTOEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGLTPVFNITGQFENKTNLK 480  
Db 421 INTOEYLDVLGRPMVLGAKAKOVQNTNYLDALGLVITGLTPVFNITGQFENKTNLK 480  
Qy 481 NQILIGVMGVDSLEDIKRLTPRTLCFNGYFAIDPNGYALLHPNLPKPKSOEPTVL 540  
Db 481 NQILIGVMGVDSLEDIKRLTPRTLCFNGYFAIDPNGYALLHPNLPKPKSOEPTVL 540  
Qy 541 DFLDAELNDIKVEIRNMIDGESGKERTLVKSQDERYIDKGNRTYTPVNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRNMIDGESGKERTLVKSQDERYIDKGNRTYTPVNGTDYSL 600  
Qy 601 ALVLPYTFYIYKAKLEETITQARSKKMKDSETLKPDPNFEESGYTFIAPRDYCNLDKI 660  
Db 601 ALVLPYTFYIYKAKLEETITQARSKKMKDSETLKPDPNFEESGYTFIAPRDYCNLDKI 660  
Qy 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELYQVYWSKQKNIKVYKAR 720  
Db 661 SDNTEFLNFEEDIRKTPNPNPCNADLINRVLLDAGFTNELYQVYWSKQKNIKVYKAR 720  
Qy 721 FVWTDGGITRVYKPEAGENQWENPETEDSFYKRSNDNDNVETAPYFNKSGPGAYESGI 780  
Db 721 FVWTDGGITRVYKPEAGENQWENPETEDSFYKRSNDNDNVETAPYFNKSGPGAYESGI 780

QY 781 MVSKEVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840  
Db 781 MVSKEVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPACGVCDCRNSDVMDCVI 840  
QY 841 LDGSGFLLMANHDYTNQIGRFFGEIDPDLMLRHLVNSVAFNKSVDYQSVCEPAGAPKQ 900  
Db 841 LDGSGFLLMANHDYTNQIGRFFGEIDPDLMLRHLVNSVAFNKSVDYQSVCEPAGAPKQ 900  
QY 901 GAGHRSAYVPSVADIQIGWATAAAMSIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
Db 901 GAGHRSAYVPSVADIQIGWATAAAMSIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQYQYFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNLIPTMVESKGTCPDTRLLI 1020  
Db 961 SCITEQYQYFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNLIPTMVESKGTCPDTRLLI 1020  
QY 1021 QAEOTSDGPNPCDMVKOPRYRKGPVDFVCFDNNVLEDYDTCGVSGLNPSLWYIIGIQFLLL 1080  
Db 1021 QAEOTSDGPNPCDMVKOPRYRKGPVDFVCFDNNVLEDYDTCGVSGLNPSLWYIIGIQFLLL 1080  
QY 1081 WLVSNGTHRL 1091  
Db 1081 WLVSNGTHRL 1091

RESULT 7

US-08-455-543A-54  
; Sequence 54, Application US/08455543A  
; Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA

COMPUTER READABLE FORM:

ZIP: 92101-2926  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A

PRIOR APPLICATION DATA:

FILING DATE: May 31, 1995  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
APPLICATION NUMBER: 07/745,206  
FILING DATE: 15-AUG-1991  
APPLICATION NUMBER: 07/620,250  
FILING DATE: 30-NOV-1990  
APPLICATION NUMBER: 07/482,384  
FILING DATE: 20-FEB-1990  
APPLICATION NUMBER: 07/603,751  
FILING DATE: 04-APR-1989  
APPLICATION NUMBER: 07/603,751  
FILING DATE: 04-APR-1989

APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1086 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-54

Query Match 99.3%; Score 5708.5; DB 1; Length 1086;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1086; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLLALTLFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTLFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
Db 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
QY 121 EVVYVNAKDDLPDKNDSEPGSORIKPVFIEDANFGQISYQAAHVHPTDIYEGSTIVL 180  
Db 121 EVVYVNAKDDLPDKNDSEPGSORIKPVFIEDANFGQISYQAAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTLSALDEVEFKKNEEDPSLLQWVFGSATGLARYYPASPVWDSNRTNPKIDLYDVR 240  
Db 181 NELNWTLSALDEVEFKKNEEDPSLLQWVFGSATGLARYYPASPVWDSNRTNPKIDLYDVR 240  
QY 241 RPWYIOGAASPDKMLILVDVSGSVGLTLKIRTSVSEMLETSLDDDFVNVASFNSNAQ 300  
Db 241 RPWYIOGAASPDKMLILVDVSGSVGLTLKIRTSVSEMLETSLDDDFVNVASFNSNAQ 300  
QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKGFSAFEQLLNYSRANCNKIIML 360  
Db 301 VSCFOHLVQANVRNKKVLDVANNITAKGTDYKGFSAFEQLLNYSRANCNKIIML 360  
QY 361 FTDGGEERAEQIEFNKYNKDKKRVFRFVSQHNVERGPIQWACENKGYEIPSGAIR 420  
Db 361 FTDGGEERAEQIEFNKYNKDKKRVFRFVSQHNVERGPIQWACENKGYEIPSGAIR 420  
QY 421 INTQEYLDVLGRPMVLGAKAKOVQMTNVYDLALELGLVTGTLPVFNITGQENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLGAKAKOVQMTNVYDLALELGLVTGTLPVFNITGQENKTNLK 480  
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPBGYVLLHPNLPKNPKSQEPVTL 540  
Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPBGYVLLHPNLPKNPKSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYDKGNRTYTTWTPVNGTDYSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSODERYDKGNRTYTTWTPVNGTDYSL 600  
QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLKPONFESGYTFTIAPRDYCNLDKI 660  
Db 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLKPONFESGYTFTIAPRDYCNLDKI 660  
QY 661 SONNTEFLNPFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNVSKQKIKGVKAR 720  
Db 661 SONNTEFLNPFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNVSKQKIKGVKAR 720



Db 656 SNNTEFLNNEFDTRKTPNNPSCNADLINRVLLDAGFTNELVQNTWSKQKNIKGVKAR 715  
QY 721 FVWTDGGITRYVPKEAGNWOENPETYEDSYKRSLDNDNTVFTAPFNKSGPGAYESGI 780  
Db 716 FVWTDGGITRYVPKEAGNWOENPETYEDSYKRSLDNDNTVFTAPFNKSGPGAYESGI 775  
QY 781 MYSKAVEIYIOGKLLKPAVGIKIDVNSWIEFNFTKTSIRDPACGVCDCCKRNSDVMDCVI 840  
Db 776 MYSKAVEIYIOGKLLKPAVGIKIDVNSWIEFNFTKTSIRDPACGVCDCCKRNSDVMDCVI 835  
QY 841 LDDGGFLMAHNDYTNIOIGRFFGEIDPSLMRHLVNTSVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 836 LDDGGFLMAHNDYTNIOIGRFFGEIDPSLMRHLVNTSVYAFNKSVDYQSVCEPGAAPKQ 895  
QY 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960  
Db 896 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 955  
QY 961 SCITEQTYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVSKGTCPCDTRLLI 1020  
Db 956 SCITEQTYFFDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVSKGTCPCDTRLLI 1015  
QY 1021 QAEQTSQGNPCDMVKOPRYRKGPVDFCNVLEDYTDGCGVSGNLPSLWYIIGIQFLL 1080  
Db 1016 QAEQTSQGNPCDMVKOPRYRKGPVDFCNVLEDYTDGCGVSGNLPSLWYIIGIQFLL 1075  
QY 1081 WLVSSTHRL 1091  
Db 1076 WLVSSTHRL 1086

## RESULT 8

US-08-223-305C-54  
; Sequence 54, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA: WO PCT/US89/01408  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0062  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1086 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-223-305C-54

Query Match 99.3%; Score 5708.5; DB 2; Length 1086;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1086; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MAAGCLIALTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLIALTLTFLQSLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNNAQVETIAARDIEKLLSNRSKALVSLALEAEKYQAAHQWREDFASN 120  
Db 61 YEKYQDLYTVEPNNAQVETIAARDIEKLLSNRSKALVSLALEAEKYQAAHQWREDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL 180  
QY 181 NELNWTSAIDVEFKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTNPKIDLYDVR 240  
Db 181 NELNWTSAIDVEFKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTNPKIDLYDVR 240  
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300  
QY 301 VSCFOHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQOLLNVNVRANCKIIML 360  
Db 301 VSCFOHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQOLLNVNVRANCKIIML 360  
QY 361 FTGGERAQEIEFNKYNKDKKVRVFRFVSGQHNHYERGPQIOMACENKGYIYEIPSGAIR 420  
Db 361 FTGGERAQEIEFNKYNKDKKVRVFRFVSGQHNHYERGPQIOMACENKGYIYEIPSGAIR 420  
QY 421 INTQEYLDVLGRPMVLADKAKOVQMTNVYLDALGLVITGTLVPVFNITGQFENKTNLK 480  
Db 421 INTQEYLDVLGRPMVLADKAKOVQMTNVYLDALGLVITGTLVPVFNITGQFENKTNLK 480  
QY 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYIYFAIDPNGYVLLHPNLPKNPKSQBPVTL 540  
Db 481 NQILGVMGVDVSLIEDIKRLTPFTLCPNGYIYFAIDPNGYVLLHPNLPKNPKSQBPVTL 535  
QY 541 DFLDALENDIKVEIRNKMIDGESGKFTFTLVKSDERYIDKGNRTYTTWTPVNGTDYSL 600  
Db 536 DFLDALENDIKVEIRNKMIDGESGKFTFTLVKSDERYIDKGNRTYTTWTPVNGTDYSL 595  
QY 601 ALVLPYTSFYIKAKLEETITQARSKGKMKDSEITLKPONFESGYTFIAPRDYCNLDKI 660  
Db 596 ALVLPYTSFYIKAKLEETITQARSKGKMKDSEITLKPONFESGYTFIAPRDYCNLDKI 655

QY 661 SNNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNBLVONYWSKQNKIRGVKAR 720  
DB 656 SNNTEFLNFEIDRKTTPNPNPCNADLINRVLLDAGFTNBLVONYWSKQNKIRGVKAR 715  
QY 721 FVVTGGITRVYPKKAGENWQENPETEYDSFYKRSIDNDNYYFTAPYFNKSGPGAYESGI 780  
DB 716 FVVTGGITRVYPKKAGENWQENPETEYDSFYKRSIDNDNYYFTAPYFNKSGPGAYESGI 775  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVPCDCRNSDYMDCVI 840  
DB 776 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPCAGVPCDCRNSDYMDCVI 835  
QY 841 LDDGGFLLMANHDDYTNQIGREFGIDPSLMRHLVNI SYAENKSYDYQSVCPEGAAPKQ 900  
DB 836 LDDGGFLLMANHDDYTNQIGREFGIDPSLMRHLVNI SYAENKSYDYQSVCPEGAAPKQ 895  
QY 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLEAVEMEDDDFTASLSKQ 960  
DB 896 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLEAVEMEDDDFTASLSKQ 955  
QY 961 SCITEQTOYFFDNDKSGFVGLDCGNCRIHPHGEKLMNTNLIIFVSKGTGTCPCDTRLII 1020  
DB 956 SCITEQTOYFFDNDKSGFVGLDCGNCRIHPHGEKLMNTNLIIFVSKGTGTCPCDTRLII 1015  
QY 1021 QAEQTSQSDGNPCDMYKQPRYKRGPDVCFDNNVLEDYTDGCGVSGNLNPSLWYIIGIQFLLL 1080  
DB 1016 QAEQTSQSDGNPCDMYKQPRYKRGPDVCFDNNVLEDYTDGCGVSGNLNPSLWYIIGIQFLLL 1075  
QY 1081 WLVSQSTHRL 1091  
DB 1076 WLVSQSTHRL 1086

## RESULT 9

US-08-455-543A-56  
; Sequence 56, Application US/08455543A  
; Patent No. 5792846

## GENERAL INFORMATION:

; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; NUMBER OF SEQUENCES: 57

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street.  
; City: San Diego  
; STATE: California  
; COUNTRY: USA

## ZIP: 92101-2926

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5

## CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,543A  
; FILING DATE: May 31, 1995  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/223,305

; FILING DATE: April 4, 1994

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-52517  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1084 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-455-543A-56

## Query Match

99.0%; Score 5691.5; DB 1; Length 1084;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 MAAGCLLALTTLFOSLLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
DB 1 MAAGCLLALTTLFOSLLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60  
QY 61 YEKYQDLYTVEPNNAQOLVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
DB 61 YEKYQDLYTVEPNNAQOLVETAAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
QY 121 EVVYNNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAHVHPTDIYEGSTVL 180  
DB 121 EVVYNNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAHVHPTDIYEGSTVL 180  
QY 181 NELNWT SALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240  
DB 181 NELNWT SALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKKIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLTIRTSVSEMLETSLDDDFNVASFNSNAQD 300  
DB 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLTIRTSVSEMLETSLDDDFNVASFNSNAQD 300  
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYNVSRANCKIIML 360  
DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYNVSRANCKIIML 360  
QY 361 FTDGGEERAQAEIFNKYNKDKKVRVFRFSVGQHNRYERGPQIWMACENKGYEIPISGAIR 420  
DB 361 FTDGGEERAQAEIFNKYNKDKKVRVFRFSVGQHNRYERGPQIWMACENKGYEIPISGAIR 420  
QY 421 INTQEYLDVLGRPMVLADGKAKQVQNTNYLDALBELGLVITGTLVPVNTGOFENKTNLK 480  
DB 421 INTQEYLDVLGRPMVLADGKAKQVQNTNYLDALBELGLVITGTLVPVNTGOFENKTNLK 480  
QY 481 NQLILGVNMGVDVSLIEDIKRLTPRFTLCPNGYFFADPNGYVLLHHPNLOPKPKPSQEPVTL 540  
DB 481 NQLILGVNMGVDVSLIEDIKRLTPRFTLCPNGYFFADPNGYVLLHHPNLOPKPKPSQEPVTL 540  
QY 541 DFLDAELENDIKVEIRNKKMIDGESGEKTFRTLVSQDERYIDKGNRTYTTWTPVNGTDYSL 600

Db 541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTPNGTDYSL 600  
QY 601 ALVLPYISYIIKALEETITQARKSKGKMDSETLKPONFESGYTFTAPRDYCNLDKI 660  
Db 601 ALVLPYISYIIKALEETITQARY-----SETLKPONFESGYTFTAPRDYCNLDKI 653  
QY 661 SDNTEFLNNEFIDRKTPNPNCSNADLINRVLLDAGFTNELVQYNSKQNIKGVKAR 720  
Db 654 SONTEFLNNEFIDRKTPNPNCSNADLINRVLLDAGFTNELVQYNSKQNIKGVKAR 713  
QY 721 FVYTDGTRVYPKEAGENQWENPETYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 780  
Db 714 FVYTDGTRVYPKEAGENQWENPETYEDSFYKRSIDNDNYVFTAPYFNKSGPGAYESGI 773  
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPCAGPVCCKRNSDMVDCVI 840  
Db 774 MYSKAVEIYIOGKLLKPAVVGKIDVNSWENFTKTSIRDPCAGPVCCKRNSDMVDCVI 833  
QY 841 LDDGGFLMANHDDYTNOIGRFGGEIDPDSLMRHLVNSIVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 834 LDDGGFLMANHDDYTNOIGRFGGEIDPDSLMRHLVNSIVYAFNKSVDYQSVCEPGAAPKQ 893  
QY 901 GAGHSAYVPSVADILIQGWATAAASWILQOFLLSLTPRLLPRLLEAVEMDDDFTSLSKQ 960  
Db 894 GAGHSAYVPSVADILIQGWATAAASWILQOFLLSLTPRLLPRLLEAVEMDDDFTSLSKQ 953  
QY 961 SCITEQTQYFFNDKSKSGVLDGNCNSRIFHGEKLMNTNLFIMVESKGTGCPDTRLLI 1020  
Db 954 SCITEQTQYFFNDKSKSGVLDGNCNSRIFHGEKLMNTNLFIMVESKGTGCPDTRLLI 1013  
QY 1021 QAEQTSQDGNPCDMQKPYRKGPDPVCFDNNVLEDYTDGCGVSGNLPSLWYIIGIQFLL 1080  
Db 1014 QAEQTSQDGNPCDMQKPYRKGPDPVCFDNNVLEDYTDGCGVSGNLPSLWYIIGIQFLL 1073  
QY 1081 WLVSQSTHRL 1091  
Db 1074 WLVSQSTHRL 1084

RESULT 10  
US-08-223-305C-56  
; Sequence 56, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; METHOD OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223.305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 52516 (P519739)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1084 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-223-305C-56

Query Match 99.0%; Score 5691.5; DB 2; Length 1084;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1083; Conservative 0; Mismatches 1; Indels 7; Gaps 1;  
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QY 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
Db 61 YEKYQDLYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
QY 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180  
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QY 181 NELNWTSSALDEVYKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKNIDLYDVR 240  
Db 181 NELNWTSSALDEVYKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKNIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
Db 241 RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTITAGITDYKKGFSFAFQOLLNINVRANCNKIIML 360  
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTITAGITDYKKGFSFAFQOLLNINVRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSQGHNYERGPQIWMACENKGYIYIPSGAIR 420  
Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSQGHNYERGPQIWMACENKGYIYIPSGAIR 420  
QY 421 INTQYLDVLRPMPVLADGKAKQVQWNTVNYLDALGLVITGTLVPFNITGTFENKTNLK 480  
Db 421 INTQYLDVLRPMPVLADGKAKQVQWNTVNYLDALGLVITGTLVPFNITGTFENKTNLK 480  
QY 481 NOLILGVNGVDVSLIEDIKRLTPRFTLCPNGYVFAIDPNGYVLLHPNLOPKNPKSQEPVTL 540

Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPLQKPKSQEPVTL 540  
Qy 541 DFLDAELNDIKVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600  
Db 541 DFLDAELNDIKVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600  
Qy 601 ALVLPYSFYIKALETITQARSKKGMKDSFELKPDNFEESGYTIAPRDYCNDLKI 660  
Db 601 ALVLPYSFYIKALETITQARY-----SEFLKPDNFEESGYTIAPRDYCNDLKI 653  
Qy 661 SDNTEFLNFEIDRTPNPNPCNADLINRVLLDAGFTNVLQNYKSKNKGKVRAR 720  
Db 654 SDNTEFLNFEIDRTPNPNPCNADLINRVLLDAGFTNVLQNYKSKNKGKVRAR 713  
Qy 721 FVVDGGITRVYKAGENWQENPETYEDSFYKRSLDNDNYYFTAPYFNKSGPGAYESGI 780  
Db 714 FVVDGGITRVYKAGENWQENPETYEDSFYKRSLDNDNYYFTAPYFNKSGPGAYESGI 773  
Qy 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDCAGPVCDCRNSDVMDCVI 840  
Db 774 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIENTKTSIRDCAGPVCDCRNSDVMDCVI 833  
Qy 841 LDGGFLLMANHDDYTNOIGREFGIDPSLMRHLVNI SYAFNKSVDYQSVCEPGAAPKQ 900  
Db 834 LDGGFLLMANHDDYTNOIGREFGIDPSLMRHLVNI SYAFNKSVDYQSVCEPGAAPKQ 893  
Qy 901 GAGHSAYVPSVADILQGWATAAANSILOQLLSLTFPRLLEAVEMDDFTASLSKQ 960  
Db 894 GAGHSAYVPSVADILQGWATAAANSILOQLLSLTFPRLLEAVEMDDFTASLSKQ 953  
Qy 961 SCITBOTQYFFDNDKSGVGLDCGNCRIHFGKLMNTNLI FIVESKGTCPCDTRLI 1020  
Db 954 SCITBOTQYFFDNDKSGVGLDCGNCRIHFGKLMNTNLI FIVESKGTCPCDTRLI 1013  
Qy 1021 QAEQTSQGNPCDMVKQPRYRKGPVDCFDNNVLEDYDCGGVSGLNPSLWYIIGIQFLLL 1080  
Db 1014 QAEQTSQGNPCDMVKQPRYRKGPVDCFDNNVLEDYDCGGVSGLNPSLWYIIGIQFLLL 1073  
Qy 1081 WLVSQSTHRL 1091  
Db 1074 WLVSQSTHRL 1084

RESULT 11  
US-08-455-543A-53  
; Sequence 53, Application US/08455543A  
; Patent No. 5792846  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,543A  
; FILING DATE: May 31, 1995  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/223,305  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-52517  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1103 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-455-543A-53

Query Match 98.7%; Score 5672; DB 1; Length 1103;  
Best Local Similarity 97.6%; Pred. No. 0;  
Matches 1083; Conservative 0; Mismatches 1; Indels 26; Gaps 2;  
Qy 1 MAAGCLLALTTLTFLQSLIGPSSEPPFPSSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
Db 1 MAAGCLLALTTLTFLQSLIGPSSEPPFPSSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60  
Qy 61 YEKYQDLYTVEPNNARQLVEITAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
Db 61 YEKYQDLYTVEPNNARQLVEITAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120  
Qy 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180  
Db 121 EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHPTDIYEGSTIVL 180  
Qy 181 NELNWTSLDVEYFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYVRR 240  
Db 181 NELNWTSLDVEYFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDLYVRR 240  
Qy 241 RPWYIQTGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDFVNVASFNSAQD 300  
Db 241 RPWYIQTGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDFVNVASFNSAQD 300  
Qy 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFQELLNLYNVRANCNKIIML 360  
Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFQELLNLYNVRANCNKIIML 360  
Qy 361 FTDGGEERAQEIFNKYKDKKVRVFRFVSGQHNYERGPQWACENKGYEYIPEISGAIR 420  
Db 361 FTDGGEERAQEIFNKYKDKKVRVFRFVSGQHNYERGPQWACENKGYEYIPEISGAIR 420

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QY 421 INTQEXLDVLRPMVLGAKQKOVQWNTNVYLDALGLVITGTLPVFNITGQFNKTNLK 480
Db 421 INTQEXLDVLRPMVLGAKQKOVQWNTNVYLDALGLVITGTLPVFNITGQFNKTNLK 480
QY 481 NQLILGVMGVDSLEDIKRLTPFTLPCNGYYPFAIDPBGVLLHPNLPK-----530
Db 481 NQLILGVMGVDSLEDIKRLTPFTLPCNGYYPFAIDPBGVLLHPNLPKPIGVGPTIN 540
QY 531 -----NPKSQEPVTLDFDLAELENDIKVEIRNMKIDGESGEKTFRLVKSQDERYI 581
Db 541 LKRRPNIQPKSQEPVTLDFDLAELENDIKVEIRNMKIDGESGEKTFRLVKSQDERYI 600
QY 582 DKGRTYTWTPVNGTDYSLALVPTYSFYIKAKLEETITQARSKGKMKDSSTLPDNF 641
Db 601 DKGRTYTWTPVNGTDYSLALVPTYSFYIKAKLEETITQARY-----SETLPDNF 653
QY 642 EESGYTFIAPRDYCNLDKISDNNTFELLNNEFIDRKTNNPNSCNADLINRVLLDAGFTN 701
Db 654 EESGYTFIAPRDYCNLDKISDNNTFELLNNEFIDRKTNNPNSCNADLINRVLLDAGFTN 713
QY 702 ELVQVWSKOKNIKGVKARFVVTGGITRVYPKEAGENMQENPETYEDSFYKRSLDNDNY 761
Db 714 ELVQVWSKOKNIKGVKARFVVTGGITRVYPKEAGENMQENPETYEDSFYKRSLDNDNY 773
QY 762 VFTAPYFNKSGPAGYSGIMVSKAVIYIQGLLKPAVVGKIDVNSWIENFTKTSIRDP 821
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QY 822 CAGPVCDCRNSDVMOCVILDDGGFLLMANHDDYTNOIGRFGCEIDPSLMRHLVNSVYA 881
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QY 882 FNKSYDQVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAASIIQQFLLSITFPR 941
Db 894 FNKSYDQVCEPAGAPKOGAGHRSAYVPSVADILQIGWATAAASIIQQFLLSITFPR 953
QY 942 LLEAVEMEDDDFTASLSKSCITEQYQYFFDNDKSGFSGLDCGNSRIFHGEKLMNTNL 1001
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QY 1062 VSGINPSLWYIIIGIQLLWLVSGSTHRL 1091
Db 1074 VSGINPSLWYIIIGIQLLWLVSGSTHRL 1103
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## RESULT 12

US-08-223-305C-53

Sequence 53, Application US/08223305C

Patent No. 5851824

## GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSES: Brown, Martin, Haller &amp; McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

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OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-223-305C-53
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## Query Match

98.7%; Score 5672; DB 2; Length 1103;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatcheq 1; Indels 26; Gaps 2;

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Db 61 YEKYQDLYTVEPNNAARQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWREFDASN 120
QY 121 EVVYVNAKDDLOPEKNDSEPGSORIKPVEIDANFQROISYQHAHVHIPTDIYEGSTIVL 180
Db 121 EVVYVNAKDDLOPEKNDSEPGSORIKPVEIDANFQROISYQHAHVHIPTDIYEGSTIVL 180
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Db 181 NELNMTSALDEVFKKNREEDPSLLMQVFGSAGTLARYYPASPVVDNSRTPNKKIDLYDVR 240
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIQGAASPKDMLILVDVSGSVSGTLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFQHLVQANVRNKKVLDAVNNTITAKGITYDKGFSFAFQOLLNYSRANCNKIIML 360
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QY 361 FTDGGEERAQEIFNKNYKDKKVRFRFVSQGHNYERGPQWACENKNGYIIPISGAI 420
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Db 361 FDGGEAQAELFNKNDKVRFRFVGQNHVERGPIQMACENKGGYYEIPISGIR 420  
Qy 421 INTQYLDVLRPMYLAGDKAKQVQWTVNYLDALGLVITGTLVPFNITGOFENKTNL 480  
Db 421 INTQYLDVLRPMYLAGDKAKQVQWTVNYLDALGLVITGTLVPFNITGOFENKTNL 480  
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Qy 531 -----NPKSQBPVTLDFDLAELENDIKVEIRKMKIDGESGKTRTLVKSQDRIY 581  
Db 541 LRKRPNTQPKSQBPVTLDFDLAELENDIKVEIRKMKIDGESGKTRTLVKSQDRIY 600  
Qy 582 DKGRTYTWTPNGTDYSLALVLPYSYIYKAKLEETITQARSKKGMKDSKSETLKPDPN 641  
Db 601 DKGRTYTWTPNGTDYSLALVLPYSYIYKAKLEETITQARY-----SETLKPDPN 653  
Qy 642 EESGYTFIAPRDYCNLDKISDNTEFLNFNEFIDRKTPNPNPSCNADLINRVLLDAGFTN 701  
Db 654 EESGYTFIAPRDYCNLDKISDNTEFLNFNEFIDRKTPNPNPSCNADLINRVLLDAGFTN 713  
Qy 702 ELVQYNSKQKNIKGVKARFVTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDY 761  
Db 714 ELVQYNSKQKNIKGVKARFVTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDY 773  
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Qy 882 FNKSYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAMSILQOFLSLTPPR 941  
Db 894 FNKSYDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAMSILQOFLSLTPPR 953  
Qy 942 LLEAVEMDDFTASLSKQSCITQTOYFFDNDKSGFSGVLDGNCNCRIFHGEKLMNTNL 1001  
Db 954 LLEAVEMDDFTASLSKQSCITQTOYFFDNDKSGFSGVLDGNCNCRIFHGEKLMNTNL 1013  
Qy 1002 IFINVESKGTCPDTRLLIAEQTSQGNPCDMYKQPRYKGPDPVCFNNVLEDYTDGCG 1061  
Db 1014 IFINVESKGTCPDTRLLIAEQTSQGNPCDMYKQPRYKGPDPVCFNNVLEDYTDGCG 1073  
Qy 1062 VSGLNPSLWYIIGIOFLLWLVSGSTHRL 1091  
Db 1074 VSGLNPSLWYIIGIOFLLWLVSGSTHRL 1103

## RESULT 13

US-08-455-543A-55  
; Sequence 55, Application US/0845543A  
; Patent No. 5792846  
; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/223,305  
FILING DATE: April 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/868,354  
FILING DATE: April 10, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/745,206  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/620,250  
FILING DATE: 30-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/482,384  
FILING DATE: 20-FEB-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/603,751  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US89/01408  
FILING DATE: 04-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/176,899  
FILING DATE: 04-APR-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-52517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-455-543A-55

Query Match 98.3%; Score 5652; DB 1; Length 1079;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1078; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

Qy 1 MAAGCLLATLTTLFQSLILIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGVGNOLVDI 60  
Db 1 MAAGCLLATLTTLFQSLILIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTAGVGNOLVDI 60  
Qy 61 YEKYODLYTVEPNNAQLVEITAARDIEKLLNSRKALVSLALEAEKQAAHQRDEFASN 120  
Db 61 YEKYODLYTVEPNNAQLVEITAARDIEKLLNSRKALVSLALEAEKQAAHQRDEFASN 120  
Qy 121 EVVYINAKDLDPEKNDSEPCSQRIKPVFIEDANFGROIYSQHAHVHTPTDIYEGSTIVL 180  
Db 121 EVVYINAKDLDPEKNDSEPCSQRIKPVFIEDANFGROIYSQHAHVHTPTDIYEGSTIVL 180  
Qy 181 NELNWTALDEVFKNKREDDPSLLWVFGSATGLARYYPASFPWVDSNRTPNKIDLYVRR 240  
Db 181 NELNWTALDEVFKNKREDDPSLLWVFGSATGLARYYPASFPWVDSNRTPNKIDLYVRR 240  
Qy 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNSNAQD 300  
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVASFNSNAQD 300

QY 301 VSCFQHLVQANVRNKKVLDAVNNTAKGTDYKKGFSFAFOLLNYSRANCKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDAVNNTAKGTDYKKGFSFAFOLLNYSRANCKIIML 360  
QY 361 FTGGERAQEIIPKNYKDKKVVFRFSVQGHNYERGIOWMACENKGYEIPSGAIR 420  
Db 361 FTGGERAQEIIPKNYKDKKVVFRFSVQGHNYERGIOWMACENKGYEIPSGAIR 420  
QY 421 INTQEVLDVLGRPMVLGAKAKOVQNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480  
Db 421 INTQEVLDVLGRPMVLGAKAKOVQNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480  
QY 481 NOLILGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLPKNSQBPVTL 540  
Db 481 NOLILGVMGVDSLEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLPKNSQBPVTL 540  
QY 541 DFLDAELNDIKVEIRNKMIDGESGKFTLTKVSDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 536 DFLDAELNDIKVEIRNKMIDGESGKFTLTKVSDERYIDKGNRTYTWTPVNGTDYSL 595  
QY 601 ALVLPYSFYIKAKLEETITQARSKKMKDSETLKPDNFEESGYTFAPRDYCNLKI 660  
Db 596 ALVLPYSFYIKAKLEETITQARY-----SETLKPNDFEESGYTFAPRDYCNLKI 648  
QY 661 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNKGVKAR 720  
Db 649 SONTEFLNNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNKGVKAR 708  
QY 721 FVYTDGGITRVYPKEAGENWQENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 780  
Db 709 FVYTDGGITRVYPKEAGENWQENPEYEDSFYKRSLDNDNYFTAPYFNKSGPGAYESGI 768  
QY 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWNIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 840  
Db 769 MYSKAVEIYIOGKLKPAVVGKIDVNSWNIENFTKTSIRDPGAPVCDCKRNSDVMDCVI 828  
QY 841 LDGGFLLMANHDDYTNQIGRFFGEIDPRLMRHLVNIISYAFNKSVDYOSVCEPGAAPKQ 900  
Db 829 LDGGFLLMANHDDYTNQIGRFFGEIDPRLMRHLVNIISYAFNKSVDYOSVCEPGAAPKQ 888  
QY 901 GAGHRSAYVPSVADILQIGWATAAWSLIQOFLSLTLPRLLEAVEMEDDDFTASLSKQ 960  
Db 889 GAGHRSAYVPSVADILQIGWATAAWSLIQOFLSLTLPRLLEAVEMEDDDFTASLSKQ 948  
QY 961 SCITEQTYFFNDKSFSGVLDGNCRSRIFHGEKLMNTNLIFIMVESKGTCTCDTRLII 1020  
Db 949 SCITEQTYFFNDKSFSGVLDGNCRSRIFHGEKLMNTNLIFIMVESKGTCTCDTRLII 1008  
QY 1021 QAEQTSDDGNPCDMVKQPRYRKGPVDFVFNNDYEDYDCGGVSGLNPLSLWYIIGIQFLLL 1080  
Db 1009 QAEQTSDDGNPCDMVKQPRYRKGPVDFVFNNDYEDYDCGGVSGLNPLSLWYIIGIQFLLL 1068  
QY 1081 WLVSNGTHRL 1091  
Db 1069 WLVSNGTHRL 1079

RESULT 14

US-08-223-305C-55  
; Sequence 55, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:

; ADDRESSER: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-223-305C-55

Query Match 98.3%; Score 5652; DB 2; Length 1079;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1078; Conservative 0; Mismatches 1; Indels 12; Gaps 2;

QY 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
Db 1 MAAGCLLALTTLFOSLLIGPSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNOLVDI 60  
QY 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
Db 61 YEKYQDLYTVEPNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120  
QY 121 EVVYVNAKDDLPKNDSEPGSORIKPVETDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
Db 121 EVVYVNAKDDLPKNDSEPGSORIKPVETDANFGRQISYQHAHVHPTDIYEGSTIVL 180  
QY 181 NELNWTSSALDEVFKKNREDDPSLLMQVFGSATGLARYYPASPWVNSRTPNKNIDLYDVR 240  
Db 181 NELNWTSSALDEVFKKNREDDPSLLMQVFGSATGLARYYPASPWVNSRTPNKNIDLYDVR 240



QY 241 RPYIOGAASPKDMLLVDSVSGSLTLKLRISVSEMLETLSDDDFVNVASFNSNAQD 300  
Db 241 RPYIOGAASPKDMLLVDSVSGSLTLKLRISVSEMLETLSDDDFVNVASFNSNAQD 300  
QY 301 VSCFQHLVQANVRNKKVLDKDAYNNITAKGIDYKKGFSFAFQQLLNNVSRANCNKIIML 360  
Db 301 VSCFQHLVQANVRNKKVLDKDAYNNITAKGIDYKKGFSFAFQQLLNNVSRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKNKDKKVRFRFSGVQHNBERGPIQWMACENKGYIIPISIGAIR 420  
Db 361 FTDGGEERAQEIFNKNKDKKVRFRFSGVQHNBERGPIQWMACENKGYIIPISIGAIR 420  
QY 421 INTQEVLDVLRPMVLGADKAKQVQNTVYLDALGLVITGLPVFNITGOFENKTNLK 480  
Db 421 INTQEVLDVLRPMVLGADKAKQVQNTVYLDALGLVITGLPVFNITGOFENKTNLK 480  
QY 481 NQILIGVMGVDSLEDIKRLTPFRFLCPNGYFAIDPNGYVLLHPLNLPKPKSOEPTVL 540  
Db 481 NQILIGVMGVDSLEDIKRLTPFRFLCPNGYFAIDPNGYVLLHPLNLPKPKSOEPTVL 540  
QY 541 DFLDAELENDIKVEIRNKMIDGESKFTRLTVKSDERYIDKGNRTYTWTPVNGTDYSL 600  
Db 541 DFLDAELENDIKVEIRNKMIDGESKFTRLTVKSDERYIDKGNRTYTWTPVNGTDYSL 600  
QY 595 DFLDAELENDIKVEIRNKMIDGESKFTRLTVKSDERYIDKGNRTYTWTPVNGTDYSL 595  
QY 601 ALVLPITYFYIYKALEETITQARSKKGKMDSEITLKDNPFEESGYTFTAPRDYCNLDKI 660  
Db 601 ALVLPITYFYIYKALEETITQARSKKGKMDSEITLKDNPFEESGYTFTAPRDYCNLDKI 660  
QY 661 SDNNTEFFLNFEFIDRTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720  
Db 661 SDNNTEFFLNFEFIDRTPNPNPCNADLINRVLLDAGFTNELVQYNSKQKNIKGVKAR 720  
QY 721 FVVDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780  
Db 721 FVVDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGI 780  
QY 769 FVVDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGI 768  
Db 769 FVVDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNVYFTAPYFNKSGPGAYESGI 768  
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDPGAGVPCDKRNSDYMDCVI 840  
Db 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWENFTKTSIRDPGAGVPCDKRNSDYMDCVI 840  
QY 841 LDGQFLLMANHDDYTNQIGRFEGIDPSLRHLNYSVYAFNKSVDYQSVCEPGAAPKQ 900  
Db 841 LDGQFLLMANHDDYTNQIGRFEGIDPSLRHLNYSVYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAASLQQLFLLSLTFPRLEAVEVEDDDFTASLSQ 960  
Db 901 GAGHSAYVPSVADILQIGWATAAASLQQLFLLSLTFPRLEAVEVEDDDFTASLSQ 960  
QY 961 SCITQOTQYFFDNDKSFSGVLDGNCNCRIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020  
Db 961 SCITQOTQYFFDNDKSFSGVLDGNCNCRIFHGEKLMNTNLFIMVESKGTCPDTRLLI 1020  
QY 1021 QAEQTSQSDGNPCDMVKQPRYKGPVDCFDNNVLEDYTDGCGVSGLNPLSLWYIIGIQFLLL 1080  
Db 1021 QAEQTSQSDGNPCDMVKQPRYKGPVDCFDNNVLEDYTDGCGVSGLNPLSLWYIIGIQFLLL 1080  
QY 1081 WLVSQSTHLL 1091  
Db 1081 WLVSQSTHLL 1091  
QY 1069 WLVSQSTHLL 1079  
Db 1069 WLVSQSTHLL 1079

## RESULT 15

US-08-435-675B-5  
; Sequence 5, Application US/08435675B  
; Patent No. 5710250  
; GENERAL INFORMATION:  
; APPLICANT: Ellis, Steven Bradley  
; APPLICANT: Williams, Mark E.  
; APPLICANT: Harpold, Michael Miller  
; APPLICANT: Schwartz, Arnold  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,675B  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/314,083  
; FILING DATE: 28-SEP-1994  
; APPLICATION NUMBER: US 07/914,231  
; FILING DATE: 13-JUL-1992  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 08-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-53193  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1106 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-435-675B-5

Query Match 95.8%; Score 5508.5; DB 1; Length 1106;

Best Local Similarity 94.7%; Pred. No. 0;

Matches 1054; Conservative 15; Mismatches 15; Indels 29; Gaps 4;

QY 1 MAAGCLLALTTLFOS--LLIGPSSEEPFPPSAVTITKSWDKMQEDLVTLAKTASGVNQLV 58  
Db 1 MAAGPLAWTLTQAWLILIGPSSEEPFPPSAVTITKSWDKMQEDLVTLAKTASGVNQLV 60  
QY 59 DIYEKYQDLYTVEPNNAQVLEIAARDIEKLSNRSKALVSLALEAEKVQAAHOREDEFA 118  
Db 61 DIYEKYQDLYTVEPNNAQVLEIAARDIEKLSNRSKALVRLALEAEKVQAAHOREDEFA 120  
QY 119 SNEVYVYNAKDLDPEKNDSEPGSQRIKPVFTEDANFRQISYQHAHVHPTDIYEGSTI 178  
Db 121 SNEVYVYNAKDLDPEKNDSEPGSQRIKPVFTEDANFRQISYQHAHVHPTDIYEGSTI 180  
QY 179 VLNELNWTSLADVEPKKNEEDPSLLWQVFGSATGLARYYPASPVWDSRTPNKIDLYDV 238  
Db 181 VLNELNWTSLADVEPKKNEEDPSLLWQVFGSATGLARYYPASPVWDSRTPNKIDLYDV 240  
QY 239 RRRPWYIOGAASPKDMLLVDSVSGSLTLKLRISVSEMLETLSDDDFVNVASFNSNA 298  
Db 241 RRRPWYIOGAASPKDMLLVDSVSGSLTLKLRISVSEMLETLSDDDFVNVASFNSNA 300  
QY 299 QDVSCFQHLVQANVRNKKVLDKDAYNNITAKGIDYKKGFSFAFQQLLNNVSRANCNKII 358  
Db 301 QDVSCFQHLVQANVRNKKVLDKDAYNNITAKGIDYKKGFSFAFQQLLNNVSRANCNKII 360  
QY 359 MLFTDGGGEERAQEIFNKNKDKKVRFRFSGVQHNBERGPIQWMACENKGYIIPISIGA 418  
Db 361 MLFTDGGGEERAQEIFNKNKDKKVRFRFSGVQHNBERGPIQWMACENKGYIIPISIGA 420

Qy 419 IRIHQEYLDVLGRPMWLAGKAKOVQNTNYYLDALBELGLVITGTLPVFNITGOFENKTN 478  
Db 421 IRIHQEYLDVLGRPMWLAGKAKOVQNTNYYLDALBELGLVITGTLPVFNITGOFENKTN 480  
Qy 479 LKNQILGVMGVDVSLIEDIKRLTFRFTLPCPNNGYFAIDPNGYVLLHHPNLOPK----- 530  
Db 481 LKNQILGVMGVDVSLIEDIKRLTFRFTLPCPNNGYFAIDPNGYVLLHHPNLOPKPIGVGIPT 540  
Qy 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDER 579  
Db 541 INLRKRRPNVQNPQSQEPVTLDFDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDER 600  
Qy 580 YIDKGNRTYTWTPVNGTDY-SLAVLPTYSFYIKAKLEETITQARSKKGMKMDSETLKP 638  
Db 601 YIDKGNRTYTWTPVNGTDYSSALVLPYSFYIKAKIEETITQARY-----SETLKP 653  
Qy 639 DNFEESGYTFIAPRDYCNDLKISDNTEFEFLNFEFIDRKTPNPNPCNADLINRVLLDAG 698  
Db 654 DNFEESGYTFIAPRDYCNDLKPSDNTEFEFLNFEFIDRKTPNPNPCNADLINRVLLDAG 713  
Qy 699 FTNELVQNYNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDN 758  
Db 714 FTNELVQNYNSKQKNIKGVKARFVVTGGITRVYPKEAGENWQENPETYEDSFYKRSLDN 773  
Qy 759 DNYVFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI 818  
Db 774 DNYVFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSI 833  
Qy 819 RDPGAGPVDCCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSPMLRHLVNI 878  
Db 834 RDPGAGPVDCCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSPMLRHLVNI 893  
Qy 879 YAFNKSVDYOSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSTILOQFLLSLT 938  
Db 894 YAFNKSVDYOSVCEPGAAPKQAGHRSAYVPSIADILQIGWATAAAWSTILOQFLLSLT 953  
Qy 939 FPRLEAVEMEDDDFTASLSKSCITQTOTYFFONDSSKFSFVLDGCGNCSRIFHGEKLMN 998  
Db 954 FPRLEAVEMEDDDFTASLSKSCITQTOTYFFONDSSKFSFVLDGCGNCSRIFHGEKLMN 1013  
Qy 999 TNLIFIMVESKGTCPDTRLLIQAEQTSFGPNPCDMVKQPRYKGPDPVCFDNNVLEDYTD 1058  
Db 1014 TNLIFIMVESKGTCPDTRLLIQAEQTSFGPNPCDMVKQPRYKGPDPVCFDNNVLEDYTD 1073  
Qy 1059 CGGVSGLNPLSLWYIIGIQFLLMLVSGSTRLL 1091  
Db 1074 CGGVSGLNPLSLWYIIGIQFLLMLVSGSTRLL 1106

Search completed: July 23, 2001, 07:38:26  
Job time: 493 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:29:43 ; Search time 84.28 Seconds  
(without alignments)  
986.075 Million cell updates/sec

Title: US-09-397-548-14  
Perfect score: 5748  
Sequence: 1 MAAGCLLATLTFLQSLIG.....IIGIOFLLWLVSSTHRL 1091

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Lasting first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5748	100.0	1091	2 JH0565	calcium channel al
2	5505	95.8	1091	2 A4147	calcium channel pr
3	5503.5	95.7	1106	1 CHRBA2	calcium channel al
4	1127.5	19.6	1091	2 T30256	calcium channel al
5	607	10.6	734	2 S44617	C50C3.11 protein -
6	580.5	10.1	1148	2 T18770	probable calcium c
7	198	3.4	1450	2 C86880	hypothetical prote
8	194.5	3.4	886	2 S54355	inter-alpha-trypsi
9	185	3.2	885	2 S30350	inter-alpha-trypsi
10	164.5	2.9	889	2 JC5576	inter-alpha-trypsi
11	161	2.8	2706	2 T28155	variant-specific s
12	159	2.8	1984	2 D44396	p-type cation tran
13	157.5	2.7	575	2 D64998	hypothetical prote
14	155	2.7	1516	2 E71619	RAD2 endonuclease
15	155	2.7	2364	2 I40884	cytotoxin L - Clos
16	154.5	2.7	946	1 IYH02	inter-alpha-trypsi
17	154.5	2.7	1315	2 T28679	fibrinogen-binding
18	153	2.7	932	2 JC5953	inter-alpha-inhibi
19	152	2.6	1291	2 S46431	botulinum neurotox
20	152	2.6	1291	2 A49777	botulinum neurotox
21	151.5	2.6	420	2 S76691	hypothetical prote
22	150.5	2.6	921	2 JC4625	inter-alpha-trypsi
23	150	2.6	654	2 A69656	methyl-accepting c
24	149	2.6	459	2 F64688	proteinase (EC 3.4
25	149	2.6	930	2 JX0368	inter-alpha-trypsi
26	148.5	2.6	2401	2 T28676	rhodopy protein -
27	148	2.6	964	2 S25855	DNA-directed DNA p
28	146.5	2.5	1285	2 B72420	hypothetical prote
29	146	2.5	4688	2 F82885	hypothetical prote

30	145.5	2.5	576	2 T47637	hypothetical prote
31	145.5	2.5	589	2 F84811	probable retroelem
32	145.5	2.5	5005	2 F82884	hypothetical prote
33	144	2.5	1087	1 S41797	cellulose 1,4-beta
34	144	2.5	1091	2 S33850	fibronectin-binding
35	143	2.5	946	2 JC5575	inter-alpha-trypsi
36	143	2.5	1864	2 T18485	hypothetical prote
37	142.5	2.5	382	2 S44618	C50C3.10 protein -
38	142	2.5	1169	2 A64505	PI15 homolog - Met
39	142	2.5	1599	2 S22737	glucosyltransferas
40	141	2.5	1252	2 B42771	reticulocyte-bind
41	140.5	2.4	2269	2 T28677	rhodopy protein -
42	140	2.4	1180	2 A28858	paraspinal crystal
43	140	2.4	2710	2 A37052	toxin A - Clostrid
44	140	2.4	3305	2 T18358	apolipoprotein prec
45	139.5	2.4	764	2 I39934	protective antigen

## ALIGNMENTS

RESULT 1  
JH0565  
calcium channel alpha-2b chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999  
C:Accession: JH0565  
R:Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B.  
Neuron 8, 71-84, 1992  
A:Title: Structure and functional expression of alpha1, alpha2, and beta subunits of  
A:Reference number: JH0564; MUID:92110010  
A:Accession: JH0565  
A:Molecule type: mRNA  
A:Residues: 1-1091 <WIL>  
A:Cross-references: GB:M6559; NID:gl79761; PIDN:AAA51903.1; PID:gl79762  
A:Experimental source: basal ganglia  
A:Note: Several conflicts are found between GenBank submission, authors' translation  
C:Comment: This protein is a subunit of the voltage dependent calcium channel.  
C:Superfamily: calcium channel alpha-2 chain  
C:Keywords: glycoprotein; phosphoprotein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>  
F:32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase  
F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #  
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: ca  
F:501/Binding site: phosphate (Thr) (covalent) #status predicted  
F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match		100.0%;	Score 5748;	DB 2;	Length 1091;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1091;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAAGCLLATLTFLQSLIGPSEPPSPSAVTIKSWDKMQEDLVTLAKTAGSNQVLVDI	60		
Db	1	MAAGCLLATLTFLQSLIGPSEPPSPSAVTIKSWDKMQEDLVTLAKTAGSNQVLVDI	60		
QY	61	YKQYQDLYTVEPNNKQLVEIAARDTEKLSNRKSKALVSLALEAEKVQAAHQWREDFASN	120		
Db	61	YKQYQDLYTVEPNNKQLVEIAARDTEKLSNRKSKALVSLALEAEKVQAAHQWREDFASN	120		
QY	121	EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGRIQISYQAAHVHIPTDIYEGSTIVL	180		
Db	121	EVVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGRIQISYQAAHVHIPTDIYEGSTIVL	180		
QY	181	NEUNWTSALDEVEKKNREEDPSLLWQVFGSATGLARYYPASPWWDNSRTNPKIDLYDVR	240		
Db	181	NEUNWTSALDEVEKKNREEDPSLLWQVFGSATGLARYYPASPWWDNSRTNPKIDLYDVR	240		
QY	241	RPVYIOGAASPKDMLILVDYSGVSGLTLLKIRTSVSEMLETISDDDFVNVASFNSNAQD	300		
Db	241	RPVYIOGAASPKDMLILVDYSGVSGLTLLKIRTSVSEMLETISDDDFVNVASFNSNAQD	300		

QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEOQLLNNVSRANCNKIIML 360  
DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEOQLLNNVSRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKYNDKKVRVFRFSGVGHNYERGPQIOWMACENKGYEYIPIPSIGAIR 420  
DB 361 FTDGGEERAQEIFNKYNDKKVRVFRFSGVGHNYERGPQIOWMACENKGYEYIPIPSIGAIR 420  
QY 421 INTQEYLDVGLRPVLAGDKAKQOVQWNTNYLDALBELGLVITGTLVPFNITGOFENKTNLK 480  
DB 421 INTQEYLDVGLRPVLAGDKAKQOVQWNTNYLDALBELGLVITGTLVPFNITGOFENKTNLK 480  
QY 481 NOLLILGVMDVDSLEIDIKRLTPRFTLCNPGYFYFAIDPNCYVLLHHPNLOPKNPKSOEPTVL 540  
DB 481 NOLLILGVMDVDSLEIDIKRLTPRFTLCNPGYFYFAIDPNCYVLLHHPNLOPKNPKSOEPTVL 540  
QY 541 DFLDAELENDIKVEIRNKNMIDGESGEKFTRLVKSODERYIDKGNRTYTWTVPNGTDYSL 600  
DB 541 DFLDAELENDIKVEIRNKNMIDGESGEKFTRLVKSODERYIDKGNRTYTWTVPNGTDYSL 600  
QY 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPONFEESGYTFTAPRDXCNDLKI 660  
DB 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPONFEESGYTFTAPRDXCNDLKI 660  
QY 661 SDNNTFEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNKIKGVKAR 720  
DB 661 SDNNTFEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNKIKGVKAR 720  
QY 721 FVYTDGGITRVYPKEAGENQWNPETIYDSFYKRSLDNDNYVFTAPYFNKSGFGAYESGI 780  
DB 721 FVYTDGGITRVYPKEAGENQWNPETIYDSFYKRSLDNDNYVFTAPYFNKSGFGAYESGI 780  
QY 781 MYSKAVEIYIQGLKLPVAVGKIDVNSHIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840  
DB 781 MYSKAVEIYIQGLKLPVAVGKIDVNSHIEFTKTSIRDPGAGVCDCKRNSDVMDCVI 840  
QY 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSYAFNKSVDYQSVCEPGAAPKQ 900  
DB 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSYAFNKSVDYQSVCEPGAAPKQ 900  
QY 901 GAGHSAYVPSVADILQIGWATAAAWSILQQLFLSLTFRLLLEAVEMEDDDFTASLSKQ 960  
DB 901 GAGHSAYVPSVADILQIGWATAAAWSILQQLFLSLTFRLLLEAVEMEDDDFTASLSKQ 960  
QY 961 SCITEQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIPIMVESKGTCPDTRLLI 1020  
DB 961 SCITEQTOYFFDNDKSFSGVLDGNCGRIFHGEKLMNTNLIPIMVESKGTCPDTRLLI 1020  
QY 1021 QABQTSQGNPCDMVKQPRYKGPVDFVCFDNNVLEDYTDGGSVSLNPSLWYIIGIQFLLL 1080  
DB 1021 QABQTSQGNPCDMVKQPRYKGPVDFVCFDNNVLEDYTDGGSVSLNPSLWYIIGIQFLLL 1080  
QY 1081 WLVSQGSTHRL 1091  
DB 1081 WLVSQGSTHRL 1091

RESULT 2  
A44147  
calcium channel protein alpha-2 chain precursor - rat  
N;Alternate names: dihydropyridine-sensitive L-type  
N;Contains: calcium channel alpha-2 chain  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 20-Aug-1999  
C;Accession: A44147  
R;Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.  
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992  
A;Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensit  
A;Reference number: A44147  
A;Accession: A44147  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1091 <KIM>

A;Cross-references: GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955  
C;Superfamily: calcium channel alpha-2 chain  
C;Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 95.8%; Score 5505; DB 2; Length 1091;  
Best Local Similarity 95.3%; Pred. No. 0;  
Matches 1040; Conservative 26; Mismatches 23; Indels 2; Gaps 2;

QY 1. MAAGCLLALTTLFOSLLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
DB 1. MAAGCLLALTTLFOSLLIGPSSEEPFSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60  
QY 61 YEKYQDLYTEPNNARQOLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN 120  
DB 61 YEKYQDLYTEPNNARQOLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEFASN 120  
QY 121 EVVYNAKDDLPENDSPGSRQIKPVIEDANGRQISYQHAHVHITDIIYEGSTIVL 180  
DB 121 EVVYNAKDDLPENDSPGSRQIKPVIEDANGRQISYQHAHVHITDIIYEGSTIVL 180  
QY 181 NELNNTSALDEVFKKRNREDDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKKIDLYDVR 240  
DB 181 NELNNTSALDEVFKKRNREDDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKKIDLYDVR 240  
QY 241 RPWYIQGAASPKDMLILVDVSGVSGTLTKLIRTSYSEMLETLSDDDFVNVASFNSAOD 300  
DB 241 RPWYIQGAASPKDMLILVDVSGVSGTLTKLIRTSYSEMLETLSDDDFVNVASFNSAOD 300  
QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEOQLLNNVSRANCNKIIML 360  
DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEOQLLNNVSRANCNKIIML 360  
QY 361 FTDGGEERAQEIFNKYNDKKVRVFRFSGVGHNYERGPQIOWMACENKGYEYIPIPSIGAIR 420  
DB 361 FTDGGEERAQEIFNKYNDKKVRVFRFSGVGHNYERGPQIOWMACENKGYEYIPIPSIGAIR 420  
QY 421 INTQEYLDVGLRPVLAGDKAKQOVQWNTNYLDALBELGLVITGTLVPFNITGOFENKTNLK 480  
DB 421 INTQEYLDVGLRPVLAGDKAKQOVQWNTNYLDALBELGLVITGTLVPFNITGOFENKTNLK 480  
QY 481 NOLLILGVMDVDSLEIDIKRLTPRFTLCNPGYFYFAIDPNCYVLLHHPNLOPKNPKSOEPTVL 540  
DB 481 NOLLILGVMDVDSLEIDIKRLTPRFTLCNPGYFYFAIDPNCYVLLHHPNLOPKNPKSOEPTVL 540  
QY 541 DFLDAELENDIKVEIRNKNMIDGESGEKFTRLVKSODERYIDKGNRTYTWTVPNGTDY 599  
DB 541 DFLDAELENDIKVEIRNKNMIDGESGEKFTRLVKSODERYIDKGNRTYTWTVPNGTDY 599  
QY 600 LALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPONFEESGYTFTAPRDXCNDL 659  
DB 600 LALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPONFEESGYTFTAPRDXCNDL 659  
QY 660 ISDNNTFEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNKIKGVKA 719  
DB 660 ISDNNTFEFLNFEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQYNSKQNKIKGVKA 719  
QY 720 RFVYTDGGITRVYPKEAGENQWNPETIYDSFYKRSLDNDNYVFTAPYFNKSGFGAYESG 779  
DB 720 RFVYTDGGITRVYPKEAGENQWNPETIYDSFYKRSLDNDNYVFTAPYFNKSGFGAYESG 779  
QY 780 IMYSKAVEIYIQGLKLPVAVGKIDVNSHIEFTKTSIRDPGAGVCDCKRNSDVMDCV 839  
DB 780 IMYSKAVEIYIQGLKLPVAVGKIDVNSHIEFTKTSIRDPGAGVCDCKRNSDVMDCV 839  
QY 840 ILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSYAFNKSVDYQSVCEPGAAPK 899  
DB 840 ILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNYSYAFNKSVDYQSVCEPGAAPK 899  
QY 900 QGAGHSAYVPSVADILQIGWATAAAWSILQQLFLSLTFRLLLEAVEMEDDDFTASLSK 959  
DB 900 QGAGHSAYVPSVADILQIGWATAAAWSILQQLFLSLTFRLLLEAVEMEDDDFTASLSK 959

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QY 960 QSCITEQYQYFPDNDKSFSGVLDGCGNSRPHGKLMNTNLIFIMVSKGTCPCDTRLL 1019
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 960 QSCITEQYQYFKNDTKSFSGVLDGCGNSRPHGKLMNTNLIFIMVSKGTCPCDTRLL 1019
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1020 IQAETSDGPNPCDMVKQPRYRKGPVDFDNNVLEDDYDTCGGVSLNPSLWIIIGIQFLL 1079
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1020 MQAETSDGPDPCDMVKQPRYRKGPVDFDNNVLEDDYDTCGGVSLNPSLWIIIGIQFLL 1079
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1080 LWLVSGSTHRL 1090
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1080 LWLVSGSRHYL 1090
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
CHRB2
N:Alternate names: dihydropyridine-binding protein, 140K
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
C:Accession: S10579; A39518; A33409
R:Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.T.; Campbell, K.P.
A>Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of
A:Reference number: S10579; MUID:88336904
A:Accession: S10579
A:Molecule type: mRNA
A:Residues: 1-1106 <ELL>
A:Cross-references: EMBL:M21948; NID:g164762; PID:AAA81562.1; PID:g164763
A:Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found
R:Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.
J.Biol. Chem. 266, 3287-3293, 1991
A>Title: Structural characterization of the dihydropyridine-sensitive calcium channel al
A:Reference number: A39518; MUID:91131638
A:Accession: A39518
A:Molecule type: Protein
A:Residues: 961-973 <AY>
A:Note: this sequence represents the amino end of a glycosylated peptide that appears af
e at the amino end and identical molecular weights (17K) following deglycosylation
R:Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.
Biochemistry 28, 7820-7828, 1989
A>Title: Subunit composition of the purified dihydropyridine binding protein from skelet
A:Reference number: A33409; MUID:90122765
A:Accession: A33409
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-44, 'S', 46-47 <HAM>
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosph
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-1106/Product: calcium channel alpha-2 chain #status predicted <WAT>
F:94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:

Query Match 95.7%; Score 5503.5; DB 1; Length 1106;
Best Local Similarity 94.68; Pred. No. 0;
Matches 1053; Conservative 16; Mismatches 15; Indels 29; Gaps 4;

QY 1 MAAGCLLALTLLFQS--LLIGPSSEEPFSAVTTKSWDKMQEDLVTLAKTASGVNQIV 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MAAGRPLAWTLTQAWLLIGPSSEEPFSAVTTKSWDKMQEDLVTLAKTASGVHQLV 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 59 DIYKYQDLYTEPNNAQLVEIARDETEKLSNRKALVSLALEAEKVQAAHQWREDA 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DIYKYQDLYTEPNNAQLVEIARDETEKLSNRKALVSLALEAEKVQAAHQWREDA 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 SNEVYYNAKDDLDPEKNDSEPGSORIKFPVIEDANFQRQSYQAAHYIPTDIYEGSTI 178
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SNEVYYNAKDDLDPEKNDSEPGSORIKFPVIEDANFQRQSYQAAHYIPTDIYEGSTI 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 179 VLNELNWTSAIDDEVFKKREDEPSSLWQVFGSATGLARYYPASPMWDSRTNPKIDLDYDV 238
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VLNELNWTSAIDDEVFKKREDEPSSLWQVFGSATGLARYYPASPMWDSRTNPKIDLDYDV 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

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QY 239 RRRPWYIQGAASPDKMLILVDYSGSVSGITLKLIRTSVSEMLETLSDDDFVNVASENSNA 298
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 RRRPWYIQGAASPDKMLILVDYSGSVSGITLKLIRTSVSEMLETLSDDDFVNVASENSNA 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 299 QDVSCFQHLVQAVNRNKKVLDVANNITAKGTDYKKGFSFAFEQLLNLYNVRANCNKII 358
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 QDVSCFQHLVQAVNRNKKVLDVANNITAKGTDYKKGFSFAFEQLLNLYNVRANCNKII 360
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 MLFTDGGEEAQAEIFNKNKDKKVRVFRFSGVGHNYERGPQIOMMACENKGYIYIIPSIGA 418
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 MLFTDGGEEAQAEIFNKNKDKKVRVFRFSGVGHNYERGPQIOMMACENKGYIYIIPSIGA 420
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 419 IRINTQEYLDVLGRPMVLADGKAKQVQWNTNVDLAELGLVITGLPVTNITQGFENKTN 478
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 IRINTQEYLDVLGRPMVLADGKAKQVQWNTNVDLAELGLVITGLPVTNITQGFENKTN 480
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 479 LKNQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYYPATDNGVYVLLHPNLQPK----- 530
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 LKNQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYYPATDNGVYVLLHPNLQPKIGVITP 540
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNMKIDGESGEKTFRTLVKSQDER 579
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 INLRKRRPNVQPKSQEPVTLDFDAELENDIKVEIRNMKIDGESGEKTFRTLVKSQDER 600
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 580 YIDKGNRTYTPVNGTDY-SIALVLPYISFYIRAKLEETITQARSKKGGKMKDSETLKP 638
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 YIDKGNRTYTPVNGTDYSSIALVLPYISFYIRAKLEETITQARSKKGGKMKDSETLKP 653
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 639 DNFEESGTYFIAPROYCNDLKTSDNTEFLNPFIDRKTNPNSCNADLNRVLLDAG 698
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 654 DNFEESGTYFIAPROYCNDLKTSDNTEFLNPFIDRKTNPNSCNADLNRVLLDAG 713
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 699 FTNELVQNTWSKQNKIKGVKARFVVTGGITRVYKPEAGENQENPETYEDSFYKRSLDN 758
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 714 FTNELVQNTWSKQNKIKGVKARFVVTGGITRVYKPEAGENQENPETYEDSFYKRSLDN 773
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 759 DNYVTAPYFNKSGAYESGIMVSKAVIYIQGKLLKPAVVGKIDVNSWIENFTKTSI 818
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 774 DNYVTAPYFNKSGAYESGIMVSKAVIYIQGKLLKPAVVGKIDVNSWIENFTKTSI 833
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 819 RQPCAGPVCDCKRNSDMDCVILDGCGFLLMANHDDYTNQIGRFFGEIDPDLMLRHVLNIS 878
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 834 RQPCAGPVCDCKRNSDMDCVILDGCGFLLMANHDDYTNQIGRFFGEIDPDLMLRHVLNIS 893
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 879 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAANSILQQFLLSLT 938
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 894 VYAFNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAANSILQQFLLSLT 953
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 939 FPRLEAVEMEDDDFTASLSKSCITEQYQYFDDNDKSFSGVLDGCGNSRIFHGEKLAN 998
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 954 FPRLEAVEMEDDDFTASLSKSCITEQYQYFDDNDKSFSGVLDGCGNSRIFHGEKLAN 1013
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 999 TNLITIMVESKTCPCDTRLLIQAQTSQPNPCDMVKQPRYRKGPVDFDNNVLEDDYTD 1058
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1014 TNLITIMVESKTCPCDTRLLIQAQTSQPNPCDMVKQPRYRKGPVDFDNNVLEDDYTD 1073
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1059 CGVSGSLNPSLWIIIGIQFLLWLVSGSPHRL 1091
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1074 CGVSGSLNPSLWIIIGIQFLLWLVSGSPHRL 1106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
T30256
calcium channel alpha-2-delta-C chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
C:Accession: T30256
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A>Title: Molecular diversity of the calcium channel alpha2delta subunit.
A:Reference number: Z20794
A:Accession: T30256
A>Status: preliminary; translated from GB/EMBL/DBJ
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A:Molecule type: mRNA  
A:Residues: 1-1091 <KLU>  
A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1  
A:Experimental source: brain  
C:Superfamily: calcium channel alpha-2 chain

Query Match 19.6%; Score 1127.5; DB 2; Length 1091;  
Best Local Similarity 28.6%; Pred. No. 4.9e-60;  
Matches 328; Conservative 230; Mismatches 451; Indels 137; Gaps 42;

QY 3 AGCLLALTLFOSLLIGPSSPPSAVTKSWDKMEDLVTLAKTASGVNQLDIYE 62  
DB 14 ASALLA-TALLYAALGDVRSQQIPLSV-VKLWASAFGEIKSIAAKYSGSOLLQKKYK 71

QY 63 KYQDLTYVPPNNARQLYEIAARDIEKLLNRSKALYSIALALEAEKVQAHOHREDFASNEV 122  
DB 72 EYKDAVIEIDGLQVLKYLAKTMEEMFHKSEAVRRLVEAAEAHLKHEFDADL---QY 128

QY 123 VYNAK--DLDPEKNDSEPSQRIKPVFTEDANFGR-QISYQAAVHIPTDIYEGSTIV 179  
DB 129 EYFNVLINERDKNLELGKEFI---LAPNDFNNLPVNISLSDVOVPTNMYNKDPAI 185

QY 180 LNEUNWTSALDEVFKNREEDPSLLMQVFGSATGLARYYPASVPWDSNRPNNKIDLYDVR 239  
DB 186 VNGVWSESLNKVFVDFNDRPSLIWYFGSAKGFRRQYPIKWEPE---NGVIAFDCR 242

QY 240 RRPWYIOGAASPRDMLILVDVSGSVSLGLTKLRTSVSEMLETISLDDDFVNVASFNSNAQ 299  
DB 243 NRKWIQAATSPKDWVILVDVSGSMGLRUTIAKQTVSSILDTGLDDOFFNIITYNEELH 302

QY 300 DVS-CFO-HLVQAVNRNKVKDAVNNTAKITDYKKGFSAFQQLNYNVSRAN--CN 355  
DB 303 YVEPLNGTLVQADRTNKEFREHLDKLPAKGIGMLDIALNEAFNILSDFNHTQGSICS 362

QY 356 KIIMFTDGGEEAQAEIFNKYN-KDKKRVRFVSQGHNYERGIOMMACENKGYIYEIP 414  
DB 363 QAIMLITDGAVDVDTIFAKYNWPNDRKVRIFTYLGREAAAFADNLKWMKANKGFFQTIS 422

QY 415 SIGAIRNTQYLDVLRPMVLADGKAKQVWNTNYLD-----ALBELGLVI--TGT 463  
DB 423 TLADVQENVMYELHLVSRPKVI--DQSHDVVWTEAYIDSTLPQAQLADQGLVMTVA 480

QY 464 LPVFNITQGENKTNLKNQILGVMGVDVLEDIKRLTPRTLCNPGYYPADIPNGVYLL 523  
DB 481 MPVFS---KONETRSKG-ILDGVGVDVPPKELLTPKIKIGIHGIFATFATNNGTILT 535

QY 524 HPNLQP---KNPKSQEP--VTLDFDLAELENDIKVEIRNMIDGESGKTRTLVKSQDE 578  
DB 536 HPELRPLYEEGKKRRKNYSVDLSEVEDRDVY-LRNAVNRKTGK--FSMEVK--- 588

QY 579 RYIDKGNRT-----YTWTPVNGTDYSALVLPY-YSFYTIKAKLEETITQARSKGKMK 631  
DB 589 KTVDKGRVLVMTNDYTYTDIKGTFPSGLVALSRGHGKYFF-----RGNVT 634

QY 632 DSEPLKPDNPEESGYTFIADRYCN-DLKISDNTEPELLNFNEFIDRKTNNPSCNADLI 690  
DB 635 IEELG--HDLHPDVSLADEWSYCNLDLPEHRLSLEAIKILKLGKEP-LLOCDKELI 691

QY 691 NRVLDAAGFTNELVQNTWS-----KOKNIKGVKAREVWTDGGITRYYP----- 733  
DB 692 QEVLFDA-VVSAPTEAVYTSIALNKSNSDKGEVAFGLTRTGLSLNLFVGAELTNQD 750

QY 734 -KEAGENWQENPEYEDSFYKRSLDN--DNYVFTAPY-----FNKSGPAGESIMVSKAV 786  
DB 751 FLKAGDENIFNADHFLPLWYRAAEQIAGSFVYSIPFSTGTVNSK-----NVVTASTSI 804

QY 787 EIIYQGLLKPAPVIGIKIDVNSWLENTEKTSIRDPACAGPVCDCKRNSDVMDCVLLDGGF 846  
DB 805 QLLDERKSPVVAAGIQMKLEFFQKFWTASROQASLDGKCSICDDDETNYCLIDNNGF 864

QY 847 LLMAHDDYTNQIGRFFGEIDPSLMRLHLNIVSVAFNKSVDYOSVCEPAGPAGQAGHR 906  
DB 906

DB 865 ILVS--EDYT-QTGDFFGEVGAVMNKLTMGSKRITLYDYQAMCR---ANKESSDAH 918  
QY 907 AVVPSVADILQIGWATAAAWSILQOFLLSLTPRLLEAVEMEDDDFTASLSK-----QS 961  
DB 919 GLDDPYKAFI-----SAKWIWTELVLFLVEF---NLCSSWHSDMTAKAQLKQTLPEP 968

QY 962 CITEQTYQFFDNDKSKFSGLVDCGNSRIFHGKLMNTNLIIFIMVESKGTCPDTRLLIQ 1021  
DB 969 CDFEYPAFVSERTIKETGTGNIACEDCSKSPVIOQIPSSNLFMVVDS--SCLCESVAPIT 1026

QY 1022 AEGTSDGPN---PCDMVKOPRYRKGPVDFCDNNVLEDYTCGGVSGLNPLSLWLIIGIOFL 1078  
DB 1027 MAPIEIRYNESLACERLKAQKIRRRPESCHGFHPEENARECGGASSLQAQ-----AALL 1080

QY 1079 LLWLVS 1084  
DB 1081 LPLVVS 1086

RESULT 5  
S44617  
C50C3.11 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: S44617  
R:Pavello, A.D.  
submitted to the EMBL Data Library, May 1993  
A:Description: Sequence of the C. elegans cosmid C50C3.  
A:Reference number: S44618  
A:Accession: S44617  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-734 <PAV>  
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650  
C:Genetics:  
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match 10.6%; Score 607; DB 2; Length 734;  
Best Local Similarity 26.6%; Pred. No. 7.7e-29;  
Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;

QY 47 LAKTASGVNLDIYKQYQDLYTVPEPNARQLVEIAARDIEKLLSNRS-----KALVSLAL 102  
DB 36 MKETFSKISHETILKQYKLVVEEQDPAELKSKKHRIEDYLVRSQFAYKAKIS--L 93

QY 103 EABKQAAHQRWEDFASNEVYVYNKADDDLDPEK-NQSEPGSRIKP-----VFIEDANF 155  
DB 94 EARSVRNDSTVNDPQSKSFIREMSAKQGNQDGTITYESNHLGKRLKVNKTSFNLQANF 153

QY 156 -GRQISYQHAHVHIPTDIYEGSTIVLNELNWTALDVEFKNREEDPSLLWQVFGSATGL 214  
DB 154 YTLPTSVSSAVHIPTDLYDRNEDLRRKIDW-SDIDAVYRTNREETKDLAFQLFCSEAGY 212

QY 215 ARYPASPWW-DNSRTPNKKIDLYDVRPPWYIQGAASPKDMLILVDVSGSVGLTLKLIR 273  
DB 213 MRYPPAASFWDNQ--DEHLDLDFCRNTEWYINSATNSKNVLIMLDMSGMLGQRYEVAK 270

QY 274 TSYSEMLETISLDDDFVNVASFNSNA-----QDVSCFQHLVQANRNKKVYLKDAVNNTAKGI 330  
DB 271 QTTEAILETLSHNDYFNIMTFSKNTFLLDGCNGTNGLLQATMRNKKALRRKMDTYQSEK 330

QY 331 TDYKKGFSAFQELLYN-----VSRANCKNIIMLFDGGEERAQEIFNKYNDKKVRF 385  
DB 331 AEYEKALPLAFVLLDINNGGDNNGACENIMLITDGPANAYKIKFIDMADKKVRF 390

QY 386 RFSVGOHNTYERGIOMMACENKGYIYEIPSIGAIRINTQYV-----DVLGRPWVLAGDKA 441  
DB 391 TFLVGEADIDFNEVREMACNRYMWHVANADYDEKIHYYIRMSRVGRRHYESQLS 450

QY 442 KOVQWNTVYLDALDELGL--VITGLPVTNITGOFENKT----- 478  
DB 451 ---WTVGYVYRERYLPRPEIFAEPVPITNQSFVAMNKMARRKIRLQKSEARSMEFVTV 507

QY 479 -----LNQILGVGVDSLEDIKRLTPRTLCPCNGYYFAIDPBGVYVLLHPNQPKNP-- 532  
 Db 508 SYPVIYNFTFMGVAAYNIPLTEVAQKSHPANIGSKSYFFMLDQNGFVMTHPOLRPIDPET 567  
 QY 533 --KSQEPVTLDFLD-----AELENDIKVEIRKNMID 561  
 Db 568 KYHKQYNMMDLLELVGQNGQNVRSQKSAVSDLVCEGSAVAECVDDLKAVRKMID 627  
 QY 562 GESGKTFRTLVKSQDERY----IDK---GNRTYTPVNGTDYSLALVLPYTSFYIKA 614  
 Db 628 CQNSD-----VQOLDVYATELLDRVYQNTYYAEICINHANFVLGLAVAKGDDYRVVK 661  
 QY 615 KLEETITQARSKKGMK 631  
 Db 682 K-----QKKYDFGRVK 692  
 RESULT 6  
 T18770  
 probable calcium channel protein - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T18770; T25249  
 R:Sulston, J.  
 submitted to the EMBL Data Library, June 1995  
 A:Reference number: 219019  
 A:Accession: T18770  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1148 <W1>  
 A:Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24F1.6  
 A:Experimental source: clone B0491  
 R:Chui, C.  
 submitted to the EMBL Data Library, June 1995  
 A:Reference number: 220004  
 A:Accession: T25249  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1148 <W2>  
 A:Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6  
 A:Experimental source: clone T24F1  
 C:Genetics:  
 A:Gene: CESP:T24F1.6  
 A:Map position: 2  
 A:Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

Query Match 10.1%; Score 580.5; DB 2; Length 1148;  
 Best Local Similarity 21.2%; Pred. No. 6.3e-27;  
 Matches 244; Conservative 217; Mismatches 437; Indels 251; Gaps 43;  
 QY 37 VDKMOEDLVTLA-----KTASGVNQLVDIYEKYQDLYTVFPNNARQLVEIAARDI 86  
 Db 99 VDTIEAPASIAQFSANILRDFETQSRFSLVQEEFEKLPDIKSKKEDAAKLVRATEHL 158  
 QY 87 EKLNSRSLVSLALEAKVQAQHWREDFASNEVYVYNAKDDLDPERNDSEPGSQR-- 144  
 Db 159 DRLVTNRVDALKLASSAASAFAV-----DEYDDOAYAVPQADKRCE 201  
 QY 145 --IKPVFIEDANFGRIQISQVH---AAVHTPTDIYEGSTIVLNLNWTSA--LDEVFKNR 197  
 Db 202 AYMKKNESDMHFVSNM--VEHNSKSGIHITVESYQCQDPRVRMDFDWTGKHLKETSMSDNK 260  
 QY 198 EEDPSLLMWQFSGATGLARYIPASPVVDNSRTPNKTLDYDVRRRPWWYIOGAASPQDMLIL 257  
 Db 261 ERAPENGHOYIGTYSGLTRMYPRRH--KVEPTPTIDLDPRFRPWFVNAESVPKDIVL 319  
 QY 258 VDYSVSGSLGTLKLTISVSEMLETSLDDDFVNVASFNSAOD-VSCFOH-LVQANVRNK 315  
 Db 320 LDYSGSVKQPTMHLIKITMYTLSTLSPNDYFYGVFYFNHFNPIISCANRTEPATTNSK 379  
 QY 316 KYLKDAVNNTAKGTDYKKGFSFAFEQL---LNNVNS-----RANCNKIIMLFTDGGEE 367

Db 380 KYFEFELGMLLEKQDQAHFATPLKFSLDVLRGNLDSNQSLFADYRSEGHKLILIFTDGVDE 439  
 QY 368 RAQEIEFN---KYNKDKKRVRFRESVGQHNHYERGPQIOWMACENKGYEYIPISGAIRINTQ 424  
 Db 440 WPHQIILDEEFQTRSELIRIFGSMGYGSLPLQOYMACKSHGGYSEIDSIWDRPQSR 499  
 QY 425 EYLDVLRPMVLAGDKAK-----QVQWTVNYLDLLEGLVITGLPVENITGQENK 477  
 Db 500 TIONVLSQ---VRGDELKGTNAEKREPSWTQLYMETQGTGPIVTLSPILT-----SEQR 551  
 QY 478 NLKNQILGVGVDSLEDIKRLTPRTLCPCNGYYFAIDPBGVYVLLHPNQPKNP-- 533  
 Db 552 IWRDQKLAGVVAIDISIKEFTKHL--TSSEQMIGYIVDNNGLIYHPQIQIPTEVHCV 609  
 QY 534 -----SQEPV-----TLDFLDAELENIDKIVEIRN 557  
 Db 610 RRSACYDAQVQKQKAGSLRVHYGFSDEVYRLVGLIDSIPITLDMVDLEGDSTAIRDLRR 669  
 QY 558 KMIDGESGKTFRTLVKSQDERYIDKGNRTYTPVNGTDYSLALV--LPTYSFYIYKAK 615  
 Db 670 -----RITTKTCYEEAIKNSKEYHCHSHKDSPTLIVVNNIOLKTVYDDSV 717  
 QY 616 LEETITQ-----ARSKKGMKDSKTLKPDNFEESGYTFIAPROYC--NDLKISDNNT 665  
 Db 718 QELGLFDNKLVTFFYPDRDVCQWKLDEYAAHDFRV--WSDISEKEICAQDMLRPRAFT 775  
 QY 666 EFLNFEETDRKTPNPNNSCNADLINRVLIDAGFTNELVQNYWSKQKNIKGVKARFVVD 725  
 Db 776 KGLGWTQSWPKSDIEHTTC-----LLAQYPENASVPHYVNS-----FVHTR 817  
 QY 726 GGITRVYPKEAGENWQENPETYEDSYKSLDNDNVVFTAPYFNKSGPGAYESGIMVSKA 785  
 Db 818 SKLTAFYPTCSSHDMKAVNKKFDEEI--KLTDNNDFV---QFSMR-----SESLIYRT 866  
 QY 786 VEYIOGKLLKPAVVGKIDVN--SWIENFTKTSIRDCAGPVCCKNSD-----VMD 837  
 Db 867 IADYDNNRL---AVGTQWKENFFDQYFNF-----RQPDWKICKRQE 908  
 QY 838 CVILDDGGFLLMANHDDYTNQIGRFEIGEIDPSLMRHLNLSVYAFNKSVDYQSVCEPGAA 897  
 Db 909 CSIITRNHGVIIASSAHRAPAHAKF---DPQLFESLVKNVLTNSVTWTEVQSECK--- 960  
 QY 898 PKGAGHRSAYVPSVADILQIGHWATAA--AWSILOQFLLSLTFPRLLEAVEDEDDFTA 955  
 Db 961 -----AKRVAPWSSAAPGSSILRYFTSI-----FKLAKTSFWR 995  
 QY 956 SLKSKQSCITEQYQYFFDNDKSKFSGLDCGNC--SRIFHGKELMNTNLIIFIMVSKGTC-- 1012  
 Db 996 NLLESALTLDVAQPSMTGNTCTFKIKPFERCMPKFFHYRMTLNITK--QLQLTGMSTCSR 1054  
 QY 1013 -----PCDTRLIOAETSQGNP-----CDMVKQPRYKGPVDCFD--N 1050  
 Db 1055 YAKLYVPVHTLTLIADACSOYRPRKRIFSEPRKLEKCDVY-HSHARRRPPALNDWKI 1113  
 QY 1051 NVLEDYDTC 1059  
 Db 1114 DLQNKHVDC 1122

## RESULT 7

C86880

hypothetical protein yvcC [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001

C:Accession: C86880

R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Eh

Genome Res. in press, 2001

A:Title: The complete genome sequence of the lactic acid bacterium.

A:Reference number: A86625

A:Accession: C86880

A:Status: preliminary

A:Molecule type: DNA



A:Residues: 1-1450 <STO>  
A:Cross-references: GB:AE005176; NID:gl2725093; PIDN:AAK06141.1; GSPDB:GN00144  
A:Experimental source: strain Il1403  
C:Genetics:  
A:Gene: yvcc

	Query Match	3.4%	Score 198;	DB 2;	Length 1450;
	Best Local Similarity	21.0%;	Pred. No. 0.0012;		
	Matches 242;	Conservative 149;	Mismatches 439;	Indels 322;	Gaps 56
QY	37	VDKQOEDLVTLAKTASGVNQLVDIYEKQDYQLVTPENNAQLVEIARQIEK-----L 89			
DB	69	INKTENDKELKLFSEGNQPIETEE--NESWTLKEKNT-----IISDFEKENECKIVL 120			
QY	90	LSNRSKALVSLALEAEKVQAAHWR---EDFA-----SNEVYVNA 127			
DB	121	RANNSISLLNLEIQADAKLIENDQVEISDILAKESTIFSILYPENNKADSKERDKNT 180			
QY	128	KDDLDPEKNDSPPGSRKTP---VPIDANFGRQISYOHAAVH-----167			
DB	181	EVLLNNSSQEBTSQLKKDSQALSYPSNFGIKASFNDLAQNYENISPEYQDETGISP 240			
QY	168	---IPTDIYEGSTIVLNELNWTSALDEVFKKNREEDPSLLNQVFGSATGLARYYPASPW 223			
DB	241	NHSWIPT---GNTTVVNHQGNSE-----SSQWDGVNSWN--GEATNLENSIYEYAG 287			
QY	224	VDN-----SRTPNKTDLV--DYRRRRPWYTGGAASPKDMLILVDSVSGSLTLK 270			
DB	288	VNNPVDFAIRKYAKETIEPGLYDVLNVRGN--VQNPKIPVDIVLVIDMSGMQGAKET 344			
QY	271	LIRTSVSEMLETSLDD---DFVNV--AFSNSNAQDVSCFQHLVQANVRNKKVKLD---A 321			
DB	345	AVROGVSDFLSTIQNTAYADYVNVGIVGYSPPGVTVTGASGYITVPI--DKVSSSESHVKS 402			
QY	322	VNNITA---KGITDYKKGFSFAFEOILLNYSRANCNKIIMLFTDGGERAQEIFNKYNK 378			
DB	403	INQALAPFGSGTFTQLGRKGTML---EODSDNQKMMILMTDG---VPTFSYKVN 455			
QY	379	DKKVR--VFRFSVGQHNTERG---PIQ---WMACENKGYIET---PSIGAIRINTQE 425			
DB	456	ASKVDNVIYGQSFASROBPGNTSKIQSPYYKIDNGSNIETROTWAATLGEAEISKQE 515			
QY	426	YLDVLGRPMVLAD-----KAKQVQNTVYLDALGLGLVITGTLPLVFNITGQPE 474			
DB	516	ISEIHTGLIGLNGDSYLSQEEVKRSKTSLIATTLGYQDANSAN-----DITDYLK 565			
QY	475	NKTN-----LKNQLIILGVGVDSVLEIDKRLPRFTLCPNGYFFAIDPQYVLLHPN 526			
DB	566	NQANVYLSRFNTITNGLIDPLGAOFEXKDTK-----FEITSVG-----604			
QY	527	LQPNPKSQEPVTLDFLOAELENDIKVEIRNKMIDGESKETFRTLKVSQDERYIDKGNR 586			
DB	605	-----EDSINLPTGKNEKGLEISLNLI--GKQEVQIHQVRLNTEFDDFKTVY 653			
QY	587	TY-----TWTPVNGT--DYSIALVLPITYFYIIRAKLE-----ETIQARSK 627			
DB	654	WYQMGNETTLTP--NGSNPDKNVNFQVPSAKSSGINLTLEKQWLANSENIPENVELLIGRR 712			
QY	628	GKKMDE-----TLKPDNFEESGYFTIAPRDYCNLDKISDNTEFLLNNEFTIDRTPNN 692			
DB	713	SAQISSDWTKTVTLKDEDDSWRSQLENLPLKYSILGEEFYIEIRKDEIVLN--SEIYDWTITGE 771			
QY	683	PSCNADLLNRVLDD---AGFTNELVQNVWSKOKIKGVKAREVTVTDGGITRVYPKEAGE 738			
DB	772	DKTTTIANTEKFRQLIKTNSHNDNEPLSEVEFVLKNSQGEIEIDKAVTN-----EKGE 822			
QY	739	NWQENPETYEDSFYKRSLLDNVNYFTAPYFNKSGPGAYESGINVSK-----AVEIYIQ 791			
DB	823	ILFDTRLNYPEYQIHEIKSPGHSLEGFWKTKT---EFENGOPILKVDGEQIALDEHYN 879			
QY	792	GKLLKPAVVGVIKIDVNSWJENFTKTSIRDPCAGVCDCKRNSDVMDCVILD-----DG-- 844			

QY 467 ENITGFENKTNLKNOLLGVGVDSLEIDKRLTPRTFLCPNGYFAIDPNGYVLLHPN 526  
Db 492 F-----YDG-----SIIVAGRLVDRMDN-----FKADVKGHGALN-- 523  
QY 527 LQPKPKSQEPVTLDFDLAELENDIKVEIRNKMIDGESGEK--TFRTLVKSQDERVIDRG 584  
Db 524 ---DLTFEEVDMEBDAALK-----EQGVIFGDYIERLWAYLTIQELLEKKRNG 572  
QY 585 NRTYTWTPVNGTDYSLA--LVLPYTSFYIKAKLETTIQAKSKKKMKMDSET-----LK 637  
Db 573 DEKENIT-ABALDLSKYHFVPLTSMVYTKPEDNEDOTSADNAGEEAFATETMTSFLT 631  
QY 638 PNFESGVTFTAPRDYCNLDKISDNNTFELNFEIDRKTPNPNPCNADLINRVLLDA 697  
Db 632 TQOSSQSPYIV-----DGDPHFIQI-----PGKNDSCFNIDEKP 668  
QY 698 GTNELVQWYNSQKNIKGVKARFVVDGTRVYPKEAGENQWENPETYDSFYKRSILD 757  
Db 669 GTVLRLIQD-----PVT--GIT-VTQIIIGD-----KRS-- 694  
QY 758 NDNYFTAPYFNKSGPGAYESGIMSKAVEITIQGLKLPAPVGVKIDVNSWIENFTKTS 817  
Db 695 NASSRTGRTYFKGLGTINAMDFRVEVTTKEILG-----TGAELETSFSLDVTVTQ 747  
QY 818 IRDPCAGPVCDCKRNSDVMDVLDG-GFLLMAN-----HDDYTQIGRFFGEIDP 868  
Db 748 -----TGLSVTNRKKNMV--VSFGDGISFVILHGWKKHPVHQDFLG-----FVVDVS 795  
QY 869 SLMRHLVNSVYAFNKSQYQSV-CEPGAAP 898  
Db 796 HRMSAQTHGLLGQFPDFKVGIRPGSDP 826  
RESULT 9  
S30350  
Inter-alpha-trypsin inhibitor heavy chain 3 precursor - human  
N:Alternate names: HC3; Inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heavy  
C:Species: Homo sapiens (man)  
C:Date: 03-May-1994; sequence\_revision 20-Feb-1995; text\_change 04-Feb-2000  
C:Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167  
R:Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin,  
Eur. J. Biochem. 212, 771-776, 1993  
A:Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-  
A:Reference number: S30350; MUID:93215656  
A:Accession: S30350  
A:Molecule type: mRNA  
A:Residues: 1-885 <BOU1>  
A:Cross-references: EMBL:X67055; NID:g288562  
R:Bourguignon, J.  
submitted to the EMBL Data Library, June 1992  
A:Reference number: S34123  
A:Accession: S34123  
A:Molecule type: mRNA  
A:Residues: 1-310, 'K', 312-343, 'R', 345-885 <BOU2>  
A:Cross-references: EMBL:X67055; NID:g288562; PIDN:CAA47439, 1; PID:g288563  
R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattei, M.G.; Passage, E.; Sallier,  
Eur. J. Biochem. 179, 147-154, 1989  
A:Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three ch  
A:Reference number: S02141; MUID:89137072  
A:Accession: S02141  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 341-356, 'G', 358-845, 'H', 847-885 <DIAL>  
A:Cross-references: EMBL:X14690; NID:g35464; PIDN:CAA32821, 1; PID:g35465  
R:Engild, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.  
J. Biol. Chem. 264, 15975-15981, 1989  
A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al  
A:Reference number: A92736; MUID:89380192  
A:Accession: D34245  
A:Molecule type: protein  
A:Residues: 30-49 <ENGI>  
R:Engild, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S.V.  
J. Biol. Chem. 266, 747-751, 1991

A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood p  
A:Reference number: A39079; MUID:91093267  
A:Accession: A39079  
A:Molecule type: protein  
A:Residues: 631-647 <ENG2>  
R:Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-  
Blochim. Biophys. Acta 1219, 551-554, 1994  
A:Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H  
A:Reference number: S50132; MUID:95002176  
A:Accession: S50133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-27 <DIA2>  
A:Cross-references: EMBL:X75318  
R:Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.  
Biochemistry 33, 7423-7429, 1994  
A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable co  
A:Reference number: A53642; MUID:94271799  
A:Accession: B53642  
A:Molecule type: protein  
A:Residues: 30-34, 'X' <WIS>  
R:Jessen, T.E.; Faarvang, K.L.; Ploug, M.  
FEBS Lett. 230, 195-200, 1988  
A:Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a  
A:Reference number: S02431; MUID:88167187  
A:Accession: A59167  
A:Molecule type: protein  
A:Residues: 30-32, 'GEKQAVDT' <JES>  
C:Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondro  
C:Genetics:  
A:Gene: GDB:ITIH3  
A:Cross-references: GDB:120109; OMIM:146650  
A:Map position: 3p13-3p12  
C:Superfamily: Inter-alpha-trypsin inhibitor complex component II  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-29/Domain: propeptide #status predicted <PRO>  
F:30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <M  
F:648-885/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:87-576/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:647/Modified site: Chondroitin sulfate ester carboxyl end (Asp) (in mature form) #s  
Query Match 3.2%; Score 185; DB 2; Length 885;  
Best Local Similarity 20.9%; Pred. No. 0.0034;  
Matches 137; Conservative 101; Mismatches 239; Indels 180; Gaps 34;  
QY 27 FPSAVTIKSWDKMOEDVTLAKTAGSVQNLVDIYEKYQDLYTVEPNARQLVEIAARDI 86  
Db 97 YGNVKEVAKQYKAVSQGTAG-----LVKASGRKL 131  
QY 87 EKLLSNRSKAL---VSLALEAEKVQAAHQWREDFASNEVVYNAKDDLPDEKNDSEPGSQ 143  
Db 132 EKFTSVNVAAGSKVTFELTYELLKRHKGK-----YEMYLKVQPK-----Q 173  
QY 144 RKPVEIDANFGRIQSYQAAVHIPTDIYEGSTIVLNELNWTLSALDEKFKKNEEDPSL 203  
Db 174 LYKHFEIE-----VDIFEPOGI-----SMLD-----AEASFI 200  
QY 204 LMQVFGSA-----TGLARYVPASPVDNSRT-PNKID-----LYDVRRRP----- 242  
Db 201 TNDLLGSALTAKSFSGKKGHVSFKPSLDQORSCTCTDLSLLNGDFTTYDVNRSPGNVQI 260  
QY 243 ---WYI-----QG-AAAPKMDLILVDVSGVSLGTLKLIRTSVSEMLETSLDSDDFVNVAS 293  
Db 261 VNGYFVHFPAQGLPVVPKNVAFVIDISGMAGRKLEQTKAALLRILEDMQEEEDYLNFL 320  
QY 294 FNSNAQDVSCF-QHLVQANVRNKKVLDAVNNTAKGITDYKGFSAFEQQLNLYNSR- 351  
Db 321 FSG---DVSTWKEHLVQATPENLQEAQTFVSKMEDKGMTNINDGLLRIGISML---NKARE 374  
QY 352 ----ANCKIMLFTDG---GEEAQAQEIFNKYNK--DKKRVFRFVSQGHNYERGPQ 400

Db 375 EHRIPERSTIVIMLTGDNANVGSRPEKIQENVRNAIGGRFPLYNLGF--NNLNYNFLE 433  
Qy 401 WMACENKGYVEISIGAIRINTQYLDVLRPMVLGADKAKQVQWTVNYLDALE----- 455  
Db 434 NMALENHGFARIEDSDADLOLQGFVEEVANPL-LTGVEMEYPE--NAILDLTQNTYQH 490  
Qy 456 ---LGLVITGTLFVNITGOFENKTNLK-----NOLILGVMGVDVSLDEDIKRLTPRFTL 506  
Db 491 FIDSEIVVAGRL-VDEDMNSF--KADVKHGATNDL---TFTTEVDMKENEK-----AL 539  
Qy 507 CPNGYFFAIDPN-----GYVLLHPNLOPK---NPKSQEPVTLDFDLAELENDIKVEIRN 557  
Db 540 QERDYIFG---NYIERLWAYLTIEQLLEKRNKHAKEKENUTARALDLSKVHFVTPUTS 596  
Qy 558 KNIDGSEKTRILVKSQDRYI-DKGNRRYTTTPVN-GTDSYSLALVLPYSFYI 612  
Db 597 MVVTKE-----DNEDERAIDKPGDAEATPVSPAMSYLTSTYQPPQNPYYV 644

RESULT 10  
JC5576  
Inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 17-Mar-1999  
C:Accession: JC5576; PC4486  
R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.  
J. Biochem. 122, 71-82, 1997  
A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors in inhibitor heavy chain family.  
A:Reference number: JC5576  
A:Accession: JC5576  
A:Molecule type: mRNA  
A:Residues: 1-889 <NA>  
A:Cross-references: DDBJ:D89287  
A:Experimental source: liver  
A:Accession: PC4486  
A:Molecule type: protein  
A:Residues: 34-53; 449-475; 509-526 <NA>  
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were that the complexes play important role for pancreatic cancer.  
C:Superfamily: inter-alpha-trypsin inhibitor complex component II  
F:236-239,664-865/Disulfide bonds: #status predicted

Query Match 2.9%; Score 164.5; DB 2; Length 889;  
Best Local Similarity 23.2%; Pred. No. 0.059;  
Matches 66; Conservative 56; Mismatches 112; Indels 51; Gaps 11;  
Qy 202 SLLQVFGSATGLARYYPASPPVNSRT-PNKID-----LYDVRER-PWYIQA-- 248  
Db 211 SALTQSGKKGHVFKPS---LQQRSCPTCTDSLLNGDFTIVYDVARESPGVQVNG 267  
Qy 249 -----ASPKMLILVDVSGVSGTLKIRTSVSEMLETLSDDDDFNVASFNS 296  
Db 268 YVHFPAQGLVPVKNIVFVIDISGMAGRIQOTRALLKILDKODDVLNILEST 327  
Qy 297 NAQDVSCFQHLVQAVNRKVKLKDANNITAKITDYKGFSAFQELN-----YVNSRA 352  
Db 328 GV--TTWKDSLVOATPANLEEARTEVRSISDOGTNINDGLLRIGRMLTDAREQHTVPR 385  
Qy 353 NCNKIIMLFTDG---GEARQEIFNKYKDKKVRVFRFVG-QHNYERGPQWACENK 407  
Db 386 STSIILML-TDGDANTGSRPEKIQENVRNAIGGRFPLYNLGFNNLNFLETMALENH 444  
Qy 408 GYVEIPISTGAIKIRINTQYLDVLRPMVLGADKAKQVQWTVNYLD 452  
Db 445 GVARIYSDANLQLOGVEEVANPL-----TNVEVE 478

RESULT 11  
T28155  
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum) (fragments  
N:Alternate names: erythrocyte membrane binding protein 1 (EMPI)

C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T28155  
R:Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.  
Nature 388, 292-295, 1997  
A:Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and requires complement  
A:Reference number: J20477; MUID:97373957  
A:Accession: T28155  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2706 <ROW>  
A:Cross-references: EMBL:Y13402; PIDN:CAA73831.1  
A:Experimental source: strain IT 4/25/5  
C:Genetics:  
A:Introns: 2493/3  
A:Note: R29R+var1

Query Match 2.8%; Score 161; DB 2; Length 2706;  
Best Local Similarity 18.2%; Pred. No. 0.56;  
Matches 183; Conservative 137; Mismatches 345; Indels 338; Gaps 46;

Qy 36 WDKMQEDLVTLAKTASGVNQLVDIYEKQDLYTVEPNA-----RQL 78  
Db 308 WFEWAEEFCIRKI-----KLENVKECRD---EPNNKYCSGDGCHCKRYLKDNTIF 358  
Qy 79 VEIARDTEKLSNRKALVSLALEAEKVQAAHQWREDFASNEVYVYNAKDDLPKNDL 138  
Db 359 IDLNCPCENACSNYK-----WIEIQKQFDKQRK--YNNEI---KIKTINNNENDK 408  
Qy 139 E-----PGSORIKPVFIEDANFGRIQISYQAAVHIPTDIYEGSTIVLNELNWTSALE 191  
Db 409 EYENLDKKGYSTIN-TFLESNLHGKQCO-----DN 438  
Qy 192 VFKNREEDPSLLQVFGSATGLARYYPASP-----WDNSRTPNKI 233  
Db 439 IDKKNKTNFKNNL-ETFGP---SGYCEACPIYGVKCSNEKCTPVTEWNSNNRLPTDT 493  
Qy 234 DLYDVRRRPWYIQAASPKDMLILVDVSGVSGTLKIRTSVSEMLETLSDDDDFNVAS 293  
Db 494 STKNL-----ATNIDMLVNDGIGNAI----- 515  
Qy 294 FNSNAQDVSCFQHLVQAVNRK-----VLKDAVNNITAKITDYKGFSAFQEL 345  
Db 516 ---DNELEKNCIKYGLKKGKQKQWQCYLLNIDOCKINNVMNSGYFDNKIAFNVLFQRL 573  
Qy 346 NYNVSRAKNIIMLFTDGGEEARQEIFNKYKDKKVRVFRFVGQHNHYERGPQWMAE 405  
Db 574 RYFVRDHNRK-----EKIDVCIKKENINENICIKRCKTN-----CE 610  
Qy 406 NKGYIYEIPSTGAIKIRI---NTQEVLDVLRPMVLGADKAKQVQWTVNYLDALEGLVIT 461  
Db 611 CVGKLEKEAEWMDINOHYNOKNHIMFLIPYITWTFYK--ITFPNDFKALE-----DV 665  
Qy 462 GTLPVFNITGQPKNTNLKNQLILGVMGVDVSLDEDIKRLTPRFTLCPNGYIYFAIDPN 521  
Db 666 DTINVLDLTKECQD--THCKIEKIRSI-DVDLKEIISWLNKIEVCKS--HDEDKHEYC 721  
Qy 522 LLHPNLOPKNPKSQEPVTLDFDLAELENDIKVEIRNKMTIDGSEKGT-----FRT 571  
Db 722 C---DILPKSVDDDEDD--EEVDEEKESSQTKRN--ISQKGGTKSASCVGACAIKVG 775  
Qy 572 LVKSQDERYID---KGNRTYTW-----TPVNGTD-----YSLALVLPYSF 609  
Db 776 VLQKQNSGNSIDCNNAKRNKKNEMQCDKNTFVDGNEGVCMPPRRKSCICIHNLTEEGTKNK 835  
Qy 610 Y-----YIKAKLEET--ITQARSKKGMKDSITLK-----PDNFEE--SGYTFIAPRDYC--N 656  
Db 836 YOLREAFIKAAKETNLLWDKYNDKNEAEELLKKGKIPEDFMIRIMFYTFGDFRDFCLEN 895  
Qy 657 DL-----KISDNNTEFLNFEFIDRK-----TPNPNPSC--NADINRVLNLDAGTNNEL 703  
Db 896 DMGKDVKYKKNINKVFNNSKRGFKKIDPENWNNENGPOIWNGLCALIHADTKDSIKN 955

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QY 704 VQNY-----W-----SKQNKIGVKARFVV 723
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Db 956 KDNKYKEVKTILAKRDGSGNMTLSEFAKPKFLRWFEVWDDYCKERQKYLEVASTCKS 1015
|||
QY 724 TDGGLTRV-----YPKEAGEWQENPETYEDSFYKRSLDN-----DNYV- 762
|||
Db 1016 IDGQLKCDRGCNKODEYKYMRRKKKEWNLODKYIKKRENGKDGKPGIIVKDYVL 1075
|||
QY 763 -----FTAPYFNKSGPGAYESGIMVSKAVEIYIQGLKLPAVVGIKIDVNSWI-- 810
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Db 1076 ANAKYLLKKRFTASCVTSSGKAQNSATEEVKKNIELSEEQY-----YDADQYCGC 1126
|||
QY 811 -----ENFTKTSIRPCAGPVCDCK-----RNSDVMDCVIL 841
|||
Db 1127 TKPTHDDKYSKISGRSNCCGLNSDAKKNKIKWRNSDEKDYAFL 1169
|||

RESULT 12
A44396
P-type cation translocating ATPase - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000
C:Accession: A44396
R:Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; Robson, K.J.
J. Cell Biol. 120, 385-398, 1993
A:title: A family of cation ATPase-like molecules from Plasmodium falciparum.
A:reference number: A44396; MUID:93132070
A:accession: A44396
A:status: preliminary; not compared with conceptual translation
A:molecule type: nucleic acid
A:residues: 1-1984 <KRI>
A:note: sequence extracted from NCBI backbone (NCBIP:122678)

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Db	765	KNIKDNNKKYIYNLELEQBEINEKKYNNKND- ---SNKTF- ---	-----LK TENEF 812
QY	426	YLDGRPMVLADK- ---AKQVOMT- ---	-----NVYLDALGLVITGTLPVFNIT 470
Db	813	KKDLLDDSQIFGDSLLADIKEYNTYTDLNNNNENKSLYEDGENF- ---ITRNEP- ---IT	866
QY	471	GQFENKTNL- ---	-----KNOLILGVMGDVSLIEDIKRLTPRTLCPN- ---G 510
Db	867	NEYEEKNNIIYISDEOKYNEEDIIPFKDIKEKENNDTSSDDFENCVSQEKIYVNEKIEE 936	
QY	511	YFPAID- ---PNGVILLHPLNQPKNKSOBPVT- ---	-----LDPLD- ---AELEN- ---DI 551
Db	927	YNNKNDKSSSSSIILEIKYKKEKDELVSPLCVLLDDEFHSNDLENNYISVSSDDM 986	
QY	552	KVEIRKNMIDGESGEKFTFTLVKSODERYIDKGNRTYTWTPVNGTDYSLALVLPYTSFY 611	
Db	987	KTNVSKNNITG- ---	-----VK- ---ENKVDKTNVEY- ---1010
QY	612	IKAKLEETIQARSKG- ---	-----KMKDSEILKPDNEESGYTF- ---INAPRDYCN 656
Db	1011	-----DKKGDDGVIEISFEDSHKLEESKFDNNNNIYDNDDELEKNLSKDYIS 1057	
QY	657	DLKISDNNTEFLNF- ---	-----NSFIDRKPNNPS- ---CNAOL 689
Db	1058	D- ---VDKNHNNYININTERGERENEFEVENKQTSFESHKSNEFICTENKSLRKQYMSKEDI 1115	
QY	690	IN- RVLLDAGFTNELQNTYWSKQKNIKGKARFVYTDGGITRVYPKEAGENWQENPETYE 748	
Db	1116	SNVRILKSDDINNLKSNQYFE- ---	-----ILLD- ---KKQVMDNFQMNIBQNN 1156
QY	749	DSFYKKSLDNDYVFTAPYFNKSGPGAVESGIMWSKAVEYI- ---	-----QGKLLK 796
Db	1157	DKLKDKLDE- ---	-----GAFYEYLEDNKIIDSYIKETNKENEELIKEYKKLK 1201
QY	797	PAYVGKIDVNSWIE- ---NFTKTS- IROPCK- AGPVCDCKRNSDVMDCVILDDGGFLLMAN 851	
Db	1202	KNNIEINDEMNDDIKLLNFFGPIPIQSPCEAEACQSYLNKNKNYCDALISDSDVLFSG 1261	
QY	852	DDTYTNQIGRFGE- ---	-----IDPSL- ---MRHLWNISV 879
Db	1262	-----KTVIKFNFKNKKTVEYKKAIEKGLGYQELINISL 1299	

[illegible]

QY 124 YNAKD-----DLDPEKNDSEPGSQRIKP-----VFIEDANFR- 157  
Db 1222 LPNAPNRVFGYEMWTPGFRSLD---NDGTLKLDRIHRYEGFYWRYEAFIADALITKL 1278  
QY 158 QISYQHAHVHPTDIVEGSTIVLNLNWTLSALDEVFKKNEEDPSLLQVQFGSATGLARY 217  
Db 1279 KRYEDTNVRINLDGNTRFIV-----PVITEQIRKN-----LSYSFYGS--GGSYS 1324  
QY 218 YPASPWVNDSTRPNKIDLYDVRRRPWYIQGAASPKDMLILVDVSGVSLTLKLRTSVS 277  
Db 1325 LSLSPYNMN-----IDLNLVENDTW-----VIDVDNVKNITIESDEIQKG 1365  
QY 278 EMLETLSDDDFVNVSFNSNAODVSCFQHLVQAVNRKVKLDAVNNITAK---GITDYK 334  
Db 1366 ELIENI-----LSKLNIEDNKII---LNNHTINFEYGDINESN 1399  
QY 335 KGFSFAFEOLLNVN-----VSRA-----NCNKIIMLFTD-----GGEERAO 370  
Db 1400 RFISTFSLIEDINIIIEIDLVSRTKILLSGNCMKLIENSIOQKIDHIGFNGEHQY 1459  
QY 371 EIFN-----KYN-----KDKYRVFRFVSQHNRYERGPIQMACENKGYEYIPSGAIR 420  
Db 1460 IPYSVIDNETKNGFDYDKSKEGLTAESNESIIRN--IYMPDSNNLFYSSKDLKDIR 1517  
QY 421 INTQEYLDVLRPWLADKAKQ-----VQWNTNYVLDALGLVITGLP 465  
Db 1518 IINK-----GDVKLLIGNFYKDDMKVLSFTIEDNTIKLNGVYLDE-----NGVAQ 1564  
QY 466 VFNITQPENKTNLKNQILGVMGVDVSLIEDIKRLTPRETLCPNGYFFAIDPNGYVLLHP 525  
Db 1565 ILKFMNNAKSALNTSNLNFLESINIK-----NIFYNNLDPNIEFILD 1609  
QY 526 NLQPNKPSQEPVTLDFLDAELENDIKVEIRNMIDGESGKFTFTLVKSODERYIDKGN 585  
Db 1610 NF-----IISGNSIQOFE-LICDKDN-----1631  
QY 586 RRYTWTVPNGTDYSALVLPYVSFYIRAKLEETITQARKKGMKDSSETLPKDPNFESG 645  
Db 1632 -----IQP-----YFINFKIKET-----SYTLVVGNRQN-- 1655  
QY 646 YTFIAPROYCNDKLTSDNTELLAFNE---FIDR---KTPNPNFSCHADLIN-----691  
Db 1656 -LIVEPSHLD--SGNISSTVINFSOKYLYGIDRYVKNVILAPNLYTDEINITPVYKP 1711  
QY 692 -----RVLLDAGFTNE-----LVQNYW-----SKQKNIKGVKARFVVT 724  
Db 1712 NYICPEVILIDANYINEKINYNINDLSIRYWDNDGSDLLILIANSEEDNQPOVKIRFV-- 1769  
QY 725 DGGITRVYPKEAGE-----NWOENPE-----TYEDSFYKR-----SLDNDNY 761  
Db 1770 -----NVFKSDTAADKLSFNFSKODSVSKIIISFSLAAYSDFGFEYFGLVSLDND-- 1822  
QY 762 VFTAPYFNKSGPGAYESGIMYSKAVEIYIOGKL--LKPAVVGIKIDVNSWIENFTKTSIR 819  
Db 1823 -----YFYINFGNMYVSGL-----IYINDSLYTFKP-----PKNNLITGFTTI--- 1860  
QY 820 DPCAGPVCDCKRNSDVMCDVILDDGGLFLMANHDDYTNOIGRFFGEIDPISLMRHLVNISV 879  
Db 1861 -----DGN-----KYFDPKTSGAASIGEI-----TIDGKD 1886  
QY 880 YAFNKSIDYQSVCEPGAAPKOGAGHRSAYVPSVADILQIGMWATAAAMSILQQFLLSLTF 939  
Db 1887 YFYN-----KOG-----ILOQGVINTSDG---LKYFAPAGTL 1915  
QY 940 PRLLAEVEME-----DDDFASLSKSCITEQTOYFFDNDSDKSFSGVLDCG 985  
Db 1916 DENLEGESVNFIGKLNIDGKYFYEDNRYAAV-EWKLLDDETYFNFNPKTGEALGLHQIG 1974  
QY 986 NCSRIFHGEKLMNTNLIPI 1004  
Db 1975 DNKYFFDDNGIMQTGFTI 1993





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:38:39 ; Search time 66.28 seconds  
(without alignments)  
563.861 Million cell updates/sec

Title: us-09-397-548-14  
Perfect score: 5748  
Sequence: 1 MAGCLLTLTLFQSLIG.....IIGIQLLLWLVSNGTHRL 1091

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5748	100.0	1091	1	CIC2_HUMAN
2	5505	95.8	1091	1	P34289 homo sapien
3	5503.5	95.7	1106	1	P34290 rattus norv
4	607	10.6	734	1	P3806 oryctolagus
5	194.5	3.4	886	1	P34374 caenorhabdi
6	182	3.2	885	1	Q61704 mus musculu
7	180.5	3.1	887	1	Q06033 homo sapien
8	164.5	2.9	886	1	Q63416 rattus norv
9	161	2.8	1829	1	P37280 mesocricetu
10	159	2.8	1956	1	Q3845 thermococcu
11	157.5	2.7	575	1	Q04956 plasmodium
12	154.5	2.7	946	1	P76481 escherichia
13	152	2.6	1290	1	P19823 homo sapien
14	151.5	2.6	420	1	P18640 clostridium
15	150.5	2.6	921	1	Q5874 synechocyst
16	150	2.6	654	1	P79263 sus scrofa
17	149	2.6	930	1	P34576 bacillus su
18	148	2.6	964	1	Q14624 h inter-alp
19	144	2.5	1087	1	P30319 choristoneu
20	143	2.5	946	1	P38535 clostridium
21	142.5	2.5	382	1	P97279 mesocricetu
22	141	2.5	1251	1	P34373 caenorhabdi
23	140.5	2.4	935	1	Q00799 plasmodium
24	140	2.4	2710	1	O2668 sus scrofa
25	140	2.4	3305	1	P16154 clostridium
26	139.5	2.4	764	1	Q25490 manduca sex
27	139	2.4	1180	1	P13423 bacillus an
28	139	2.4	1513	1	P16480 bacillus th
29	137	2.4	984	1	STU1_YEAST
30	136.5	2.4	3063	1	P38198 saccharomyc
31	135.5	2.4	946	1	Q3591 streptococc
32	134.5	2.3	2077	1	Q99715 homo sapien
33	133	2.3	862	1	Q61703 mus musculu
					P52340 human herpe
					O51737 borrelia bu

34	133	2.3	1323	1	ADRI_YEAST	P07248 saccharomyc
35	132.5	2.3	547	1	SYM_BUCAI	P57210 buchnera ap
36	132.5	2.3	929	1	CAIC_NOTVI	Q91145 notophthalm
37	132.5	2.3	1679	1	Y109_YEAST	P40457 saccharomyc
38	132	2.3	697	1	YE9C_SCHPO	O13773 schizosacch
39	131.5	2.3	1018	1	YC14_METJA	Q58611 methanococc
40	131	2.3	1634	1	DPOL_METJA	Q58295 methanococc
41	131	2.3	1658	1	YM67_YEAST	Q03661 saccharomyc
42	130.5	2.3	987	1	YD94_METJA	Q58789 methanococc
43	129	2.2	1244	1	Y307_MYCPN	P75342 mycoplasma
44	128.5	2.2	1254	1	UBPC_YEAST	P39538 saccharomyc
45	128	2.2	1113	1	Y140_MYCPN	P75033 mycoplasma

## ALIGNMENTS

RESULT 1  
CIC2\_HUMAN  
ID AC P54289; STANDARD; PRT; 1091 AA.  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE DIHYDROXYRINDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA  
DE SUBUNITS PRECURSOR.  
GN CACNA2D1 OR CACNL2A OR CCHL2A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92110010; PubMed=1309651;  
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R.,  
RA Velicelebi G., Ellis S.B., Harpold M.M.;  
RT "Structure and functional expression of alpha 1, alpha 2, and beta  
subunits of a novel human neuronal calcium channel subtype.";  
RL Neuron 8:71-84(1992).  
CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN  
EXCITATION-CONTRACTION COUPLING.  
CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:  
ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS  
HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE AND  
AORTA TISSUES.  
CC -!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM  
A PRECURSOR FORM (BY SIMILARITY).  
CC -!- SIMILARITY: TO OTHER SPECIES ALPHA-2 SUBUNIT.  
-----  
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EMBL; M76559; AAA51903.1; -;  
MIM; I14204; -;  
InterPro; IPR002035; -;  
Pfam; PF00092; vwa; 1.  
PROSITE; PS50234; VWFA\_DOMAIN; 1.  
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
Calcium channel; Glycoprotein; Phosphorylation; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT  
(BY SIMILARITY).  
FT CHAIN 945 1091 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY  
SIMILARITY).  
FT TRANSMEM 446 469 POTENTIAL.  
FT TRANSMEM 906 930 POTENTIAL.

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FT TRANSMEM 1067 1086 POTENTIAL
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 769 769 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 883 883 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 973 973 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 986 986 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 501 501 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 833 833 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 833 833 PHOSPHORYLATION (BY CAPK)
FT SEQUENCE 1091 AA; 123183 MW; 2E4E13EE29A47837 CRC64;

Query Match 100.0%; Score 5748; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGCLLALTLTQSLIGPSSEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLALTLTQSLIGPSSEPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKQDLYTVEPNAROLVETARDIEKLSNRSKALVSALAEKVOAARHOREDFASN 120
DB 61 YEKQDLYTVEPNAROLVETARDIEKLSNRSKALVSALAEKVOAARHOREDFASN 120

QY 121 EVVYNKADLDPEKNDSEPGSORIKPFVIEDANFGRQISYQAAHVHPIDIEGSTITV 180
DB 121 EVVYNKADLDPEKNDSEPGSORIKPFVIEDANFGRQISYQAAHVHPIDIEGSTITV 180

QY 181 NELNWTSALEDFVKKNEEDPSLLQVFGSATGLARIYPASPWWDSNRTNPKIDLYDVR 240
DB 181 NELNWTSALEDFVKKNEEDPSLLQVFGSATGLARIYPASPWWDSNRTNPKIDLYDVR 240

QY 241 RPWYIQGAASPDKMLILVDVSGVSGTGLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300
DB 241 RPWYIQGAASPDKMLILVDVSGVSGTGLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300

QY 301 VSCFQHLVQAVNRKVKLDVANNITAKGIDYKKGFSFAFEQQLNLYNVRANCKITIML 360
DB 301 VSCFQHLVQAVNRKVKLDVANNITAKGIDYKKGFSFAFEQQLNLYNVRANCKITIML 360

QY 361 FTDGGERAQBIFNKNKDKKRVFRSVGOHNVYERGPIONMACENKGYEIPSGAIR 420
DB 361 FTDGGERAQBIFNKNKDKKRVFRSVGOHNVYERGPIONMACENKGYEIPSGAIR 420

QY 421 INTQEYLDVLRPMVLAGDRAKQVQWNTNVLDLELGLVITGTLVPENITQEPENKTNL 480
DB 421 INTQEYLDVLRPMVLAGDRAKQVQWNTNVLDLELGLVITGTLVPENITQEPENKTNL 480

QY 481 NQLILGVMDVDSLEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLPKNKPSQEPVTL 540
DB 481 NQLILGVMDVDSLEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLPKNKPSQEPVTL 540

QY 541 DFLDAELNDIKVEIRKMKIDGSGEKTFTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600
DB 541 DFLDAELNDIKVEIRKMKIDGSGEKTFTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600

QY 601 ALVLPYTFYIYKAKLEETITQARKSKGKDKSETLKPDPNFESGYTFIAPROYCNDLKI 660
DB 601 ALVLPYTFYIYKAKLEETITQARKSKGKDKSETLKPDPNFESGYTFIAPROYCNDLKI 660

QY 661 SDNTEFLNFEIDRKTNNPNSCNADLNRLVLLDAGFTNELVQVWSKQKNIKGVKAR 720
DB 661 SDNTEFLNFEIDRKTNNPNSCNADLNRLVLLDAGFTNELVQVWSKQKNIKGVKAR 720

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## RESULT 2

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CIC2_RAT ID CIC2_RAT STANDARD; PRT; 1091 AA.
AC P54290;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
DE CACNA2D1 OR CACNL2A OR CCHL2A.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228762; PubMed=1314383;
RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
RT "Rat brain expresses an alternatively spliced form of the
dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3251-3253(1992).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
SPLICING.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
A PRECURSOR FORM (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
-----
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CC EMBL; M86621; AAA41088.1; -
DR

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DR InterPro: IPR002035;
DR Pfam: PF00092; tva; 1.
DR PROSITE: PS0234; VWA_DOMAIN; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 944
FT CHAIN 945 1091
FT CHAIN 945 1091
FT TRANSMEM 445 468
FT TRANSMEM 906 930
FT TRANSMEM 1067 1086
FT CARBOHYD 92 92
FT CARBOHYD 136 136
FT CARBOHYD 184 184
FT CARBOHYD 323 323
FT CARBOHYD 347 347
FT CARBOHYD 474 474
FT CARBOHYD 584 584
FT CARBOHYD 593 593
FT CARBOHYD 663 663
FT CARBOHYD 769 769
FT CARBOHYD 812 812
FT CARBOHYD 876 876
FT CARBOHYD 883 883
FT CARBOHYD 973 973
FT CARBOHYD 986 986
FT MOD_RES 500 500
FT MOD_RES 833 833
FT SEQUENCE 1091 AA; 123822 MW; 7054907D9D343B34 CRC64;

Query Match 95.8%; Score 5505; DB 1; Length 1091;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 1040; Conservative 26; Mismatches 23; Indels 2; Gaps 2;

Qy 1 MAAGCLLATLTFLQSLIGSPSEPPSPVAVTIKSWDKMQEDLVLTAKTAGSVNQLVDI 60
Db 1 MAAGCLLATLTFLQSLIGSPSEPPSPVAVTIKSWDKMQEDLVLTAKTAGSVNQLADI 60

Qy 61 YEKQDLYTVEPNARQLVETAAARDIEKLLNSRKALVSLALEAEKVAQAQHWREDFASN 120
Db 61 YEKQDLYTVEPNARQLVETAAARDIEKLLNSRKALVSLALEAEKVAQAQHWREDFASN 120

Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVIEDANFGROIYSQHAHVHTPTDIYEGSTIVL 180
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVIEDANFGROIYSQHAHVHTPTDIYEGSTIVL 180

Qy 181 NELNWTSALEDEVFKKREDEPSSLLWQVFGSATGLARYYPASPVDNSTRPNKIDLYDVR 240
Db 181 NELNWTSALEDEVFKKREDEPSSLLWQVFGSATGLARYYPASPVDNSTRPNKIDLYDVR 240

Qy 241 RPWTIOGAASPDMLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVAFSNSNAQD 300
Db 240 RPWTIOGAASPDMLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVAFSNSNAQD 299

Qy 301 VSCFQHLVQANVRKVKLVKDAVNITAKGIDYKKGFSFAEQLLNNVSRANCKIIML 360
Db 300 VSCFQHLVQANVRKVKLVKDAVNITAKGIDYKKGFSFAEQLLNNVSRANCKIIML 359

Qy 361 FTDGGEERAQEIFKYNKKKRVFRSVSGQHYNTERGPIQWACENKGYEYIIPSIGAIR 420
Db 360 FTDGGEERAQEIFKYNKKKRVFRSVSGQHYNTERGPIQWACENKGYEYIIPSIGAIR 419

Qy 421 INTQEYLDVLRPMVLADGKAKQVQWNTNVLDALELGIVTGLTFVFNITQGFENKTNLK 480
Db 420 INTQEYLDVLRPMVLADGKAKQVQWNTNVLDALELGIVTGLTFVFNITQGFENKTNLK 479

Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKPKSQEPVTL 540

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Db 480 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKPKSQEPVTL 539
Qy 541 DFLDAELENIDKVEIRNKMIDGESGEKFTRLVKQSDERYIDKGNRTYTWTPVNGTDS- 599
Db 540 DFLDAELENIDKVEIRNKMIDGESGEKFTRLVKQSDERYIDKGNRTYTWTPVNGTDS- 599
Qy 600 LALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLPDNPFEESGYTFIAPRDCNDLK 659
Db 600 LALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLPDNPFEESGYTFIAPRDCNDLK 659
Qy 660 ISDNNTTELLAFNERIDRKTNNPCNADLNRVLLDAGFTNELQVNTWSKOKNKGKVA 719
Db 660 PSNNTEFLNFNEFIDRKTNNPCNADLNRVLLDAGFTNELQVNTWSKOKNKGKVA 719
Qy 720 RFVVDGGITRVYPKEAGENQENPETEDSFYKRSNDNDNTVFTAPYFNKSGPAYESG 779
Db 720 RFVVDGGITRVYPKEAGENQENPETEDSFYKRSNDNDNTVFTAPYFNKSGPAYESG 779
Qy 780 IMVSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCV 839
Db 780 IMVSKAVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDVMDCV 839
Qy 840 ILDDGGFLLMANHDDYTNOIGRFGCEIDPSLMRHLVNSVYAFNKSIDYQSVCEPAAPK 899
Db 840 ILDDGGFLLMANHDDYTNOIGRFGCEIDPSLMRHLVNSVYAFNKSIDYQSVCEPAAPK 899
Qy 900 QGAGHRSAYVPSVADILQIGWATAAASILQQLLSLTPFRLLEAVEMEDDDFTASLSK 959
Db 900 QGAGHRSAYVPSVADILQIGWATAAASILQQLLSLTPFRLLEAVEMEDDDFTASLSK 959
Qy 960 QSCITEQTYQFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMWESKGCPCDTRLL 1019
Db 960 QSCITEQTYQFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMWESKGCPCDTRLL 1019
Qy 1020 IOAETSQDPNPMQVOPRYKGPVDCVFNNDVLDYDTCGGVSGNLPSLWYIIGIQFL 1079
Db 1020 IOAETSQDPNPMQVOPRYKGPVDCVFNNDVLDYDTCGGVSGNLPSLWYIIGIQFL 1079
Qy 1080 LWLVSQSGTHRL 1090
Db 1080 LWLVSQSGTHRL 1090

RESULT 3
CIC2_RABIT STANDARD; PRT; 1106 AA.
AC P13806;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Oryctolagus cuniculus (Rabbit);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88336904; PubMed=2458626;
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,
RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A.,
RA Schwartz A., Harpold M.M.;
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2
RL subunits of a DHP-sensitive calcium channel.";
RN Science 241:1661-1664(1988).
RP [2]
RP SEQUENCE OF 961-973.
RX MEDLINE=91131638; PubMed=1847144;
RA Jay S.D., Sharp A.H., Kahl S.D., Vedvick T.S., Harpold M.M.,
RA Campbell K.P.;
RT "Structural characterization of the dihydropyridine-sensitive calcium

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RESULT 4
UN36_CAEEL STANDARD; PRT; 734 AA.
AC P34374;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE UNC-36 PROTEIN.
GN UNC-36 OR UNC-72 OR C50C3.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderidae; Caenorhabditis.
OX NCBI_taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohlschlag P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38 (1994).
CC -1- SIMILARITY: TO CALCIUM CHANNEL ALPHA-2B SUBUNIT.
CC -----
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CC -----
DR EMBL; L14433; AAA27969.1; -
DR PIR; S44617; S44617.
DR WormPep; C50C3.11; CE00117.
DR InterPro; IPR002035; -
DR Pfam; PF00092; vva; 1.
DR PROSITE; PS0234; VVFA_DOMAIN; 1.
KW Ionic channel; Ion transport; Voltage-gated channel; Calcium channel;
KW Glycoprotein.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 734 AA; 85034 MW; CCFB78C8DE4B7F CRC64;

Query Match 10.6%; Score 607; DB 1; Length 734;
Best Local Similarity 26.6%; Pred. No. 8.9e-28;
Matches 180; Conservative 127; Mismatches 258; Indels 112; Gaps 20;

QY 47 LAKTAGSNQNLVDIYEQDLYTEPNARQVLEAARDIEKLNSRS-----KALVSLAL 102
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
36 MKEFTKISHETILKQNEKLEVEEQFPRAELKSKHRIEDYLVRSQFAYKAKIS--L 93
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
103 EAEKQVAAHQREDFASNEVYVYNAKDDLPDK-NDSEFGSQRIKP-----VFTDANF 155
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
94 EARSVRNDSTVNDPQSKSFIRFMSAKQNGDGTIYESNHLGKRLKLVNETKSFNLQANF 153
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
156 -GRQISYQAAHVHPTDIYESTVNLNWTSLDVEFKKNREDDPSLLNQVFGSATGL 214
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 154 YTLPTSSVSSAVHIPTPLYDRNEDLLRKIDW-SDIDAVYRTNREETKDIAFQFCSEAY 212
QY 215 ARYPASPWW-DNSRTPNKIDLYDVRRRPWYIQGAASPKDMLILVDVSGVSLTKLIR 273
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
213 MEYYPAAWFWNQ--DEHLDLDFDCRNTWYINSATNSKNVLLMDMSGMLGORVEVAK 270
QY 274 TSVSEMLETSDDDDFVNVASFNSNA---QDVSCFQHLVQANVRNKVLKADVNNITAKGI 330
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
271 QTTEAILLETLSHNDYFNIMTFSKNTFLDCCNGTNGLLQATWRNKKALRRKMDTYQSEK 330
QY 331 TDYKKGFSFAFOLLNYN-----VSRANCKIIMLTFTDGEERAQEIFKNYKNDKKRVYF 385
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
331 ABEYKALPFAFSVLLDINGGDNRRGACENVIMLTIDGAPNAYKIFDMYNADKKRVF 390
QY 386 RFSVGQHNYERGIQWMACENKGYIYEIPSGAIRINTQEYL-----DVLGRPMVLAGDKA 441
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
391 TFLVGDGAIDFNEVREMACNRRGYVHVANMADVDEKIHYYIRMSRVVGRHYKESGQLS 450
QY 442 KOVQNTNYVLDALGL--VITGTLPVFNITQGFENKTN----- 478
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
451 ---WWTGVYRERLYLPRPEIFAEPVITNQSPAVNMKASRRKIRLQKSEARSMEFTTV 507
QY 479 ----LKNOLLILGVMGVDSLEDIKRLTPRETLCPNGYFAIDPNGYVLLHPNLQKNP-- 532
Db 508 SYPVIVNETFMGAAVNIPLTEVAQKSHPANIGSKSYFFMLDQNGFVMTHPQLRPIDPFT 567
QY 533 --KSEPTVTLFDL-----AELENDIKVEIRNKMD 561
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
568 KYHKQYNNMDELLEVGQNVNRSSQKSVQSVDLVCSGANVAECVDLLRAVRKMIID 627
QY 562 GESGEKTFRLVKSQDERY----IDK---GNRTYVTPVNGTDYSLALVLPYFSFYIKA 614
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
628 CDNSD-----VQQLDVLVYATELLDRVTPQTNTTYAACINHANFVLGLAVARGDDYRVYK 681
QY 615 KLEETITQARSKGKMK 631
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
682 K-----QKKYDFGRVK 692

RESULT 5
ITH3_MOUSE STANDARD; PRT; 886 AA.
AC Q61704;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY
DE CHAIN H3).
GN ITIH3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=Liver;
RX MEDLINE=95194326; PubMed=7534067;
RA Chan P., Risler J.-L., Raquez G., Sallier J.-P.;
RT "The three heavy-chain precursors for the inter-alpha-inhibitor
RT family in mouse: new members of the multicopper oxidase protein group
RT with differential transcription in liver and brain."
RL Biochem. J. 306:505-512(1995).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONIN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONIN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.

```

[illegible]







DR Pfam: PF00092; vwa: 1.  
DR PROSITE: PS50234; VWFA\_DOMAIN: 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 21 POTENTIAL.  
FT PROPEP 22 33 BY SIMILARITY.  
FT CHAIN 34 647 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
FT FT  
FT PROPEP 648 887 BY SIMILARITY.  
FT DOMAIN 282 442 VWFA.  
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT BINDING 647 647 CHONDROITIN 4-SULFATE, CROSS-LINK SITE  
FT (BY SIMILARITY).  
SQ SEQUENCE 887 AA; 99097 MW; 389F0FF96D514096 CRC64;

Query Match 3.1%; Score 180.5; DB 1; Length 887;  
Best Local Similarity 18.5%; Pred. No. 0.0052;  
Matches 173; Conservative 139; Mismatches 350; Indels 275; Gaps 39;

QY 27 FFSATYIKSWDKQEDLYLAKTAGSVNQLVDIYKQDLYTVEPNARQLVEIARADI 86  
DB 101 YPGSVKEVAQKQYKAVSQGKTAG---LVKASGRKLEKFTSVNVAAGSKVIFELTY 156  
QY 87 EKLNSRKALVSLALEAKVQAAHOWRED---FASNEVVYVNAKDDLDPEKNDSEPGSQ 143  
DB 157 EELL-KRNGKYEYKQPKQLVHFHEDAHIFEPQGISMLDA----- 199  
QY 144 RIKPFIEDANFGROISYOHAAVHIPTDIYEGSTIVLNELNWTLSALDEVFKKNREEDPSL 203  
DB 200 -----DASE-----ITNDL-LGSALTAKSF----- 217  
QY 204 LMQVGSATGLARYPASVWNSRT-PNKID-----LYDVRRP-----WY 244  
DB 218 -----SGKGHVSFPLSPQDSQSCPTCTDSLLGDFTIYDVNRESPGNVQVINGYF 269  
QY 245 I-----QG-AASPDKMLIYDVSGVSGTLKLTISVSEMETLSDDDFVNVAFSNSA 298  
DB 270 VHFAPQGLPVVPKNIATFIDVSGMSGKRIQOTREALKILDDMKEDYLFILFSTGV 329  
QY 299 QDVSCFQHLVQAVNRNKKYKDAVNNTAKGTIDYKGFSAFEOELNLYNVRAN----- 353  
DB 330 --TTWKDLVVKATPANLEARAFVKNIRDSNTNINDGLRGIEL--NKAREHLYPE 384  
QY 354 -CNKIIMLTGQ-----GEERAQEIFKNKKVRFPSVG-QHNYERGPQWACENK 407  
DB 385 RSTSLVMTDGTANTGESRPEKIOENVRNAIRKFPPLYNLGFNGNLYNLESLEALNH 444  
QY 408 GYYPEIPSGAIRINTQYDLVGRPMVLGAKQVQVNTVYLDLLEGL--VITGTLPL 465  
DB 445 GFARRIYEDSASLOQGYEEVAPLL-----TNELEYEPENAILDLTRNSYP 493  
QY 466 VFNITQFENKTNKLNILVGMVDVSLDIKRLTPFCNGYFAIDPNGYVLLHP 525  
DB 494 HP-----YIG-----SEIVVAGRLVDRVND-----FRADVKHGHALN- 526  
QY 526 NLOPKNPKSQEPVTLDFDALENDIKVEIRNMIDGESGKTF-----RTLVKSQDER 579  
DB 527 -----DLTTEEDVMKEMDAALK-----EQGYIFDGYIERLWAYLTTEQLLEKRNAR 574  
QY 580 YIDKGNRTTTPVNGTDSLVA--LVLPYSFYIKAKLEETITQARSKGKMKOSET-- 635  
DB 575 GDEKENIT-----AEALELSLKYHFVTLPTLSMVVTVPEDNEQDTALADPGBEAISASTA 629  
QY 636 -LAPDNFEESGYTFIAPRYCNDLKSIDNNTPELLNF---NEFIDRKTNPNSCNADLN 691  
DB 630 YLTSQOSSHSPIYY-----DGDPHFIQVPGKNDITICNIDEKPGCTVLUSLQ 677  
QY 692 RVLIDAGFTNELQYVWSKQKNIKGVKARFVVDGGITRVYKPEAGENQENPETYEDSF 751  
DB 678 DPTVGIATVQII-----GEKGNASRTCKT----- 704

QY 752 YKRLSDNDNVFTAPYFNKSGPGAYESIMVSKAVEIYIOGKLLKPAVVVGIKIDVNSWIE 811  
DB 705 -----YFGKLGCIANAWMDFRLEVTEKILGN-----GDALSTFSWLD 742  
QY 812 NFTKYSIRDCAGPVCDCRNSDVMDCVILDDG-GFLMAN-----HDDYTNQIGRF 862  
DB 743 TVTVTQ-----TGLSVTINRKKNMV--VSFDDGISFVILVHQVWKKHVPVHQDFLG----- 790  
QY 863 FGEIDPSLMRHLVNLVSVAFNKSYDYQSV-CEPGAAP 898  
DB 791 FYVDVSHRMSAQTHGLLGQFFQFPDFKVDVVRPGSDP 827

RESULT 8  
ITH3\_MESAU STANDARD; PRT; 886 AA.  
ID ITH3\_MESAU  
AC P97280;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY  
DE CHAIN H3) (HC3).  
GN ITH3.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=97420688; PubMed=9276673;  
RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;  
RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain  
RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:  
RT implications for the evolution of the inter-alpha-trypsin inhibitor  
RT heavy chain family";  
RL J. Biochem. 122:71-82(1997).  
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY  
CC SIMILARITY).  
CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.  
CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY  
CC SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL: D89287; BAA13940.1;  
CC InterPro: IPR002035;  
DR Pfam: PF00092; vwa: 1.  
DR PROSITE: PS50234; VWFA\_DOMAIN: 1.  
KW Serine protease inhibitor; Repeat; Signal; Multigene family;  
KW Glycoprotein.  
FT SIGNAL 1 18 POTENTIAL.  
FT PROPEP 19 30 BY SIMILARITY.  
FT CHAIN 31 646 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
FT H3.



Db 867 NGEVFKVIGETIDRYMEBQKDKVTDVNTDTEVLDNIFAFSLNKESKSEIKKVKAL-- 924

QY 723 VTDGGITRVYPKEAGE 738

Db 925 -----IRHKYGEAYE 935

RESULT 10

ATX1\_PLAFA

ID ATX1\_PLAFA STANDARD; PRT; 1956 AA.

AC Q04956;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE PROBABLE CATION-TRANSPORTING ATPASE 1 (EC 3.6.1.-).

OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI\_TaxId=5833;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-T9/96;

RX MEDLINE=93132070; PubMed=8421054;

RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,

RA Robson K.J.;

RT "A family of cation ATPase-like molecules from Plasmodium

RT falciparum";

RL J. Cell Biol. 120:385-398(1993).

CC -/- CATALYTIC ACTIVITY: ATP + H(2)O -&gt; ADP + ORTHOPHOSPHATE.

CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

CC -/- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2

CC ATPASES). SUBFAMILY V.

CC -----

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CC -----

CC EMBL: X65738; CA446646.1; -

DR InterPro; IPR001757; -

DR Pfam; PF00122; E1-E2\_ATPase; 4.

DR PROSITE; PS00154; ATPASE\_E1\_E2; 1.

KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.

FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 36 58 POTENTIAL.

FT DOMAIN 59 61 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 62 80 POTENTIAL.

FT DOMAIN 81 407 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 408 427 POTENTIAL.

FT DOMAIN 428 440 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 441 462 POTENTIAL.

FT DOMAIN 463 1818 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1819 1837 POTENTIAL.

FT DOMAIN 1838 1845 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1846 1863 POTENTIAL.

FT DOMAIN 1864 1881 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1882 1905 POTENTIAL.

FT DOMAIN 1906 1928 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1929 1952 POTENTIAL.

FT DOMAIN 1953 1956 CYTOPLASMIC (POTENTIAL).

FT MOD\_RES 496 496 PHOSPHORYLATION (PROBABLE).

FT METAL 1760 1760 MAGNESIUM (BY SIMILARITY).

FT METAL 1764 1764 MAGNESIUM (BY SIMILARITY).

FT DOMAIN 246 251 POLY-ASN.

FT DOMAIN 252 256 POLY-LYS.

FT DOMAIN 937 941 POLY-ASN.

FT DOMAIN 1344 1347 POLY-LYS.

FT DOMAIN 1363 1372 POLY-ASN.

FT DOMAIN 1680 1684 POLY-ASN.

SQ SEQUENCE 1956 AA; 230285 MW; AE708AAE99009335 CRC64;

Query Match

Best Local Similarity 2.8%; Score 159; DB 1; Length 1956;

Matches 179; Conservative 144; Mismatches 359; Indels 366; Gaps 45;

QY 58 VDIYEKYQDLYTVEPNNAQVLEIAARDIEKLKLSNR-----SKALVSLALEAEK 106

Db 100 INVY-RYNTSYIISSS-----ELVPGDIYEIKNNMTIPCDTIILSGSVTMEHMLTGES 152

QY 107 VQAQHQRWEDFASNEVYVNAKDDLDPEKD-----SEPGSORIKPVFIEDANFGROIS 160

Db 153 V-PIHKERLFFEGNAIINKNNKYSNDEKDDYLRYYNNHASIMIKRNLHIEETLCKKOR 211

QY 161 YQHAHVHIPTDIYEGSTIVLNELNW-TSALDEVFKNREEDPSLLMQVFGSATGLARYYP 219

Db 212 EYKSNTH-----DLCSMNKLCYNNIYDDVHKNNKMD----- 244

QY 220 ASPWVDNSTPNKIDLYVRRRPWTIQGA-ASPKDMLILVDVSGSVGLTKLI RTSVSE 278

Db 245 ---YNNNNNNKKKKINLN---FVKGTIINSNLLY----- 275

QY 279 MLETLSDDDFVNVASFNSNAQDVSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFS 338

Db 276 -----DDKIGVNIFF---DDVNNMKH---KFNQRNINYNKDTNNL-----EYNNKIR 317

QY 339 FAFEOQLNYNVRANCKIIMLFTDGEERAQIFNKYNKDKKRVRFVSQGHNYERGP 398

Db 318 YIYDCLLKVEAISQKNKIY-----SNEDINKY----- 346

QY 399 IOWMACENKGYEYIPEISGAIRINQOEYLDVGRPMVLAG-----DKAKQV 444

Db 347 ----MLYGGTVVLSYLNKIKYNNKEENRIIGL-VIKTGFITTKGIVNNILYHKKEL 401

QY 445 QWTVNYDLALEGLVITGTLVPFNTIGQFENKTNLKNOLIG-----V 487

Db 402 NLINDSYKELII-LIYALFSVILYILYSNNYTHIIKCLDIITDAIPALPTILT 460

QY 488 MGVDSLEIDKRLTPRTICPGNYIFA-----IDPNGYVLLHPNLQ-----PKMKPSQ 535

Db 461 VGISAISRLKKKFSICSLCPHKINIAGQINTMVPDKTG-TLTENNLFQIGIITQNKKNK 519

QY 536 EPVTLDFDAELENDIKVEIRKNKMDIGESGEKTFRLVLVSQDERYIDKGNRYTWTVPNG 595

Db 520 NMLS-DFIHK-----EMNTESIYHSKDDNNIHNKN----- 549

QY 596 TDSLALVLTYSFYVYKAKLEETITQARSKGKMKD-----SETLKPDPNEESG 645

Db 550 -----SIIEYIKDNMKNLHTSSK-KKSITKERSNFLVQTIKSCLLKDHYIEKK 599

QY 646 YTFIAPRDYCNLKDINN-TEFLN-----FNEF--IDRKTNNPNSCNADLINRVLD 696

Db 600 KEYTNTYCNLDHINDSTCSSYLLNSETKDAYCEYNNIDH-----LCD---INKNMD 650

QY 697 AGFTNELVQNYWSKQNIKGVARFVVTGGITRVYPKEAGENQWENPETEYDSFKRSL 756

Db 651 INSKNELMGKYSKNELMGTKITNELM-----GKYSKNEL 684

QY 757 DNDNYVFTAPYFNKSGPAYESIMVSKAVEIYIOGKLLKPAVVG-----IKIDVNSWI 810

Db 685 -----MGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNEL 737

QY 811 ENFTKTSIRD-PCAGPVCDCKRNSDYMDCV-----ILDDGGFLMANHDDYTNIGRF--- 862

Db 738 MNCNDNYNDYPCD---YNNCNCNDYHRLHYHNKDNSFNIPPEKNKSYNNISEHIKI 794

QY 863 -----FGEIDPSLMRHLNIVSVAF-----NKSIDYQ 889

Db 795 NYPLLEALACCHTILSKVNNKIMGDVLEILMFNTCDMLNNNSFIIEKKKNCSDYEQ 854

QY 890 SVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAWSILOQFLSLTFLPRLEAVE 949

Db 855 KI---DGDKNIGANDERCHLNN-----NLVSYNLIKRF----- 884



[6] SEQUENCE OF 55-64.  
 RN TISSUE-Plasma;  
 RC MEDLINE=93039735; PubMed=1384548;  
 RA Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,  
 RA Tartar A., Fournet B., Mizon J.;  
 RA "the heavy chains of human plasma inter-alpha-trypsin inhibitor: their  
 RT isolation, their identification by electrophoresis and partial  
 RT sequencing. Differential reactivity with concanavalin A";  
 RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).  
 [7]  
 RN SEQUENCE OF 55-64 AND 681-702, AND CROSS-LINK STRUCTURE.  
 RX MEDLINE=93232026; PubMed=7682553;  
 RA Enghild J.J., Salvessen G., Thøgersen I.B., Valnickova Z.,  
 RA Pizzo S.V., Hetta S.A.;  
 RA "presence of the protein-glycosaminoglycan-protein covalent cross-link  
 RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain  
 RT 2/bikunin";  
 RL J. Biol. Chem. 268:8711-8716(1993).  
 [8]  
 RN SEQUENCE OF 67-101, AND HYALURONAN BINDING.  
 RC TISSUE-Serum;  
 RX MEDLINE=94075371; PubMed=7504674;  
 RA Huang L., Yoneda M., Kimata K.;  
 RA "A serum-derived hyaluronan-associated protein (SHAP) is the heavy  
 RT chain of the inter-alpha-trypsin inhibitor";  
 RL J. Biol. Chem. 268:26725-26730(1993).  
 [9]  
 RN SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.  
 RC TISSUE-Plasma;  
 RX MEDLINE=94229087; PubMed=7513643;  
 RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,  
 RA Chmalkski C., Fournet B., Mizon J.;  
 RA "Chondroitin sulphate covalently cross-links the three polypeptide  
 RT chains of inter-alpha-trypsin inhibitor";  
 RL Eur. J. Biochem. 221:881-888(1994).  
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A  
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,  
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE  
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE  
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.  
 CC -1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM  
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, H2  
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2  
 CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND  
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.  
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN  
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.  
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 VMFA DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; X07173; CAA30160.1; ALT\_SEQ.  
 DR EMBL; M18193; RAA60558.1; --  
 DR EMBL; M33033; AAA59195.1; --  
 DR PIR; S00346; IYHU2.  
 DR PIR; B34245; B34245.  
 DR GlycoSuiteDB; P19823; --  
 DR MIM; 146640; --  
 DR InterPro; IPR002035; --  
 DR Pfam; PF00092; vwa; 1.  
 DR PROSITE; PS50234; VMFA\_DOMAIN; 1.  
 DR Serine protease inhibitor; Repeat; Signal; Multigene family;  
 KW Glycoprotein.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 54

FT	CHAIN	55	702	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2.
FT	PROPEP	703	946	VMFA.
FT	DOMAIN	308	468	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	118	118	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	445	445	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	671	671	CARBOXYLATION.
FT	MOD_RES	282	282	CARBOXYLATION.
FT	MOD_RES	283	283	CHONDROITIN 4-SULFATE, CROSS-LINK SITE.
FT	BINDING	702	702	CHONDROITIN 4-SULFATE, CROSS-LINK SITE.
FT	CONFLICT	674	674	P -> A (IN REF. 2 AND 3).
FT	CONFLICT	705	705	F -> S (IN REF. 2 AND 3).
FT	CONFLICT	729	729	N -> D (IN REF. 2 AND 3).
FT	CONFLICT	731	731	V -> A (IN REF. 2 AND 3).
FT	CONFLICT	374	374	K -> L (IN REF. 5).
FT	SEQUENCE	946 AA;	106436 MW;	1478CF3E8F3BA776 CRC64;

Query Match 2.7%; Score 154.5; DB 1; Length 946;  
 Best Local Similarity 19.9%; Pred. No. 0.18;  
 Matches 133; Conservative 106; Mismatches 259; Indels 171; Gaps 29;

QY	33	IKSWDKMOEDLVTLAKTAGSVNOLVDIYKQDLYTVEPNNAQQLVEIAARDIEKLISN 92
Db	26	LSEFVD--YEDVLVEL---APGKQLVAENRRYQRLSGESEMEEVDQVTLYSYKQVST 80
QY	93	RSKALVSLALEAEKVQAAHQWRE-----DFASN-----EV 122
Db	81	ITSRMATTMIQSKVNNSPQPNVFDVQIPKGAFFSNFMTVDGKTRSSIKETKTVGRA 140
QY	123	VYINAK-----DDLDEPKNDSE---PGSQRKIPVFIEDANFGROISYQH--- 163
Db	141	LYAQAARAKGTAGLVRSALDMMENFRTEVNVLPKAGVQFELHYOEVRKRLGSTEHRILY 200
QY	164	----AAVHIPTDIEGSTIVLNELNMTSALD-----EVFKKNREE-----DPSLLMQVF 208
Db	201	QPGELAKHLEVDVWVIEPQGLRFLHVPDTFEGHDGVPVLSKGOQKAHVSEKFPVAAQ-- 258
QY	209	GSATGLARYYPASFWVDNSRTPNKIDLYDVRRP-----WYIQGAAS-----PK 252
Db	259	-----RICPSCR--ETAVDGELVLYLVKREKAGELEVFGYFVHFAPDNLDPK 309
QY	253	DMLLLVDVSSVSLTKLIRTSVSEMLETSLDSDDDFVNVASFNSNAQDVSCFQHLVQANV 312
Db	310	NILFVIDVSGMMGVKMKQVTEAMKTIILDLRAEDHFSVIDFNQIR--TWRNDLISATK 367
QY	313	RNKKVLKDAVNNITAKGITYKKGF---SEAFQQLNMYNSRANCKIIMLETDG---G 365
Db	368	TQVADAKRYTEKTPSGGTNINEALLRAIFILNEANNLGLDPSVSLIILVSDGDTVG 427
QY	366	EERAQEIFNKYNKDKKVRVFRFSVQ-----HNYERGIQWM-----ACENK 407
Db	428	ELKLSKIQKNVENIQDNISLFLSGMGFDVYDFLKLRLSNENHGIAQRIYGNQDTSQLK 487
QY	408	GYVEI--PSIGAIRIN--TQEVLDVL-----GRPWVLG--DKAKOVQVNTYLD 452
Db	488	KFYQNVSTPLLRNVQFNYPHTSVTDVTQNNFHNFGYSEIYVAGKFDPAK-----LD 539
QY	453	ALELGLVITGTLVPFNTITGQFNKTNLKNQILGVMGVDSLEDI-----KRLTFRFTLCP 508
Db	540	QIE--SVITA-----TSANTQVLVLETLAQMDLQDFLSKDKHADPFR-K 582
QY	509	NGYFAIDPNGYVLLHPNLQPKPKSQEPVTLDFDLAELENDIKVEIRNMKIDEGSEK 568
Db	583	LWAYLTIN--QLIAERSLAP-TAAAKRRITRSLQMSLDHIVTTLTSLVIENAEAGDER 638
QY	569	FRLVKSQD 577;
Db	639	MLADAPPQD 647

RESULT 13  
 BXCL\_CLOBO

ID AC BXCL\_CLOBO STANDARD; PRT; 1290 AA.  
DT P18640;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE BOTULINUM NEUROTOXIN TYPE C1 PRECURSOR (EC 3.4.24.69) (BONT/C1)  
DE (BONTOLYLIN C1)  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90370487; PubMed=2204031;  
RA Hausser D., Exlund M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,  
RA Boquet P., Popoff M.R.;  
RT "Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";  
RL Nucleic Acids Res. 18:4924-4924(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TYPE C STOCKHOLM / C-ST;  
RX MEDLINE=91024998; PubMed=2222445;  
RA Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,  
RA Yokosawa N., Takeshi K., Syuto B., Oguma K.;  
RT "The complete nucleotide sequence of the gene coding for botulinum  
type C1 toxin in the C-ST phage genome.";  
RL Biochem. Biophys. Res. Commun. 171:1304-1311(1990).  
RN [3]  
RP SEQUENCE OF 2-25.  
RC STRAIN=TYPE C STOCKHOLM / C-ST;  
RX MEDLINE=88153072; PubMed=2450068;  
RA Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,  
RA Oguma K.;  
RT "Establishment of a monoclonal antibody recognizing an antigenic site  
common to Clostridium botulinum type B, C1, D, and E toxins and  
tetanus toxin.";  
RL Infect. Immun. 56:898-902(1988).  
RN [4]  
RP IDENTIFICATION OF SUBSTRATE.  
RX MEDLINE=94038966; PubMed=7901002;  
RA Blas J., Chapman E.R., Yanasaki S., Binz T., Niemann H., Jahn R.;  
RT "Botulinum neurotoxin C1 blocks neurotransmitter release by means of  
cleaving APC-1/syntaxin.";  
RL EMBO J. 12:4821-4828(1993).  
CC -|- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER  
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED  
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD  
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT  
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC  
ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.  
CC -|- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A  
HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,  
WHILE THE N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL  
FORMATION AND TOXIN BINDING, RESPECTIVELY.  
CC -|- SUBCELLULAR LOCATION: SECRETED.  
CC -|- MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF  
BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.  
CC -|- MISCELLANEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C  
STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE  
BACTERIOPHAGE.  
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC  
METALLOPROTEASES); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN  
SUBFAMILY.  
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CC -----  
CC EMBL; X66433; CAA47060.1; -

DR EMBL; X72793; CAA51313.1; -  
DR EMBL; X53751; CAA37780.1; -  
DR EMBL; D90210; BAA14235.1; -  
DR EMBL; X62389; CAA44263.1; -  
DR PIR; S11291; S11291.  
DR PIR; A35396; A35396.  
DR PIR; A43503; A43503.  
DR MEROPS; M27.002; -  
DR InterPro; IPR000130; -  
DR InterPro; IPR000395; -  
DR Pfam; PF01742; Peptidase\_M27; 1.  
DR PRINTS; PR00760; BONTOLYLIN.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.  
FT INIT\_MET 0  
FT CHAIN 1 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN.  
FT METAL 449 1290 BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN.  
FT METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 229 229 BY SIMILARITY.  
FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).  
FT DISULFID 436 452 INTERCHAIN (PROBABLE).  
FT CONFLICT 84 84 P -> T (IN REF. 2).  
SQ SEQUENCE 1290 AA; 148734 MW; 71FBE379F97129E8 CRC64;  
  
Query Match 2.6%; Score 152; DB 1; Length 1290;  
Best Local Similarity 20.3%; Pred. No. 0.4;  
Matches 205; Conservative 125; Mismatches 346; Indels 334; Gaps 54;  
  
QY 106 KVOAAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSQRK---PVFIEDANFGR----- 157  
DB 138 KTRQNNWVKGSINPSVIITG-----PRENIIDETSTFKLTNTTFAAQEGFGALSIIS 192  
QY 158 -----QISYQHAHVPTDIYEGS-----TIVLNELNMTSALDEVK---KNRE 198  
DB 193 ISPREMLYSNAT---NDVGEGRFSKSEFCMDPILILMHELN--HAMHNLGYIAPNDQ 246  
QY 199 EDPSSLQVFGSATGLARYP-----ASPVDNSTPNKIDLYDVRRRPWYTGGAASPKD 253  
DB 247 TTSSTVTSNIFYSQYNVKLEYAEIYAFGGPTID--LIPKSARKYFEKALDYRSRAKRLN 304  
QY 254 MLILVDVSG---SVSGSLTLKLIR-----TSVSEMLETLSDDDFYNVASFNADVSCF 304  
DB 305 SITTANPSFNKYIGYKQKLIRKYRFVVSSEGEV--TVNRKRFVEL--YNELTQIFTEF 360  
QY 305 QHLVQANVRNKKV-LKDAVNNTAK---GITDYKKGFSFAFEQL-----LNVNVR----- 351  
DB 361 NYAKIYVQNKKIYLSNVYTPVTANILDDNVYDIQNGFNIPKSNLNLVFMGQNLSPAL 420  
QY 352 --ANCKIMLFT-----DGGEERAQEIFNK-----YNKD-----KKVVRP 386  
DB 421 RKNVPENMLYLFTEFKCHAIDG-----RSLYNKTLDRELLYKNTDLPFIGDISVKTDI 475  
QY 387 FSVGQHNYERGPIONMACENKGYVEIPSIGAIRI--NFOEY--LDVL----- 430  
DB 476 FURKIDNEETVI-----YYPDNVSDQVILSKNTSEHGQDLLYPSIDSEILP 526  
QY 431 GRPMVLADKAKOVQWNT--VYLDALGLVITGTLPVFNITGQFNKTN----- 478  
DB 527 GENQVYDNRNTQNDYLSNYYSLEOKL-----SDNVDEFTFTRSTEEALDNSAKVYTFP 582  
QY 479 -LKNQLILGVMG-----VDVSLIEDIKRLTRFPLCPNGYFAIDPNGYVLLHNPLOPK 530  
DB 583 TLANKVNAVQGLFLMWANDVVEFTTNILRKDLDKISDVSAIIP-----YIGPALNIS 638  
QY 531 NPKSDEPTVLDP-----LDAELENDI-----KVEIRNKMDGESGEKTFRL 572  
DB 639 NSVRGNFTFAVGTGVTILLFAFPFETPALGAFVYSKVQVERNEII-----KTIDNC 692  
QY 573 VKSQSDERYDKGNRTYTW-----TPVNGTDYSLALVLPYTSFYVIKAKLEETITQ 622  
DB 693 LQRIKRWKD---SYENWMTWLSRIITQFNNISQMYDSL-NYQAGAIAKAKID----- 742

QY 623 ARSKGKMKDSELPK--DNFESGYTFIAPRDYCNLDKISDNNTTEFLNNEFI----- 675  
DB 743 LEYKYSKSGDKENIKSOVENLKN-----LDVKIS-----EAMNNINKFIRECSV 787  
QY 676 -----DRKTPNPNNSCADLINRVLLDA----- 697  
DB 788 TYLFKNMLPKVIDELNEFORNT-----RAKLIN--LIDSHNIIIVGEVDKILKAKVNNFSF 839  
QY 698 -----GFTN-----ELVQNYW-----SKOKNIKGYKARFVYTDGITRYVPKEAGE 738  
DB 840 QNTIPNFISYTNNSLLKDIINEYFNINDSKILSQNRKNTLVDTS-----YNAEYSE 894  
QY 739 --NQENPERYEDSFYKRSLDNDVYFTAPYFNKSGPGAYESGIMVSKAVEYIYQKILK 796  
DB 895 EGDVQLNP-----IF--PFDEKLSSGEDRGKVIYQENIYVNSWYE 935  
QY 797 PAVYGKIDVNSWIENTKTSIRDCAGPVCDCRNSDVMDVLDGDFLLMANHD----- 853  
DB 936 SFSISFWIRKNSVNLPGVTIID-----SVKNNSGWSIGIISNLFVTLKQNEDESEQ 988  
QY 854 -----DYTNQIGR-----PFGEIDPSLMRLHLNIVSYAFNKSVDYQSVCE 893  
DB 989 SINFSDISNNAFGYNKWFVVTNNMVG---NMKIYINGKLIDTIKVKRE 1035

## RESULT 14

Y103\_SYNY3  
ID Y103\_SYNY3 STANDARD; PRT; 420 AA.  
AC Q55874;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HYPOTHETICAL 45.8 KDA PROTEIN SLL0103.  
GN SLL0103.  
OS Synecochystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synecochystis.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96127529; PubMed=8590279;  
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
Sugiura M., Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
Synecochystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
region from map positions 64% to 92% of the genome.";  
RL DNA Res. 2:153-166(1995).  
CC -1- SIMILARITY: TO E.COLI YF8K.  
CC  
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CC  
CC EMBL; D64004; BAA10635.1; --  
DR InterPro; IPR002035; --  
DR Pfam; PF00092; vwa; 1.  
DR PROSITE; PS50234; VWFA\_DOMAIN; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 420 AA; 45849 MW; E7111B51478E74F3 CRC64;

Query Match 2.6%; Score 151.5; DB 1; Length 420;  
Best Local Similarity 20.8%; Pred. No. 0.085;  
Matches 85; Conservative 85; Mismatches 183; Indels 55; Gaps 16;  
QY 251 PKDMLIVDVSGSVGTLTKLRTSVSEMLETSDDDFVNVASFNSNAQDVSCFQHLVQA 310  
DB 41 PLNLCVLDSHSGMDGQPLETKVSAALGLDRLEEDDLRLSVAFDRHRAKIV-----IENQ 95  
QY 311 NVRNKKVLKDAVNNTAKGITDYKGFSAFEQLLNIVNSRANCKIIMLFTDGGERAQ 370

DB 96 QVRNGAATAKATERLAKGEGTAIDEGKLIGQEAAGKREDRVs---HIFLLTDGENEHD 152  
QY 371 E-----IFKNYKDKKVRVRFESVGOHNYERGPIONMACENKG--YYEIPSGAIRINTQ 424  
DB 153 NDRCKLKTVASDYKLTVHTLGFGDH-WNQDVLEAIAASAQSLSYIENPS-EALHTFRQ 210  
QY 425 EYLDVLRPMVLGDKAKQVQWTVNYLDALGLG-----LVITGTLVPFNITGFENKTNLK 480  
DB 211 LF-----QRMSNVGLTNAHL-LLELAPOAHLAI--VKPAQVSPETMDLT-VQ 254  
QY 481 NQLILGVGVDSLEDIKRLTPRFTLCRPNGYFAIDPNGYVLLHNPLOPKNKSOE----- 536  
DB 255 NQGAEEVRLGLMDTQERV-----LLNLNLYDQLLPGOHVIGQVQIRYDDPASGOTNLL 309  
QY 537 ----PVTLDLDALENDIKVEIRNMIDGESGKT--PRTLVKSODERYIDKGNRTYTW 590  
DB 310 SDPLPLTIQ-VOTQYQSPDVQVQESILTLAKYRQTIAETKLKAGDRGAATMLQTAAK 368  
QY 591 TPVNGTDYSLALVLTYSFYIKAKLEETITQARSKKGMKDSITLKP 638  
DB 369 TALQMGDKNGATILQTN-----TRLQSGEDLSEGDKKTRMVKSTLIQ 413

## RESULT 15

ITH4\_PIG  
ID ITH4\_PIG STANDARD; PRT; 921 AA.  
AC P79263;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY  
DE CHAIN H4) (INTER-ALPHA-TRYPsin INHIBITOR FAMILY HEAVY CHAIN-RELATED  
DE PROTEIN) (IHRP) (MAJOR ACUTE PHASE PROTEIN) (MAP).  
GN ITI4 OR IHRP.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-36; 695-703 AND 710-722.  
RX TISSUE=Liver;  
RC MEDLINE=96271024; PubMed=8830057;  
RA Hashimoto K., Tohe T., Sumiya J.-I., Sano Y., Choi-Miura N.-H.,  
Ozawa A., Yasue H., Tomita M.;  
RT "Primary structure of the pig homologue of human IHRP: inter-alpha-  
RT trypsin inhibitor family heavy chain-related protein.";  
RL J. Biochem. 119:577-584(1996).  
RN [2]  
RP PRELIMINARY SEQUENCE OF 267-556 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=90371455; PubMed=1697703;  
RA Buchman T.G., Cabin D.E., Vickers S., Deutschman C.S., Delgado E.,  
Sussman M.M., Bulkeley G.B.;  
RT "Molecular biology of circulatory shock. Part II. Expression of four  
RT groups of hepatic genes is enhanced after resuscitation from  
RT cardiogenic shock.";  
RL Surgery 108:559-566(1990).  
RN [3]  
RP SEQUENCE OF 28-54 AND 223-240.  
RC TISSUE=Serum;  
RX MEDLINE=96013138; PubMed=7556597;  
RA Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A.,  
Garcia-Gil A., Lampreave F., Pineiro A.;  
RT "The major acute phase serum protein in pigs is homologous to human  
RT plasma kallikrein sensitive PK-120.";  
RL FEBS Lett. 371:227-230(1995).  
CC -1- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.  
CC -1- TISSUE SPECIFICITY: LIVER-SPECIFIC.  
CC -1- INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC  
CC SHOCK.  
CC -1- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).  
CC -1- PTM: CLEAVED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA



CC FRAGMENTS.  
CC -!- SIMILARITY: BELONGS TO THE ITH FAMILY.  
CC -!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.  
CC -!- CAUTION: REF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER  
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CC -----  
CC EMBL: U43164; AAD00024.1; -;  
CC EMBL: S82800; AAB46821.1; -;  
CC EMBL: M29507; -; NOT\_ANNOTATED\_CDS.  
CC InterPro: IPR002035; -;  
CC Pfam: PF00092; vwa; 1.  
CC PROSITE: PS50234; VWFA\_DOMAIN; 1.  
CC Serine protease inhibitor; Repeat; Signal; Multigene family;  
CC Glycoprotein.  
CC SIGNAL 1 27  
CC CHAIN 28 921 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN  
CC H4.  
CC DOMAIN 270 428 VWFA.  
CC CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CONFLICT 49 50 HT -> SK (IN REF. 3).  
CC CONFLICT 703 703 D -> H (IN REF. 1; AA SEQUENCE).  
CC SEQUENCE 921 AA; 102146 MW; E2BF9525DE8D07C CRC64;

Query Match 2.68; Score 150.5; DB 1; Length 921;  
Best Local Similarity 19.9%; Pred. No. 0.3;  
Matches 156; Conservative 100; Mismatches 264; Indels 265; Gaps 36;  
Qy 4 GCLLALTLT-----FQSLIGSSEPPPSAVTIKSWYDK---MOED--- 43  
Db 10 GLLLVLPALLAVLOSTAKHNDINIYSLTVDSKSSRFATHVTSRVVKNKSAVQEAFTQ 69  
Qy 44 -----LVTLAKTAGVNLVDIYEK--YQDLYT-VEPNNAQLVEIAARDIEKL--- 89  
Db 70 MELPKAFITNFSMIIDGVTPYNIKEKAAAEQYSAVARGESAGLVATGRTKTEQFOVA 129  
Qy 90 LSNRSKALVSLALEAEKVAQAAHQWREDFASNEVYVYNAKDDLDPEKNDSEPGSQRIKPVF 149  
Db 130 VSVAPAAKVTFELVYELLARH-----LGYIELLLKIQPQ-----QLVRHLQ 171  
Qy 150 IEDANFGHQ-ISKY-QHAAVHIPTDIYEGSTIVLNE---LAWTSALDEVEKKNREEDPSL 203  
Db 172 MDIHFEQGISFLETESTFTWELAEALTSQNKTAHIFKPTLSQ-OKSPQQQETV 230  
Qy 204 L-----WQVFGSATG-----LARYYPASFWVDNSRTPNKKIDLYDVRPWPYIQG 247  
Db 231 LDGNFIVRYDVRTVTGSIQIENGIFYVHFAPEW----- 266  
Qy 248 AASPKDMLILVDVSGSYGLTKLIRTSVSEMLETSLDDDFVNVASFNNAQDVSCFOHL 307  
Db 267 SAIPKNVIFVDTSGMGRKIQTREALIKILGDLGSRDQFNLYVFSGEAPR-----RRA 322  
Qy 308 VQAVRNKVLKDAVNITAKGIDYKKGFSAFEPQLLNYNVSRANCNKI-----IM 359  
Db 323 VAASAENVEEAKSYAAEIHAGGGTINNDMLMAVQLL-----ERANRELLPARSVFII 377  
Qy 360 LFTDG-----GEERAQEIFNKYNKDKKVRV-----FRFSVQGHNYERGPQIOWMA 403  
Db 378 LTTDGDPTVGETNPSKI-----QKNVREADGQHSFLCLGFGFDVPVAFLEK-----MA 426  
Qy 404 CENKG-----YY-----YEIPSGAIRINTQYLDVL--GR 432

Db 427 LENGGLARIYEDSDSALQLEDFYQEVANPLRLVAFEPYS-NAVEEVTQDNFRLEFFKGS 485  
Qy 433 PMVLAG---DKAKQVQWTVNVLDALELGLVITGTLFVFNITQGFENKTKLNQLILG--- 486  
Db 486 ELVWAGKLRDQSPDV-----LSAKVRGQLHMEVNTFVMSRVAEQEAELSPKY 534  
Qy 487 -----VMGVVDSLEDI--KRLTPFTLCPNGYYPFADPNNGYVLLHPNL 527  
Db 535 IFHSPMERLWAYLTIQQLLAQTVSASDAEKALAEARALSLSLNYSFVTPLTSMVITKPEG 594  
Qy 528 QPKNPKSOEPVTLDFDLAELENDIKVEIRNMIDGESGEKTFRTLVKSQDSEYIDKGNRT 587  
Db 595 QEQSQVAERP-----VENGROGNTSHGHSF-----QFHSVGDR 630  
Qy 588 YWTFVNGTDSYSLALVLPITYFYIKAKLEETITQARSKKGMKDKSETLKPDPNFESGYT 647  
Db 631 SRLTGGSSVD-----PVFS-----HRRGWKGQAQ-----GFEMSY- 661  
Qy 648 FIAPR 652  
Db 662 -LPPR 665

Search completed: July 23, 2001, 07:47:59  
Job time: 560 sec



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OM protein - protein search, using sw model

Run on: July 23, 2001, 07:37:14 ; Search time 125.88 Seconds

(without alignments)  
1146.686 Million cell updates/sec

Title: US-09-397-548-14

Perfect score: 5748

Sequence: 1 MAGCCLALTLTFLQSLIG.....IIGIQFLMLVSGSTHRL 1091

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5714.5	99.4	1110	4 Q9YU00	Q9YU00 homo sapien
2	5635	98.0	1091	6 Q77732	Q77732 sus scrofa
3	5562	96.8	1091	11 Q9ERS3	Q9ERS3 rattus norv
4	5498	95.7	1103	11 Q08532	Q08532 mus musculu
5	3972	69.1	745	4 Q9UDQ3	Q9UDQ3 homo sapien
6	3075	53.0	1150	4 Q9NY47	Q9NY47 homo sapien
7	3047.5	53.0	1143	4 Q9NY48	Q9NY48 homo sapien
8	3045.5	53.0	1156	11 Q9EGG2	Q9EGG2 mus musculu
9	3034.5	52.8	1145	4 Q9Y268	Q9Y268 homo sapien
10	3013.5	52.4	1076	4 Q9UEW0	Q9UEW0 homo sapien
11	2844	49.5	975	4 Q9NSA6	Q9NSA6 homo sapien
12	1127.5	19.6	1091	11 Q9Z1L5	Q9Z1L5 mus musculu
13	1050.5	18.3	997	4 Q9NT16	Q9NT16 homo sapien
14	937	16.3	2190	5 Q9NK64	Q9NK64 drosophila
15	920	16.0	2172	5 Q9VJ40	Q9VJ40 drosophila
16	897.5	15.6	1191	5 Q9VJN7	Q9VJN7 drosophila
17	892.5	15.5	1255	5 Q9NK83	Q9NK83 drosophila
18	875	15.2	170	4 Q9UDL7	Q9UDL7 homo sapien
19	851.5	14.8	1022	5 Q9V6T7	Q9V6T7 drosophila

20	738.5	12.8	519	4 Q9NY18	Q9NY18 homo sapien
21	580.5	10.1	1148	5 Q17517	Q17517 caenorhabd
22	514.5	9.0	104	4 Q9UD81	Q9UD81 homo sapien
23	506	8.8	100	6 Q9GLH1	Q9GLH1 bos taurus
24	498.5	8.7	121	4 Q9UD82	Q9UD82 homo sapien
25	492.5	8.6	223	11 Q9R142	Q9R142 mus musculu
26	482	8.4	98	4 Q9UDU5	Q9UDU5 homo sapien
27	465	8.1	97	4 Q9UD80	Q9UD80 homo sapien
28	402	7.0	77	4 Q95026	Q95026 homo sapien
29	344	6.0	1185	4 Q9HCJ9	Q9HCJ9 homo sapien
30	224.5	3.9	1449	5 Q9V917	Q9V917 drosophila
31	170.5	3.0	494	5 Q9U7P4	Q9U7P4 eufollicul
32	167	2.9	796	1 Q9HJRO	Q9HJRO thermoplasm
33	161	2.8	2706	5 Q15870	Q15870 plasmodium
34	156.5	2.7	903	6 Q9GLY5	Q9GLY5 cryptotolagus
35	155	2.7	1516	5 Q96154	Q96154 plasmodium
36	155	2.7	2364	2 Q66342	Q66342 clostridium
37	154.5	2.7	1315	2 Q86488	Q86488 staphylococ
38	153	2.7	932	11 Q35802	Q35802 rattus norv
39	152.5	2.7	789	2 Q45793	Q45793 bacillus th
40	152	2.6	1105	14 Q9EM28	Q9EM28 ansacta moo
41	151.5	2.6	2867	5 Q9N2M3	Q9N2M3 plasmodium
42	150.5	2.6	2771	5 Q26216	Q26216 plasmodium
43	150	2.6	946	6 Q9GLY6	Q9GLY6 cryptotolagus
44	149	2.6	459	2 Q25905	Q25905 helicobacte
45	149	2.6	930	4 Q9UQ54	Q9UQ54 homo sapien

#### ALIGNMENTS

RESULT 1

Q9YU00 PRELIMINARY; PRT; 1110 AA.  
AC Q9YU00;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAY-2001 (TRENBLrel. 16, Last annotation update)  
DE DIHYDROXYRIDINE RECEPTOR ALPHA 2 SUBUNIT.  
GN CACNA2D1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20003942; PubMed=10534405;  
RA Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;  
RT "Genomic structure and functional expression of a human alpha(2)/delta  
RL calcium channel subunit gene (CACNA2).";  
RL Genomics 61:201-209(1999).  
DR EMBL; AF083854; AAF03259.1; JOINED.  
DR EMBL; AF083817; AAF03259.1; JOINED.  
DR EMBL; AF083818; AAF03259.1; JOINED.  
DR EMBL; AF083819; AAF03259.1; JOINED.  
DR EMBL; AF083820; AAF03259.1; JOINED.  
DR EMBL; AF083821; AAF03259.1; JOINED.  
DR EMBL; AF083822; AAF03259.1; JOINED.  
DR EMBL; AF083823; AAF03259.1; JOINED.  
DR EMBL; AF083824; AAF03259.1; JOINED.  
DR EMBL; AF083825; AAF03259.1; JOINED.  
DR EMBL; AF083826; AAF03259.1; JOINED.  
DR EMBL; AF083827; AAF03259.1; JOINED.  
DR EMBL; AF083828; AAF03259.1; JOINED.  
DR EMBL; AF083829; AAF03259.1; JOINED.  
DR EMBL; AF083830; AAF03259.1; JOINED.  
DR EMBL; AF083831; AAF03259.1; JOINED.  
DR EMBL; AF083832; AAF03259.1; JOINED.  
DR EMBL; AF083833; AAF03259.1; JOINED.  
DR EMBL; AF083834; AAF03259.1; JOINED.  
DR EMBL; AF083835; AAF03259.1; JOINED.  
DR EMBL; AF083836; AAF03259.1; JOINED.  
DR EMBL; AF083837; AAF03259.1; JOINED.

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DR EMBL; AF083838; AAF03259.1; JOINED.
DR EMBL; AF083839; AAF03259.1; JOINED.
DR EMBL; AF083840; AAF03259.1; JOINED.
DR EMBL; AF083841; AAF03259.1; JOINED.
DR EMBL; AF083842; AAF03259.1; JOINED.
DR EMBL; AF083843; AAF03259.1; JOINED.
DR EMBL; AF083844; AAF03259.1; JOINED.
DR EMBL; AF083845; AAF03259.1; JOINED.
DR EMBL; AF083846; AAF03259.1; JOINED.
DR EMBL; AF083847; AAF03259.1; JOINED.
DR EMBL; AF083848; AAF03259.1; JOINED.
DR EMBL; AF083849; AAF03259.1; JOINED.
DR EMBL; AF083850; AAF03259.1; JOINED.
DR EMBL; AF083851; AAF03259.1; JOINED.
DR EMBL; AF083852; AAF03259.1; JOINED.
DR EMBL; AF083853; AAF03259.1; JOINED.
DR EMBL; AF083854; AAF03259.1; JOINED.
DR InterPro; IPR000885; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
DR ProDom; PD002078; -. 1.
KW Receptor.
SQ
SEQUENCE 1110 AA; 125307 MW; 8358DC6AD489C074 CRC64;

Query Match          99.4%; Score 5714.5; DB 4; Length 1110;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1088; Conservative 1; Mismatches 2; Indels 19; Gaps 1;

QY 1 MAAGCLLATLTLFQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLATLTLFQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTFVFNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDFASN 120
DB 61 YEKYQDLYTFVFNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDFASN 120

QY 121 EYVYNAKDDLPEKNDSPGSGORIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180
DB 121 EYVYNAKDDLPEKNDSPGSGORIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180

QY 181 NELNWTSAIDVEFKKREDDPSLLQVFGSAGTLARYYPASPWNDSRTPNKLIDLYDVR 240
DB 181 NELNWTSAIDVEFKKREDDPSLLQVFGSAGTLARYYPASPWNDSRTPNKLIDLYDVR 240

QY 241 RPYIOGAASPKDMLTLVDVSGSVGLTKLRTSVSEMLETSDDDFVNVASFNSNAOD 300
DB 241 RPYIOGAASPKDMLTLVDVSGSVGLTKLRTSVSEMLETSDDDFVNVASFNSNAOD 300

QY 301 VSCFOHLVQANVRNKKVLKADAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360
DB 301 VSCFOHLVQANVRNKKVLKADAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360

QY 361 FTDGGERAQEIFNKYKDKKVRVFRFSGVQHNYBERGPTQWACENKGYIIPISGAIR 420
DB 361 FTDGGERAQEIFNKYKDKKVRVFRFSGVQHNYBERGPTQWACENKGYIIPISGAIR 420

QY 421 INTQEYLDVLGRPMVLGAKAKOVQNTVYLDALGLVITGTLPVNITGOFENKTNLK 480
DB 421 INTQEYLDVLGRPMVLGAKAKOVQNTVYLDALGLVITGTLPVNITGOFENKTNLK 480

QY 481 NQILGVGMGVDSLEDKRLTPRFTLCPNGYFYAIDPNGYVLLHPNLPK----- 530
DB 481 NQILGVGMGVDSLEDKRLTPRFTLCPNGYFYAIDPNGYVLLHPNLPKIGVGIGPTIN 540

QY 531 -----NPKSQEPVTLDFDALENDIKVEIRNKMIDGSEKTFRTLKVSQDERVI 581
DB 541 LRKRPNINQPKSQEPVTLDFDALENDIKVEIRNKMIDGSEKTFRTLKVSQDERVI 600

QY 582 DKGNRYYTTPVNGTDSLALVLPYTSFYIIKAKLEETITQARSKKGKMKDSETLKPDNF 641
DB 601 DKGNRYYTTPVNGTDSLALVLPYTSFYIIKAKLEETITQARSKKGKMKDSETLKPDNF 660

QY 642 EESGYTFIAPROYCNDLKISDNNTFELNFEFIDRKTPNPNNSCNADLINRVLLDAGFTN 701
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DB 661 EESGYTFIAPROYCNDLKISDNNTFELNFEFIDRKTPNPNNSCNADLINRVLLDAGFTN 720
QY 702 ELVQYNSKQKNIKGVKARFVYTDGITRVYPKEAGENQENPETEYDSFYKRSLDNDY 761
DB 721 ELVQYNSKQKNIKGVKARFVYTDGITRVYPKEAGENQENPETEYDSFYKRSLDNDY 780
QY 762 VFTAPYFNKSGPGAYESGLMWSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP 821
DB 781 VFTAPYFNKSGPGAYESGLMWSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDP 840
QY 822 CAGPVCDCKRNSDMVDCVTLDDGFLMANHDDYTNQIGRFFGEIDPDSLMRHLVNSIYVA 881
DB 841 CAGPVCDCKRNSDMVDCVTLDDGFLMANHDDYTNQIGRFFGEIDPDSLMRHLVNSIYVA 900
QY 882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADIILQIGWATAAAWSILQOFLLSLTFFR 941
DB 901 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADIILQIGWATAAAWSILQOFLLSLTFFR 960
QY 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLCGNCSTRIFHGEKLMNTNL 1001
DB 961 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLCGNCSTRIFHGEKLMNTNL 1020
QY 1002 IFIMVESKGTCPDTRLLIQAQTSQDGNPCDMVQKQPRYKRGPDVCFDNNVLEDYDCGG 1061
DB 1021 IFIMVESKGTCPDTRLLIQAQTSQDGNPCDMVQKQPRYKRGPDVCFDNNVLEDYDCGG 1080
QY 1062 VSGLPNSLWYIIIGIOFLLLMLVSGSTHRL 1091
DB 1081 VSGLPNSLWYIIIGIOFLLLMLVSGSTHRL 1110

RESULT 2
QY 077773 PRELIMINARY; PRT; 1091 AA.
ID 077773
AC 077773;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-2 DELTA SUBUNIT PRECURSOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
ON NCBI_TaxID=9823;
RX NCBI_TaxID=9823;
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RX MEDLINE=98411353; PubMed=9738015;
RA Brown J.P., Gee N.S.;
RT "Cloning and deletion mutagenesis of the alpha2 delta calcium channel
RT subunit from porcine cerebral cortex. Expression of a soluble form of
RT the protein that retains [3H]gabapentin binding activity.";
RL J. Biol. Chem. 273:25458-25465(1998).
DR EMBL; AF077665; AAC36289.1; -.
DR InterPro; IPR002035; -.
DR Pfam; PF00092; vwa; 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 1091 VOLTAGE-DEPENDENT CALCIUM CHANNEL
FT ALPHA-2 DELTA SUBUNIT.
SQ SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9EE60E CRC64;

Query Match          98.0%; Score 5635; DB 6; Length 1091;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1068; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAAGCLLATLTLFQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
DB 1 MAAGCLLATLTLFQSLIGPSSSEPPFSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLYTFVFNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVAQAAHQWREDFASN 120
```

Db 61 YEKYQDLTVTPNNARQVETAAARDIEKLLNSRKALVRLALEAEKVQAAHQWRDFASN 120  
 Qy 121 EYVYNAKDDLDPEKNDSQSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
 Db 121 EYVYNAKDDLDPEKNDSQSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
 Qy 181 NELNWTSALEDFVFNKREEDSLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
 Db 181 NELNWTSALEDFVFNKREEDSLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
 Qy 241 RPWYIQAASPKDMLILVDVSGVSGTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIQAASPKDMLILVDVSGVSGTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
 Qy 361 FTDGGEERAQEIFAKYKNDKKVRVFRFSGVGHNYERGPIONMACENKGYEYIPIGAI 420  
 Db 361 FTDGGEERAQEIFAKYKNDKKVRVFRFSGVGHNYERGPIONMACENKGYEYIPIGAI 420  
 Qy 421 INTQBYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLPVFNITGOFENKTNLK 480  
 Db 421 INTQBYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLPVFNITGOFENKTNLK 480  
 Qy 481 NOLILGVMGVDSLEDIKRLTPRTLCPCNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 Db 481 NOLILGVMGVDSLEDIKRLTPRTLCPCNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 Qy 541 DFLDAELENDIKVEIRNKMIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
 Qy 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEEESGYTFIAPRDYCN 660  
 Db 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEEESGYTFIAPRDYCN 660  
 Qy 720 SDNNTFELNNEFIDRKTTPNPNCSNADLINRVLLDAGFTNELVQYWSKOKNKGVRAR 720  
 Db 720 SDNNTFELNNEFIDRKTTPNPNCSNADLINRVLLDAGFTNELVQYWSKOKNKGVRAR 720  
 Qy 721 FVVTGGITRTVYKREAGENWQENPETEYEDSYKRSLDNDNTVETAPYFNKSGPGAYES 780  
 Db 721 FVVTGGITRTVYKREAGENWQENPETEYEDSYKRSLDNDNTVETAPYFNKSGPGAYES 780  
 Qy 781 MYKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 Db 781 MYKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840  
 Qy 841 LDDGGFLMANHDDYTNQIGRFFGIDPSLMRHLVNIYSVAFNKSVDYQSCPEGAPKQ 900  
 Db 841 LDDGGFLMANHDDYTNQIGRFFGIDPSLMRHLVNIYSVAFNKSVDYQSCPEGAPKQ 900  
 Qy 901 GAGHRSATVPVADTLOIGWATAAASILQOFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
 Db 901 GAGHRSATVPVADTLOIGWATAAASILQOFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960  
 Qy 961 SCITEQTYFFDNDKSKSGVLDGNCNCRIFHVEKLMNTNLIIFINVESKGTCPDTRLLI 1020  
 Db 961 SCITEQTYFFDNDKSKSGVLDGNCNCRIFHVEKLMNTNLIIFINVESKGTCPDTRLLI 1020  
 Qy 1021 QAEQTSQDPNCDVMKQPRYKRGDPDVCNDNVEDYTCGGVSGNLNPLSWYIIGQIFLL 1080  
 Db 1021 QAEQTSQDPNCDVMKQPRYKRGDPDVCNDNVEDYTCGGVSGNLNPLSWYIIGQIFLL 1080  
 Qy 1081 WLVSSTH 1088  
 Db 1081 WLLSGSRH 1088

RESULT 3  
 Q9ERS3

ID Q9ERS3 PRELIMINARY; PRT: 1091 AA.  
 AC Q9ERS3;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE VOLTAGE-GATED CALCIUM CHANNEL ALPHA2/DELTA-1 SUBUNIT.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-SUPERIOR CERVICAL GANGLIA;  
 RA Lin Y., Lipscombe D.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF286488; AAG28164.1;  
 FT VARIANT 209 212 GSAT -> AADR.  
 FT VARIANT 338 338 S -> T.  
 FT VARIANT 599 600 SL -> RY.  
 FT VARIANT 869 869 S -> R.  
 SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;  
 Query Match 96.8%; Score 5562; DB 11; Length 1091;  
 Best Local Similarity 96.1%; Pred. No. 0;  
 Matches 1047; Conservative 24; Mismatches 19; Indels 0; Gaps 0;  
 Qy 1 MAAGCLLATLTTLFQSLIGPSSEPPFPSPVAVTIKSWDKMOEDLVTLAKTAGSGVNLVDI 60  
 Db 1 MAAGCLLATLTTLFQSLIGPSSEPPFPSPVAVTIKSWDKMOEDLVTLAKTAGSGVNLADI 60  
 Qy 61 YEKYQDLTVTPNNARQVETAAARDIEKLLNSRKALVRLALEAEKVQAAHQWRDFASN 120  
 Db 61 YEKYQDLTVTPNNARQVETAAARDIEKLLNSRKALVRLALEAEKVQAAHQWRDFASN 120  
 Qy 121 EYVYNAKDDLDPEKNDSQSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
 Db 121 EYVYNAKDDLDPEKNDSQSRQIKPVFIEDANFGROISYQHAHVHIPTDIYEGSTIVL 180  
 Qy 181 NELNWTSALEDFVFNKREEDSLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
 Db 181 NELNWTSALEDFVFNKREEDSLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240  
 Qy 241 RPWYIQAASPKDMLILVDVSGVSGTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 Db 241 RPWYIQAASPKDMLILVDVSGVSGTLKIRTSVSEMLETSLDDDFVNVASFNSNAQD 300  
 Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQLLNNVSRANCKIIML 360  
 Qy 361 FTDGGEERAQEIFAKYKNDKKVRVFRFSGVGHNYERGPIONMACENKGYEYIPIGAI 420  
 Db 361 FTDGGEERAQEIFAKYKNDKKVRVFRFSGVGHNYERGPIONMACENKGYEYIPIGAI 420  
 Qy 421 INTQBYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLPVFNITGOFENKTNLK 480  
 Db 421 INTQBYLDVLRPMVLADGKAKQVQWNTNYLDALGLVITGTLPVFNITGOFENKTNLK 480  
 Qy 481 NOLILGVMGVDSLEDIKRLTPRTLCPCNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 Db 481 NOLILGVMGVDSLEDIKRLTPRTLCPCNGYFFAIDPNGYVLLHPNLPKPKSQEPVTL 540  
 Qy 541 DFLDAELENDIKVEIRNKMIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
 Db 541 DFLDAELENDIKVEIRNKMIDGESGKTRFLVKSQDERYIDKGNRTYTWTPVNGTDSL 600  
 Qy 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEEESGYTFIAPRDYCN 660  
 Db 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSKSETLKPDPNFEEESGYTFIAPRDYCN 660  
 Qy 661 SDNNTFELNNEFIDRKTTPNPNCSNADLINRVLLDAGFTNELVQYWSKOKNKGVRAR 720  
 Db 661 SDNNTFELNNEFIDRKTTPNPNCSNADLINRVLLDAGFTNELVQYWSKOKNKGVRAR 720

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Db 661 SONNTEFLNNEFIDRKTNNPNSCNTDLINRILLDAGFTNELVQWNSKQKNIGVKAR 720
QY 721 FVYTDGITRVYPKEAGENQWNPETIYEDSFYKRSLDNDNNYVFTAPYFNKSPGAYESGI 780
Db 721 FVYTDGITRVYPKEAGENQWNPETIYEDSFYKRSLDNDNNYVFTAPYFNKSPGAYESGI 780
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWNIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
QY 841 LDGGGFLMANHDDYTNQIGRFFGIDPSLRLHVNISYAFNKSVDYOSVCEPGAAPKQ 900
Db 841 LDGGGFLMANHDDYTNQIGRFFGIDPSLRLHVNISYAFNKSVDYOSVCEPGAAPKQ 900
QY 901 GAGHSAYVPSVADILQIGWATAAWSLLOQLFLSLFPRLLEAVEVEMDDFTASLSKQ 960
Db 901 GAGHSAYVPSVADILQIGWATAAWSLLOQLFLSLFPRLLEAVEVEMDDFTASLSKQ 960
QY 961 SCITEQTOYFFNDNDSKFSGLDCGNCISRFHGEKLMNTNLFIMVESKGTCPDTRLII 1020
Db 961 SCITEQTOYFFNDNDSKFSGLDCGNCISRFHGEKLMNTNLFIMVESKGTCPDTRLII 1020
QY 1021 QAEQTSQSDGPNCDVMKQPRYKRGPDVCFDNNVLEDYDCGGVSGLNPLSLWYIIGIOFLLL 1080
Db 1021 QAEQTSQSDGPNCDVMKQPRYKRGPDVCFDNNVLEDYDCGGVSGLNPLSLWYIIGIOFLLL 1080
QY 1081 WLVSQSTHRL 1090
Db 1081 WLVSQSTHRL 1090

RESULT 4
ID 008532 PRELIMINARY; PRT: 1103 AA.
AC 008533; 008534; 008535; 008536;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA
DE SUBUNITS PRECURSOR.
GN CACNA2D1 OR CACNA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97113514; PubMed=8955374;
RA Angelotti T.; Hofmann F.;
RL FEBS Lett. 397:331-337(1996).
CC -1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
CC EXCITATION-CONTRACTION COUPLING.
CC -1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
CC ALPHA-1, ALPHA-2, BETA AND GAMMA.
CC -1- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-
CC LINKED.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN, ISOFORMS 2A-2E,
CC ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE
CC SEQUENCE SHOWN HERE IS THAT OF ISOFORM 2A.
CC -1- TISSUE SPECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND
CC AORTA, 2B IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS
CC EXPRESSED IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN
CC SMOOTH MUSCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE
CC CARDIOVASCULAR SYSTEM.
CC -1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
CC A PRECURSOR FORM.
CC -1- SIMILARITY: TO OTHERS SPECIES ALPHA-2 SUBUNIT.
DR EMBL; 073484; AAB50139.1; -
DR EMBL; 073485; AAB50140.1; -
DR EMBL; 073483; AAB50138.1; -
DR EMBL; 073486; AAB50141.1; -

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DR EMBL; U73487; AAB50142.1; -
DR MGD; MGI:88295; Cacna2d1.
DR InterPro; IPR002035; -
DR Pfam; PF00092; vwa; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Phosphorylation; Signal;
KW Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 957
FT CHAIN 958 1103
FT TRANSMEM 446 469
FT TRANSMEM 918 942
FT TRANSMEM 1079 1098
FT MOD_RES 501 501
FT MOD_RES 845 845
FT CARBOHYD 92 92
FT CARBOHYD 136 136
FT CARBOHYD 184 184
FT CARBOHYD 324 324
FT CARBOHYD 348 348
FT CARBOHYD 475 475
FT CARBOHYD 604 604
FT CARBOHYD 613 613
FT CARBOHYD 675 675
FT CARBOHYD 781 781
FT CARBOHYD 824 824
FT CARBOHYD 888 888
FT CARBOHYD 895 895
FT CARBOHYD 985 985
FT CARBOHYD 998 998
FT VARSPPLIC 531 549
FT VARSPPLIC 531 554
FT VARSPPLIC 644 644
FT SEQUENCE 1103 AA; 124629 MW; 10377384735120D4 CRC64;

Query Match 95.7%; Score 5498; DB 11; Length 1103;
Best Local Similarity 93.9%; Pred No. 0;
Matches 1042; Conservative 24; Mismatches 18; Indels 26; Gaps 2;

QY 1 MAAGCLLALTTLFOSLLIGPSEEPFPPSAVTIKSWVDKMQEDLVLTAKTAGSVNOLVDI 60
Db 1 MAAGCLLALTTLFOSLLIGPSEEPFPPSAVTIKSWVDKMQEDLVLTAKTAGSVTQADI 60
QY 61 YEKYQDLTYVEPNNAQLVEIAARQIEKLLSNRSKALVSIALEAEKVQAAHQWREDFASN 120
Db 61 YEKYQDLTYVEPNNAQLVEIAARQIEKLLSNRSKALVSIALEAEKVQAAHQWREDFASN 120
QY 121 EVVYINAKDDLPEKNDSEPGSORIKPVFIEDANFGROIYSQHAAVHIPTDIYEGSTIVL 180
Db 121 EVVYINAKDDLPEKNDSEPGSORIKPVFIEDANFGROIYSQHAAVHIPTDIYEGSTIVL 180
QY 181 NELNWTSDALDEVFKKREEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
Db 181 NELNWTSDALDEVFKKREEDPSLLMQVFGSATGLARYYPASPVWDNSRTPNKIDLYDVR 240
QY 241 RPWYIOGASPKDMLILVDVSGVSGSLTLKLRTSVSEMLETSLDDDFVNVASFNSNAQD 300
Db 241 RPWYIOGASPKDMLILVDVSGVSGSLTLKLRTSVSEMLETSLDDDFVNVASFNSNAQD 300
QY 301 VSCFOHLVQANVRNKKVLKADAVNNITAKGTDYKKGFSFAFEOQLLNYSRANCNKIIML 360
Db 301 VSCFOHLVQANVRNKKVLKADAVNNITAKGTDYKKGFSFAFEOQLLNYSRANCNKIIML 360
QY 361 FTDGGERAQEILFNKYNKDKKVRVFRFSYGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
Db 361 FTDGGERAQEILFNKYNKDKKVRVFRFSYGOHNYERGPQIOWMACENKGYIYEIPSGAIR 420
QY 421 INTQEYLDVLGRPWLADGKAKQVQWNTNYLDALEGLVITGLTPVFNITGQFENKTNLK 480
Db 421 INTQEYLDVLGRPWLADGKAKQVQWNTNYLDALEGLVITGLTPVFNITGQFENKTNLK 480

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QY 481 NQILGVGMGVDSLEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPNLPK-----530  
Db 481 NQILGVGMGVDSLEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPNLPKPIGVGPIPTIN 540  
QY 531 -----NPKSQEPVTLDFDAELENDIKVEIRNMIDGESGKFTFTLVKSQDERVI 581  
Db 541 LRRKRRNVQNPQSQEPVTLDFDAELENDIKVEIRNMIDGESGKFTFTLVKSQDERVI 600  
QY 582 DKGNYRTWTPVNGTYSALVLPYSFYIYAKLEBETIQARSKKGMKDSLTKPDNP 641  
Db 601 DKGNYRTWTPVNGTYSALVLPYSFYIYAKLEBETITQARY-----SETLKPDPNF 653  
QY 642 EESGYTFIAPDYCNLDKISDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFN 701  
Db 654 EESGYTFIAPDYCNLDKISDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFN 713  
QY 702 ELVQNTWSQKNIKGKARFVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 761  
Db 714 ELVQNTWSQKNIKGKARFVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNY 773  
QY 762 VFTAPFNKSGPAGESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIENFTKTSIRDP 821  
Db 774 VFTAPFNKSGPAGESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIENFTKTSIRDP 833  
QY 822 CAGPVCDCRNSDMVDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSIYA 881  
Db 834 CAGPVCDCRNSDMVDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSIYA 893  
QY 882 FNKSYDYQVQCPGAPKAGHRSAYVPSVADIQIGWATAAAWSIIQQFLLSLTFPR 941  
Db 894 FNKSYDYQVQCPGAPKAGHRSAYVPSIADIQIGWATAAAWSIIQQFLLSLTFPR 953  
QY 942 LLEAVEMEDDDTASLSKQSCITEQTFYFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNL 1001  
Db 954 LLEAVEMEDDDTASLSKQSCITEQTFYFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNL 1013  
QY 1002 IFIMVESKTCPCDRLMQAQTSDGPNPCDMVKQPRYKRGPDVCFDNNVLEDYDCGG 1061  
Db 1014 IFIMVESKTCPCDRLMQAQTSDGPNPCDMVKQPRYKRGPDVCFDNNVLEDYDCGG 1073  
QY 1062 VSGLNPSLWIIQIOFLLMLVSGSSTRLL 1091  
Db 1074 VSGLNPSLWIIQIOFLLMLVSGSSTRLL 1103  
RESULT 5  
Q9UDQ3 ID Q9UDQ3 PRELIMINARY; PRT; 745 AA.  
AC Q9UDQ3  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TremBLrel. 14, Last annotation update)  
DE WUGSC:H\_DJ0560014.1 PROTEIN (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99063792; PubMed=9847074;  
RA Sulston J.E., Waterston R.;  
RT "Toward a complete human genome sequence.";  
RL Genome Res. 8:1097-1108(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX Mead K., Bauer C.;  
RA "The sequence of Homo sapiens PAC clone RP4-560014.";  
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX Waterston R.H.;  
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [4]

RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC006145; RAD20938.1;  
DR InterPro; IPR002035;  
FT NON\_TER 1  
SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;  
Query Match 69.1%; Score 3972; DB 4; Length 745;  
Best Local Similarity 99.7%; Pred. No. 3.4e-247;  
Matches 743; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 347 YNVSRRANCNKIIMLFTDGGEEAQAEIFNKYKDKKVVFRFVSQGHYQNGRPIQWMAEN 406  
Db 1 YNVSRRANCNKIIMLFTDGGEEAQAEIFNKYKDKKVVFRFVSQGHYQNGRPIQWMAEN 60  
QY 407 KGYYEIPISGAIIRINQYLDVGRPMVLADGAKAKOVQWNTVYLDALGLVITCTLPV 466  
Db 61 KGYYEIPISGAIIRINQYLDVGRPMVLADGAKAKOVQWNTVYLDALGLVITCTLPV 120  
QY 467 FNITGOFENKTNLKNOLILGVMGVDVSLIEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPN 526  
Db 121 FNITGOFENKTNLKNOLILGVMGVDVSLIEDIKRLTFRFTLCPNGYFAIDPNGYVLLHPN 180  
QY 527 LQPKNPKSQEPVTLDFDAELENDIKVEIRNMIDGESGKFTFTLVKSQDERYIDKGNR 586  
Db 181 LQPKNPKSQEPVTLDFDAELENDIKVEIRNMIDGESGKFTFTLVKSQDERYIDKGNR 240  
QY 587 TYTWPVNGTYSALVLPYSFYIYAKLEBETIQARSKKGMKDSLTKPDNPESGY 646  
Db 241 TYTWPVNGTYSALVLPYSFYIYAKLEBETIQARSKKGMKDSLTKPDNPESGY 300  
QY 647 TFIAPDYCNLDKISDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQN 706  
Db 301 TFIAPDYCNLDKISDNTEFLNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQN 360  
QY 707 YWSKQKNIKGARFVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAP 766  
Db 361 YWSKQKNIKGARFVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYVFTAP 420  
QY 767 YFNKSGPAGESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIENFTKTSIRDPGAPV 826  
Db 421 YFNKSGPAGESGIMVSKAVEIYIQGLKLPVAVGIKIDVNSWIENFTKTSIRDPGAPV 480  
QY 827 CDCRNSDMVDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSIYAFNKS 886  
Db 481 CDCRNSDMVDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNSIYAFNKS 540  
QY 887 DYQSVCEPGAAPKAGHRSAYVPSVADIQIGWATAAAWSIIQQFLLSLTFPRLEAV 946  
Db 541 DYQSVCEPGAAPKAGHRSAYVPSVADIQIGWATAAAWSIIQQFLLSLTFPRLEAV 600  
QY 947 EMEDDDDTASLSKQSCITEQTFYFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNLIFMV 1006  
Db 601 EMEDDDDTASLSKQSCITEQTFYFFDNDKSFSGVLDCGNCRIHFHGEKLMNTNLIFMV 660  
QY 1007 ESKGTCPCDRLMQAQTSDGPNPCDMVKQPRYKRGPDVCFDNNVLEDYDCGGVSGLN 1066  
Db 661 ESKGTCPCDRLMQAQTSDGPNPCDMVKQPRYKRGPDVCFDNNVLEDYDCGGVSGLN 720  
QY 1067 PSLWYIIGIQFLLMLVSGSSTRLL. 1091  
Db 721 PSLWYIIGIQFLLMLVSGSSTRLL 745  
RESULT 6  
Q9NY47 ID Q9NY47 PRELIMINARY; PRT; 1150 AA.  
AC Q9NY47  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)



DE	CALCIUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GN	CACNA2D2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
NP	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=THYROID;
RA	Klugbauer N.;
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RP	[2]
NP	SEQUENCE FROM N.A.
RC	TISSUE=THYROID;
RA	Hobom M., Dai S., Marais E., Lacinova L.;
RT	"Neuronal distribution and functional characterization of the calcium
RT	channel alpha2delta-2 subunit.";
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AJ251368; CAB86193.1; -.
DR	InterPro: IPR002035; -.
SQ	SEQUENCE 1150 AA; 129875 MW; 37B75F687AFE573C CRC64;
<p>Query Match 53.5%; Score 3075; DB 4; Length 1150;            Best Local Similarity 54.3%; Pred. No. 3.5e-189;            Matches 595; Conservative 176; Mismatches 295; Indels 30; Gaps</p>	
QY	7 LAITLTLLFQSLILGSPSEPPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDIYEKYQD 66
DB	44 LWLLPLPLLAAPGASVYFPQOHTQHWARKLEDVGVMRIFGGVQQLREIYKDNKN 103
QY	67 LYTVPPNARQLVEIARDIETKLLNSRKALSVLALAEKVAQAAHQWREDFASNEVYYN 126
DB	104 LFEQENEPQKLVEKVAGDIESLLDRKVAQLKELADAAENFQKAHRWQDNKEEDIVYD 163
QY	127 AKDDL---DPEKNDSPGSO--RIKPVFTIEDANFGQISYQHAHVHPDITVEGSTVLN 181
DB	164 AKADAELDDPSESDVERGSKASTLRDLFDIEDPNFKNKVNSYAAVQIPTDYKGSTVLN 223
QY	182 ELNWTSAIDVEFKKNEEDPDLQWQVFGSATGLARYYPASPWDSNRTPNKIDLDYDVR 241
DB	224 ELNWTALELVFNENRRQDPTLQWQVFGSATGVTRYIPATPW----RAPKIDLDYDVR 279
QY	242 PWYIQGAASPDKMLILVDVSGSYSGLTLLKIRTSVSEMLETISDDDFVNAVFSNSAQDV 301
DB	280 PWYIQGASSPKDVIIVDVSYSVGLTKLMKTSVCEMLDTLSDDDYVNAVSEFKAQPV 339
QY	302 SCFQHLVQANVRNKKVLKDAVNNTAKGITYDYKKGSFAPQLLNYNVSRANCKNIIMLF 361
DB	340 SCFTHLVQANVRNKKVFEKAVQGWAKGTTGYKAGFEYADQLQNSNITRANCKNIMMF 399
QY	362 TDGGEERAQEIFKNYN-KDKKVVRFVSQGHNYERGPLOWACENKGYVYEIPSGIR 420
DB	400 TDGEDRVQDVFKEIKNPNTRVFTFSQGHNYDVTPIQWACANKGYFEIPSGIR 459
QY	421 INTOEYDLVGRPMVLADGAKAQOVNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
DB	460 INTOEYDLVGRPMVLAKGAKQOVNTVYEDALGLVITGTLPVFNITQ--DGPGEKK 517
QY	481 NQLILGVMGVDVSLDIKRLTPFTLCPNGYVFAIDPNGYVLHLHPNLQPKNPKSQEPVTL 540
DB	518 NQLILGVMGIDVALNDIKRLTPNTILGANGYVFAIDLNGYVLHLHPNLKPTQTNFREPVTL 577
QY	541 DFLDAELENDIKVEIRKNKMDGSEKTEFTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
DB	578 DFLDAELENKEEIRSMIDGANKHKHQINTLVKLSDERYIDVTWNTYTWPIRSTNYSL 637
QY	601 ALVLPTYSFYIYIKALFEETITQARSKKGMKDSKSETLKPONFESGYTFIAPRDYCNLDKI 660
DB	638 GLVLPPYSTYFLQANLSDQILQVLRISKLKDEFFLPSFSEGHVFVTAPEYCKDINA 697
QY	661 SDNNTFELLNPFNEFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNVYSKQK-NIKGVKA 719

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698  SDNTEFLAKNFELMEKVTPDSKQCNFFLLNLIDTGTITQOLVERVWRDOLNTYSLLA 757
QY 720  RFVVTGGITRVYPKEAGENWOENPETEYDSFYKRSLDNDNYFTAFYFNK-SGPGAYES 778
Db 758  VFAATDGGITRVFPNKAAEDWTENPEPNASFYRSRLDNHGCVFKPPHQDALLRPLELN 817
QY 779  ---GIMVSKAVEIYTOGKLLKPAVVGKIDVNSWIENF-----TKTSIRDP--CAGP--- 825
Db 818  DTVGILVSTAVELSLGRFTLRPAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-SPNSH 876
QY 826  -VCDCKRNSDMVDCVTLDDGGFLLMANHDDVTNQIGRFGFIDEISLMRHLWNISVAFNFK 884
Db 877  CEMDCFVNEEDLLCVLDDGGFLVLSNQHQHWDQVGRFSEVDANLMLALYNNNSFYTRKE 936
QY 885  SYDYSQVCEPGAAPKQAGHRSAIYVPSVADLIQIGWATAAASLIQOFLLSLTFPRLLE 944
Db 937  SYDYQAACAPQPPGNLGAAPRGVFTVADEFNLAWMTSAAASLFLQQLLYGLIYHSWFQ 996
QY 945  AVEMEDDDTASLSKOSCITEQTOYFFONDSKSFSGVLDDCGNCSRIHPGKLMNTLIFI 1004
Db 997  ADPAEAG-SPETRESSCVMKQTYFGSVNAYSNAIIDCGNCSRLFHAQRLTNTLLFV 1055
QY 1005  MVESKGTGCPCDVRLIIQAQSTSDGNGPCDMVKQPRYRKGPDPVCFDNNVLEDTDCGGVSG 1064
Db 1056  VAKPCLSCQCEAGRLLQKETHSDGFEQCELQVRPYRGRGPHICFDYNATEDSDCGRGAS 1115
QY 1065  LNPFSLYIIGIQFLLL 1080
Db 1116  FPPSLGLVLSQLLLL 1131

RESULT 7
QYNY48  PRELIMINARY; PRT; 1143 AA.
ID QYNY48
DC QYNY48;
DT 01-OCT-2000 (TreeBLrel. 15, Created)
DT 01-OCT-2000 (TreeBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TreeBLrel. 16, Last annotation update)
DE CALCUTUM CHANNEL, ALPHA 2/DELTA SUBUNIT 2.
GS CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid:9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=HEART;
RC Klugbauer N.;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Heart;
RC Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the calcium
channel alphadelta-2 subunit.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AJ251367; CAB86192.1;
DR InterPro; IPR002035;
SQ SEQUENCE 1143 AA; 129084 MW; 492556C919A0CE5 CRC64;

Query Match 53.0%; Score 3047.5; DB 4; Length 1143;
Best Local Similarity 54.1%; Pred. No. 2.1e-187;
Matches 593; Conservative 174; Mismatches 292; Indels 37; Gaps

QY 7 LATLTLTQSLIIGPSSSEPFPSAVTIKSWDKMDLVTAKTASGVNQLVDIYEKYQD 66
Db 44 LWLLLPPLPILAAPGASAFVFFQQTQHWARRLSEQVDGVMRFFGGVQQLREIYKDNRN 103
QY 67 LYTVEPNNAQLVIEAARDIEKLLNSRKSALYSLSALEAKVQAAHQWDFASNEVYYN 126
Db 104 LFEVORNEPOKLVKVGADIESLLDKVOAKRLADAAENFOKAHRWODNKKEEDIVYD 163

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Query Match 53.08; Score 3047.5; DB 4; Length 1143;

Best Local Similarity	54.18;	Pred. No. 2.1e-187;
Matches	593;	Conservative
	174;	Mismatches
	292;	Indels
	37;	Gaps
	14;	

QY 7 LALTTLFQSLIGPSSEEPFSAVIKSWVDKMQEDLVTAKTASGVNQLVDIYEKYQD 66

44 Y W Y D Y I T A B D C A S A Y C E F O O U M Q U N A B D Y E A E V D C I M B P I E C C V O O I B R I Y K D N B N 103

DD 44 LWLLEFLEFLWAAFGASATSEFFQHHIMQBWAANAEEQEVDGVMKRTFGVAVQTAKETINDIAN TO

QY 67 LYTEPNNAQLVEIAARDIEKLLSNRSKALVSLAEKVAHQWREDFASNEVVYN 1266

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db      104 LEEVOENEPOKLVEKVAGDIESLLDRKVOALKRLADAAENFOKAHRWODNIKEEDIVYYD 163

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100

QY 127 AKDDL---DPEKNDSEPSQ--RIKPVIEDANFGROISYQHAAYHIPTDIYEGSTIVLN 181  
DB 164 AKADAELDDPESEDVERGSKASTLRLDIEDPNFNKNVNSYAAVOIPTDIYKGSTIVLN 223  
QY 182 ELNWT-SALDEVFKNREDEPSLLWVFGSATGLARYYPASPVVDNSRPNKIDLDYDVR 241  
DB 224 ELNWT-TEALENFMENRDPDILLWVFGSATGVTRYATPW----RAPKKIDLDYDVR 279  
QY 242 PWYIOGAASPKDMLILVDVSGVSGLTILKIRTSYSEMLETSLDSDDFVNVASFNSAODV 301  
DB 280 PWYIOGASSPKDMLIIVDVSGVSGLTILKIRTSYSEMLETSLDSDDFVNVASFNEKAQPV 339  
QY 302 SCFOHLVQANVRNKKVLDKAVNNITAKGTIDYKKFSAFEOQLLANNYSRANCKIIMLF 361  
DB 340 SCFTHLVQANVRNKKVFEAOGVMKAGTGYKAGFEAFDQLQNSITRANCKNIMWF 399  
QY 362 TDGGERAQEIKFNKN--KDKKRVFRFSYGOHNYERGERGIOWMACENKGYIYPIPSIGAIR 420  
DB 400 TDGGERQDVFEKYNWPNRTVFTFSGOHNYDVTPLQWACANKGYIYPIPSIGAIR 459  
QY 421 INTQBYLDVLRPMVLGADKAKOVQNTNYYLDALBELGLVITGTLPVFNITGOFENKTNLK 480  
DB 460 INTQBYLDVLRPMVLGADKAKOVQNTNYYLDALBELGLVITGTLPVFNITGOFENKTNLK 517  
QY 481 NQILILGVMDVSLDIEKLTFRFTLPCPNYGFADPNYVLLHNPLOPKNSQEPVTL 540  
DB 518 NQILILGVMDVSLDIEKLTFRFTLPCPNYGFADPNYVLLHNPLOPKNSQEPVTL 577  
QY 541 DFLDAELENDIKVEIRNKNMIDGSEKFTLTKVKSODERYIDKGNRTYTWTPVNGTDSL 600  
DB 578 DFLDAELENDIKVEIRNKNMIDGSEKFTLTKVKSODERYIDKGNRTYTWTPVNGTDSL 637  
QY 601 ALVLPYTSYIYAKLEETITQARSKKGMKDSITLKPONFESGYTFTAPRDYCNLDKI 660  
DB 638 GLVLPYTSYIYAKLEETITQARSKKGMKDSITLKPONFESGYTFTAPRDYCNLDKI 690  
QY 661 SONNTEFLNFEEDRKTPNPNPCNADLINRVLDDAGFTNELVQNYWSKQK--NIKGVKA 719  
DB 691 SONNTEFLNFEEDRKTPNPNPCNADLINRVLDDAGFTNELVQNYWSKQK--NIKGVKA 750  
QY 720 RFVVDGGITRVYKPEAGNWOENPETEDSYKRSLSLNDNVTFTAPYFNK--SGPGAYES 778  
DB 751 VFAATDGGITRVYKPEAGNWOENPETEDSYKRSLSLNDNVTFTAPYFNK--SGPGAYES 810  
QY 779 ---GIMVSKAVEIYIOGKLLKPAVGIKIDVNSWIENE-----TKTSIRDP--CAGP--- 825  
DB 811 DTVGILVSTAVELSLGRRTLRPAVGVKLDLEAWAEKFKVLASNRTHQDQPKC--GPNSH 869  
QY 826 -VDCRNSDVMDCVILDDGGFLMANHDDYTNQIRFFGEIDPSLMRLHVLNLSVYAFNK 884  
DB 870 CEMDCVNNEDLLCVLDDGGFLMANHDDYTNQIRFFGEIDPSLMRLHVLNLSVYAFNK 929  
QY 885 SYDYSVCEPAGAPKOGAGHRSAYPSVADILQIGWATAAASWILQOFLLSLTPRLLE 944  
DB 930 SYDYSVCEPAGAPKOGAGHRSAYPSVADILQIGWATAAASWILQOFLLSLTPRLLE 989  
QY 945 AYEMEDDDFTASLSKQSCITEQYTFDNDKSKFSGVLDCGNCRSRIFHGKELMNTNLIPT 1004  
DB 990 ADPAEAG--SPETRESSCYMKQTYVYFSGVSNASYNALIDCGNCSRLFAQLRNTNLLFV 1048  
QY 1005 MYESKGTCDFTLLIOAQBTSDGPNPCDMVKQPRYKGPVDFDNNVLEDYTDGCGVSG 1064  
DB 1049 VAEKPLCSQCEAGRLQKETHSDGPEQCELVORPRYRRGFCFDYNATEDSDCGRGAS 1108  
QY 1065 LNPSLWYIIGIOFLLL 1080  
DB 1109 FPPSLGVLSLQLLLL 1124

RESULT 8  
Q9EOG2  
ID Q9EOG2  
AC Q9EOG2;

DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE VOLTAGE-DEPENDENT CALC10M CHANNEL ALPHA-2-DELTA-2 SUBUNIT.  
GN CACNA2D2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC -STRAIN=TKDU;  
RX MEDLINE=21015416; PubMed=11130987;  
RA Barclay J., Rees M.;  
RT 'Genomic organization of the mouse and human alpha2delta2 voltage-  
RL dependent calcium channel subunit genes.';  
RL Mamm. Genome 11:1142-1144(2000).  
DR EMBL; AF247139; AAG47846.1; -  
SQ SEQUENCE 1156 AA; 130611 MW; A732545A2B302A52 CRC64;

Query Match 53.0%; Score 3045.5; DB 11; Length 1156;  
Best Local Similarity 53.6%; Pred. No. 2.8e-187;  
Matches 590; Conservative 181; Mismatches 296; Indels 33; Gaps 15;

QY 6 LLALTLTLFQSLIGP--SSEEPFSAVTIKSWDKMOEDLVTLAKTASGVNOLVDIYKY 64  
DB 45 LLLLPPLLLLTAPGASAYSFPQOHTMOWHARLEQIDGVMRIFGQVQOIREYKDN 104  
QY 65 QDLYTEPNRNRQLVEIARADIEKLSNRKSKALVSLALEAEKVAQAAHOREDFASNEVY 124  
DB 105 RNLFVEQNEPQKLVKAGVAGIESLDRKVQALKRLADAAENFQKRAHRQDNKEEDIMY 164  
QY 125 YNAKDDL---DPEKNDSEPSQ--RIKPVIEDANFGROISYQHAAYHIPTDIYEGSTIV 179  
DB 165 YDAKADAELDDPESEDVERGSKASTLRLDIEDPNFNKNVNSYAAVOIPTDIYKGSTIV 224  
QY 180 LNELNWT-SALDEVFKNREDEPSLLWVFGSATGLARYYPASPVVDNSRPNKIDLDYDVR 239  
DB 225 LNELNWT-SALDEVFKNREDEPSLLWVFGSATGLARYYPASPVVDNSRPNKIDLDYDVR 280  
QY 240 RRPWTIOGAASPKDMLILVDVSGVSGLTILKIRTSYSEMLETSLDSDDFVNVASFNSAQ 299  
DB 281 RRPWTIOGAASPKDMLIIVDVSGVSGLTILKIRTSYSEMLETSLDSDDFVNVASFNEKAQ 340  
QY 300 DYSCFQHLVQANVRNKKVLDKAVNNITAKGTIDYKKFSAFEOQLLANNYSRANCKIIM 359  
DB 341 PVSCFTHLVQANVRNKKVFEAOGVMKAGTGYKAGFEAFDQLQNSITRANCKNIM 400  
QY 360 LFTDGGEEAQAQEIFNKN--KDKKRVFRFSYGOHNYERGERGIOWMACENKGYIYPIPSIGA 418  
DB 401 MFTDGGEDRVQVFEKYNWPNRTVFTFSGOHNYDVTPLQWACANKGYIYPIPSIGA 460  
QY 419 IRIHQEYLDVLRPMVLGADKAKOVQNTNYYLDALBELGLVITGTLPVFNITGOFENKTN 478  
DB 461 IRIHQEYLDVLRPMVLGADKAKOVQNTNYYLDALBELGLVITGTLPVFNITGOFENKTN 518  
QY 479 LKNQLILGVMDVSLDIEKLTFRFTLPCPNYGFADPNYVLLHNPLOPKNSQEPV 538  
DB 519 KKNQLILGVMDVSLDIEKLTFRFTLPCPNYGFADPNYVLLHNPLOPKNSQEPV 578  
QY 539 TLDLDAELENDIKVEIRNKNMIDGSEKFTLTKVKSODERYIDKGNRTYTWTPVNGTDSL 598  
DB 579 TLDLDAELENDIKVEIRNKNMIDGSEKFTLTKVKSODERYIDKGNRTYTWTPVNGTDSL 638  
QY 599 SLALVLPYTSYIYAKLEETITQARSKKGMKDSITLKPONFESGYTFTAPRDYCNLD 658  
DB 639 SLGLVLPYTSYIYAKLEETITQARSKKGMKDSITLKPONFESGYTFTAPRDYCNLD 698  
QY 659 KISDNNTFLLNFEEDRKTPNPNPCNADLINRVLDDAGFTNELVQNYWSKQK--NIKGV 717  
DB 699 NASDNSTEFKDFIELMEKVTIPDSKOCNNFLLNHLNLTGTITQOLVERVWRDQDLNYSL 758

718 KARFVVTGGITRVYKPEAGENWENPETYEDSFYKRSILDNDNYVFTAPYFNK-SGPGAY 776  
 Db 759 LAYFAATDGGITRVFNKAAEDWENPENFASFRSDNHCYIFKPHQDSLLRPLEL 818  
 QY 777 ES---GIMVSKAVEIYIOGKLKAPVVGKIDVNSWENF-----TKTSIRDP--CAGP- 825  
 Db 819 ENDTVGVVSTAVELSLGRTRLRPAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-GPS 877  
 QY 826 ---VCCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFEGEIDPSLMRHLVNSVXAF 882  
 Db 878 SHCEMCEVNNEDLLCVLDDGGFLVLSNQHNDQVGRFFSEVDANLMLALNNSFYTR 937  
 QY 883 NKSYDQSVCEPGAAPKQAGHRSAYVPSVAADTLQIGWATAAASILQOFLSLFFPRL 942  
 Db 938 KESYDQACAPOPPGNLGAAPRGVFPVPIADPLNLAWTSAASWSLFOQLLYGLYHSW 997  
 QY 943 LEAVEMEDDDFTASLSKQSCITQTOYTFDNDKSFSGVLDCGNSRIFGHEKLMNTLI 1002  
 Db 998 FOADPAEAG-SPETRESSCVMKQTOYFGSVNASYNAIIDCGNSRLFAORLTNTNLL 1056  
 QY 1003 FIMVESKGTCPDTRLLIOAEQ--TSDGNPCDMVKQPKRGPDVCFDNNVLEDYDCG 1060  
 Db 1057 FVVAEPLSCQCEAGRLAKETHCPADGPEQCELVORPRYRGPHICFDYNATEDSDCG 1116  
 QY 1061 GVSGLNPLSWYIIGIQFLIL 1080  
 Db 1117 RGASFPSGLVLSLQALL 1136

RESULT 9  
 QY268 PRELIMINARY; PRT; 1145 AA.  
 AC QY268;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE KIAA0558 PROTEIN.  
 GN KIAA0558.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Sekido Y., Duh F.-M., Latif F., Ding J., Lin J., Mathis M.,  
 RA Minna J.D.;  
 RT "Gene 26, a new candidate human tumor suppressor gene located in the  
 RT 3p21.3 small cell lung cancer homozygous deletion region homologous to  
 RT a voltage gated calcium channel alpha 2/ delta subunit."  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,  
 RA Zabarovsky E., Johnson B., Lerman M.I.;  
 RT "A new alpha 2 delta subunit of the L-type voltage gated calcium  
 RT channel resides in the lung cancer critical region on 3p21.3."  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=98290545; PubMed=9628581;  
 RX Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro."  
 RL DNA Res. 5:31-39(1998).  
 DR EMBL; AF040709; AAC70914.1; -  
 DR EMBL; AF042792; AAB96913.1; -  
 DR EMBL; AB011130; BAA25484.1; -  
 DR InterPro; IPR002035; -  
 QY SEQUENCE 1145 AA; 129268 MW; 9ADA4807FC70971B CRC64;

Query Match 52.8%; Score 3034.5; DB 4; Length 1145;  
 Best Local Similarity 53.9%; Pred. No. 1.4e-186;  
 Matches 592; Conservative 175; Mismatches 292; Indels 39; Gaps 15;  
 QY 7 LAITLTFLQSLLIGSSSEPPFPSSAVTIKSWDKMQDLVTLAKTASGVLVDIYEKYOD 66  
 Db 44 LWLLPLLLPAAAGASAYSFFQOHTMQHARLEGEVDGVMRIFGVQOLREIYKDNRN 103  
 QY 67 LYTVPNNARQLVEIAAROEIKLLSNRSKALVSLALEAEKVQAAHQRDFASFNEVYIN 126  
 Db 104 LFEVQENEPQKLVKEVAGDIESLLDRKQVALRLADAENFOKAHRWQDNKEEDIVYD 163  
 QY 127 AKDDL--DPERKNDSPGSG--RIKPVFTEDANFGQISYQHAHVIPDTDIYEGSIVLN 181  
 Db 164 AKADAELDPESEDVERGSKASTLRDLDFIEDPNFKKNVYSYAQVQIPTDIYKGSVILN 223  
 QY 182 ELNWTLSALDEVEKKKNEEDPSLLWQVFGSATGLARYYPASPMWVDSNRTPNKIDLYDVR 241  
 Db 224 ELNWTLEALNVFENRRODPTLLWQVFGSATGVTRYYPATPW---RAPKKIDLYDVR 279  
 QY 242 PWYOGAASPOMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVVASFNSAQDV 301  
 Db 280 PWYIOGASSPKDMVIIVDVGSGVSGLTLLKMKTSVCEMLDTLSDDDVNVVASENEKAQV 339  
 QY 302 SCFOHLVQANVRNKVLDVANNITAKGIDYKKGFSFAFEQLLNLYNVSPRANCKIIMLF 361  
 Db 340 SCFTHLVQANVRNKVFKVKAQVGVAKGTGKAGGEYAFDQLQNSNITRANCKNIMMF 399  
 QY 362 TDGGERAQEIFNKYN-KDKYRVFRFSVQGHNYERGPIQWMACENKGYEIPSGAIR 420  
 Db 400 TDGGERVQDVEKYNPNRTVRFVTFVSGHNYDVTPLQWACANKGYFEIPSGAIR 459  
 QY 421 INTQEYLDVLRPMVLGAKAKOVQNTNYLDALEGLVITGLTPVFNITGQENKTNLK 480  
 Db 460 INTQEYLDVLRPMVLGAKAKOVQNTNYVEDALGLVITGLTPVFNITGQ--DGPCEK 517  
 QY 481 NQLILGVMDVYSLEDKRLTPRETLCPNGYIFAIDPNGVLLHPNLPKNPKSQBPVTL 540  
 Db 518 NQLILGVMDIVALNDIKRLTPNTITGLANGYIFAIDNLGVLLHPNLPKQTTNFRPVT 577  
 QY 541 DFLDAELENDIKVEIRKNKIDGESGEKTFRTLVKSDERYIDKGNRTYTWTPVNGDYSL 600  
 Db 578 DFLDAELENDENKEEIRSMIDGNKHKQIRTLVKSLDERYIDETVNTWPIRSNYSL 637  
 QY 601 ALVLPYSYIYKALEETITQARKKGMKSETLKPONFESGTYTFIAPRYCNDLKI 660  
 Db 638 GLVLPYSYIYKALNSDQILQ-----VKYFELLPSSESEGHVFIAPREYCKDLNA 690  
 QY 661 SDNTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGETNELVQNVWSKQ-NIKGVKA 719  
 Db 691 SDNTEFLNFIEMEKVTPDSKQCNFLLHNLITDGTITQQLVERVWRDQDLNTYSLA 750  
 QY 720 RFVVTDDGTRVYKPEAGENWENPETYEDSFYKRSILDNDNYVFTAPYFNK-SGPGAY 778  
 Db 751 VFAATDGGITRVFNKAAEDWENPENFASFRSDNHCYIFKPHQDALLRPLELEN 810  
 QY 779 ---GIMVSKAVEIYIOGKLKAPVVGKIDVNSWENF-----TKTSIRDP--CAGP- 825  
 Db 811 DIVGILVSTAVELSLGRTRLRPAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-GPNSH 869  
 QY 826 -VCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFEGEIDPSLMRHLVNSVXAF 884  
 Db 870 CEMDCVNNEDLLCVLDDGGFLVLSNQHNDQVGRFFSEVDANLMLALNNSFYTRKE 939  
 QY 885 SYDYQSVCEPGAAPKQAGHRSAYVPSVAADTLQIGWATAAASILQOFLSLTFPRLLE 944  
 Db 930 SYDYQACAPOPPGNLGAAPRGVFPVPIADPLNLAWTSAASWSLFOQLLYGLYHSW 989  
 QY 945 AVEMEDDDFTASLSKQSCITQTOYTFDNDKSFSGVLDCGNSRIFGHEKLMNTNLI 1004  
 Db 990 ADPAEAG-SPETRESSCVMKQTOYFGSVNASYNAIIDCGNSRLFAORLTNTNLLFV 1048

QY 1005 MYESKGTCPDTRLLIQARQ--TSDGNPCDMVKQPRYKRGPDVCFDNNVLEDYTDGCV 1062  
 DB 1049 VAEKPLCSCEAGRLQKTHCPADGPEQCELVQPRYRGRPHICFDYNATEDSDCGRG 1108  
 QY 1063 SGLNPSLWIIIGTQFLL 1080  
 DB 1109 ASFPPLSGVLVSLQLLLL 1126

RESULT 10  
 Q9UEW0 PRELIMINARY; PRT; 1076 AA.  
 AC Q9UEW0;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE ALPHA 2 DELTA CALCIUM CHANNEL SUBUNIT ISOFORM II.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wei M.-H., Latif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,  
 Zabarovsky E., Johnson B., Lerman M.I.;  
 RT "A new alpha 2 delta subunit of the L-type voltage gated calcium  
 channel resides in the lung cancer critical region on 3p21.3";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF042793; AAB96914.1; -  
 DR InterPro; IPR002035; -  
 SQ SEQUENCE 1076 AA; 122116 MW; EEC474836B7EDA85 CRC64;

Query Match 52.4%; Score 3013.5; DB 4; Length 1076;  
 Best Local Similarity 54.4%; Pred. No. 2.9e-185;  
 Matches 583; Conservative 174; Mismatches 276; Indels 39; Gaps 15;

QY 33 IKSVDKMGEDLVTKTASGVNQLVDIYKEKYQDLTYVTPNNARQLVETAAKDIEKLSN 92  
 DB 1 MGHWRRLQEQVDGVMRIFGGVQQLREIYKDNRLNFEVQENEPQKLVKRVAGDIESLLDR 60  
 QY 93 RSKALVSLALEAKKQAAHOWEDFASNEVYVYNAKDDL--DPEKNDSEPGSQ--RIKP 147  
 DB 61 KVQALKRLADAENQKARHWDNKEEDIVYDKADAELDDPESEVERGSKASTLRL 120  
 QY 148 VFIEDANFGQISYQAAHYHIPTDIYEGSTIVLNELNMTSALDEVEFKKNEEDPSLLWQV 207  
 DB 121 DRIEDPNFKKNYSYAAVQIPTDIYKGVSTVILNLTNLTALNLTALNLTALNLTALNLT 180  
 QY 208 FGSATGLARYYPASPVWNSRTPNKLIDYVRRRPWYIQGAASPKDMLILVDVSGVSGL 267  
 DB 181 FGSATGVTRYYPATPW---RAPKKIDLYVRRRPWYIQGASSPKDMVIIVDVSGVSGL 236  
 QY 268 TLKLIPTVSEMLTSLDDDFNVASFNSAODVSCFQHLVQANVKNKVLKDVANNITA 327  
 DB 237 TLKLMKTSVCEMLTSLDDDFNVASFNSAODVSCFQHLVQANVKNKVLKDVANNITA 296  
 QY 328 KGITDYKGFSAFQOLLNYSRANCKNIIMLFTDGGEEAQEIENKYN-KDKKRVFR 386  
 DB 297 KGITDYKGFSAFQOLLNYSRANCKNIIMLFTDGGEEAQEIENKYN-KDKKRVFR 356  
 QY 387 FSVGQHNYSRGPIONMACENKYYEIPISGAIRINTQYLDVLRPMVLGAKAQVQW 446  
 DB 357 FSVGQHNYSRGPIONMACENKYYEIPISGAIRINTQYLDVLRPMVLGAKAQVQW 416  
 QY 447 TNYVLDALGELVITCTLVFVNITGOFENKTNLKNQILIGVGVDSLEDKRLPRFTL 506  
 DB 417 TNYVLDALGELVITCTLVFVNITGOFENKTNLKNQILIGVGVDSLEDKRLPRFTL 474  
 QY 507 CPNGYFAIDPNGYVLLHNPAPKPKSQEPVTLDFDLAELENDIKVETRNKMDGESGE 566  
 DB 475 GANGYFAIDPNGYVLLHNPAPKPKSQEPVTLDFDLAELENDIKVETRNKMDGESGE 534

QY 567 KYFRLVKSQDERYIDKGNRTYTWTPVNGTDYSLALVLPYTFYFYIKAKLETITQARSK 626  
 DB 535 KQIRTLVSLDERYIDVTRNTYTWPIRSTNYSGLVLPYTFYFYIQANLSQILQ----590  
 QY 627 KGMKMDSETLKPDPNFESEGYTFIAPRDYCNLDKISDNNTFEFLNFEFFDRKTPNPNPCN 686  
 DB 591 ---VKYFEFLPSSFESEGHVFIAPREYKCDLNASDNNTFEFLNFEFFDRKTPNPNPCN 647  
 QY 687 ADLINRVLLDAGTINELVQYWSKQ-NIKGVKARFVVTDDGTRIVYPRKEAGENWOENPE 745  
 DB 648 NELLHNLILDGTITQOLVERVWRDQDLNTYSLAVFAATDGGITRVFPNKAEDWTENPE 707  
 QY 746 TYEDSFYKRSNDNDNVFTAPYFNK-SGPGAYES---GIMWSKAVEIYIQGLLKPAVVG 801  
 DB 708 PFNASFYRRSLDNHGVYFKPHQDALLRPLELENDVGVILVSTAVELSLGRTRLPVAVG 767  
 QY 802 IKIDVNSWTENF---TKTSIRDP--CAGP---VCDCKRNSDVMDCVILDDGGFLMA 850  
 DB 768 VKLDLEAWAEKVKVLASNRTHQDQOKC-GPNSHCEMCEVANNEDLLCVLDDGGFLVLS 826  
 QY 851 NHDDTNTQIGREFGEIDPSLMRHLVNIYAFNKNYSYQVCEPCEPAAKQAGHRSAYVP 910  
 DB 827 NQNHQWDQVGRFESEVDANLMLALYNNSTYTRKESYDYQACAPQPPGNLGAAPRGVFP 886  
 QY 911 SVADILQIGWATAAAMSILQOFLSLTPRLLAEVEMEDDDFTASLSKQSCITEQTQYF 970  
 DB 887 TVADEFLNLAWTSAASLSFLQQLLYGLYHSWFQDPABAEAG-SPETRESSCVMKQOTY 945  
 QY 971 FNDKSFSGVLDGCGNCSFRIFHGEKLMNTLFIIMVESKGTCPDTRLLIQARQ--TSDG 1028  
 DB 946 FGSVNASYNAIIDCGNCSRLFAQRUTNLLFVVAEKLPCQCEAGRLLQKETHCPADG 1005  
 QY 1029 PNPCDMVKQPRYKRGPDVCFDNNVLEDYTDGCGVSGNLPSLWIIIGTQFLL 1080  
 DB 1006 PEQCELVQPRYRGRPHICFDYNATEDSDCGRGASFPPLSGVLVSLQLLLL 1057

RESULT 11  
 Q9NSAG PRELIMINARY; PRT; 975 AA.  
 AC Q9NSAG;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE LUAC11.1 (CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA 2D SUBUNIT  
 DE (KIAA0358)) (FRAGMENT).  
 GN LUAC11.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barlow K.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z84492; CAB41767.2; -  
 DR InterPro; IPR002035; -  
 FT NON\_TER 1 1  
 SQ SEQUENCE 975 AA; 110192 MW; C7874D46B88242BF CRC64;

Query Match 49.5%; Score 2844; DB 4; Length 975;  
 Best Local Similarity 56.5%; Pred. No. 2e-174;  
 Matches 548; Conservative 147; Mismatches 239; Indels 36; Gaps 14;

QY 132 DPEKNDSEPGSQ--RIKPVFIEDANFGQISYQAAHYHIPTDIYEGSTIVLNELNWTSL 189  
 DB 2 DPESEVERGSKASTLRLDIEDPNFKKNVYSYAAVQIPTDIYKGVSTVILNLTALN 61  
 QY 190 DEVFKKNEEDPSLLWQVGSATGLARYYPASPVWNSRTPNKLIDYVRRRPWYIQGA 249  
 DB 62 ENFVFNRRQDPTLLMQVFGSATGVTRYYPATPW---RAPKKIDLYVRRRPWYIQGAS 117

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QY 250 SPKDMILLVDVSGVSGILTKLIRTSVSEMLETLDSDDFVNVASFNASNAQDYSCFQHLVQ 309
DB 118 SPKDMVIIIVDVGSGVSGILTKLIRTSVSEMLETLDSDDFVNVASFNASNAQDYSCFQHLVQ 177
QY 310 ANYRNKKVLKDAVNNITAKGIDYDKGKFATFQQLNLYNVSRANCKIIMLTFTDGEERA 369
DB 178 ANYRNKKVKEAVOGVAKGTGYKAGFEYAFDOLNSNITRANCKIMMTDGDGEDRV 237
QY 370 QETFNKN-KKKVVRFSVGOHNYRGPIONMACENKGYEIPSGAINTQEYLD 428
DB 238 QVFEKYNPNRTVRVFTSVGOHNYRGPIONMACENKGYEIPSGAINTQEYLD 297
QY 429 VLGRPMVLACDRAKQVQWNVYLDALGLVITGTLFVNITQFENKTNLKNLILGVW 488
DB 298 VLGRPMVLACDRAKQVQWNVYLDALGLVITGTLFVNITQFENKTNLKNLILGVW 355
QY 489 GVDVSLDKRLTPRTTCLPNGYFAIDPNGVYLLHPNLPQNKPSQEPVTDFDADAELE 548
DB 356 GIDVALNDIKRLTPNITLPGANGVYFAIDPNGVYLLHPNLPQNKPSQEPVTDFDADAELE 415
QY 549 NDIVKVRNKKMDGEGEFTFLYKSDQERIDKGNRYTTPVNGTDSLALVLPYTS 608
DB 416 DENKEIRSMIDGNKGHQIRTLVKSLSDERIDEYTRNITVPIRSTNYSGLVLPYTS 475
QY 609 FYVIAKLEETITQARSKKMKDSETLKPDNFEESGYTFIAPRDYCNLKTSDNNTEFL 668
DB 476 TFLQANLSDQILQ-----VKYFELPSSFESGHHVFIAPREYCKDLNADNNTEFL 528
QY 669 LNFNEIDRKTNPNSCNADLNIRVLLDAGFNELQNTVWSKQK-NIKGVKARFVVTGG 727
DB 529 KNFELMEKVTDPKSCNKNFLLHNLIDTGTQQLVRYVRDQDLNTYSLLAVFAATDGG 588
QY 728 ITRVYKPEAGENQWENPEYEDSFYKRSLDNDNYTAPFNK-SGPGAYES---GIMVTS 783
DB 589 ITRVFPNKAEDTENPEPNASFYRRSLDNHGYEKKPPHQDALLRPLELNDTVGILVS 648
QY 784 KAVEIYTOGKLLPAPVVGKIDVNSNIENF-----TKTSIRDP--CAGP---VCDCKRN 832
DB 649 TAVELSLGRTRLAPVGVVKLDLEAAEKFVLAISRNRTHQDQPKC-GPNSCEMDCEVN 707
QY 833 SDVMDCVLLDDGFLMANHDDYTNOIGRFFGEBIDPSLMRLHVNISVYAFNKSXDYQSV 892
DB 708 NEDLLCVLLDDGFLVSNQONHWDQVGRFFSEVDANLMLALYNNSFYRKESYDQAAAC 767
QY 893 EPGAAKQAGHRSVAVPSVADILQGWATAAASILQOFLSLTFPLLEAVEMEDDD 952
DB 768 APQPPGNLGAAPRGVFPVTVADFLNLAWNTSAAASLFOQLLYGLIYHSWFQADPAEAG 827
QY 953 FTASLSKQSCITQOTQYFFDNDSKFSGLVDCGNCGRIFHGEKLMNTLIFIMVESKGTG 1012
DB 828 -SPETRESSCMKQOTQYFGSVNASYNAIDCGNCSRLFHAQRLTNLLFVVAEPLCS 886
QY 1013 PCBTRLLIQAQ--TSDGNPCDMVKQPRYKRGPDVCFDNNVLEDYDCGGVSGNPLSLW 1070
DB 887 QCEAGRLLOKETHCPADGPQCELVQRPVRRGPHICFDYNATEDSDCGRGASFPFSLG 946
QY 1071 YIIGIQFLLL 1080
DB 947 VLVSQQLLLL 956

RESULT 12
Q921L5 PRELIMINARY; PRT; 1091 AA.
AC Q921L5;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE CALCIUM CHANNEL ALPHA-2-DELTA-C SUBUNIT.
GN CACNA2D3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
TISUE=BRAIN;
RX MEDLINE=99098955; PubMed=9880589;
RA Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).
DR EMBL; AJ010949; CAA09423.1; -.
DR MGD; MGI:1338890; Caccna2d3.
DR InterPro; IPR002035; -.
SQ SEQUENCE 1091 AA; 122777 MW; 7AEE2BDA10077A0A CRC64;

Query Match 19.6%; Score 1127.5; DB 11; Length 1091;
Best Local Similarity 28.6%; Pred. No. 6.4e-64;
Matches 328; Conservative 230; Mismatches 451; Indels 137; Gaps 42;

QY 3 AGCLLALTTLTLOSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTAGVYNQLVDIYE 62
DB 14 ASALLA-TALLYAALGDVVRSEQQIPLSV-VKLWASAFGEIKSAKYSGSOLLQKKYK 71
QY 63 KYQDLYTEPNNARQLVEIARDIEKLNSRKALVSLALEAKVQAAHQWREDFASNEV 122
DB 72 EYEKDAVEIEIDGLQLVKKLAKIMEEMFHKSEAVRRLVEAAEAHLKHEFDADL---QY 128
QY 123 VYNNAK--DDLDPEKNDSEPGSQRIKPVFIEDANRGR-QISYQHAHVHIPTDIYEGSTIV 179
DB 129 EYFNVLINERDKDGNFLGKEFI---LAPNDHFNNLPVNISLSVQVPTNMYNKDPAI 185
QY 180 LNELNWTALDDEVFKKNREDDPSLLWQVFGSATGLARYYPASPVDNSRTPNKIDLYDVR 239
DB 186 VNGVYWSLAKVFDNDRDPSLWQYFGSAKGPQYPGIKWEPDE---NGVIAFDCR 242
QY 240 RRPWTIQGAASPKDMLILVDVSGVSGELTKLIIRTSVSEMLETLDSDDFVNVASFN 299
DB 243 NRKWTQAAATSPKVVILVDVSGMKRLTIKATQTVSSILDTLGDGDDFFNIITYNEELH 302
QY 300 DYS-CFO-HLVQANVRNKKVLDAVNNITAKGIDYDKGKFATFQQLNLYNVSRAN--CN 355
DB 303 YVEPLCNGTLVQADRTNKEHREHLDKLFAGKIGMLDIALNEAFNLISDFNHTGQSGIS 362
QY 356 KIIMLTDDGGEERAQEIFNKYN-KDKKVRVFRFSVGOHNYRGPIONMACENKGYEIP 414
DB 363 QAIMLTIDGAVDTYTFIAKYNWPKRKRIFTYLIGREAFADNLKWKMACANKGPFQTLS 422
QY 415 SIGAIRINTQEYLDVLGRPMVLACDRAKQVQWNVYLD-----ALELGLVI--TGT 463
DB 423 TLADVQENVMYELHLVLSRPKVI--DOEHVWVWTEAYIDSTLPAQAKLADDQGLVLTVA 480
QY 464 LPVFNITQFENKTNLKNLILGVNCGVDVSLIEDIKRLTPRTCLPNGYFAIDPNGYVLL 523
DB 481 MPVFS---KQNETRSG--ILGVVGTDPVVKELLTIPIKYLGIHGYAFATNNGIIT 535
QY 524 HPNLOP---KNPKSREP--VTLDLDALENDIKVIRNKMIDGESGEKTFRTLKQSD 578
DB 536 HPFLRPLYEEGKRRKPNYSVDLSEVEDRDDV-LRNAMVNRKTKG--FSMEVK---- 588
QY 579 RYIDKGNRT-----YTWTVPVNGTDYSALVLT-YSFYIIRAKLEETITQARSKK 631
DB 589 KTVDKGRVLVMTNDYYTDIKGTFPSLGVSLSRGHGKYFF-----RGNTV 634
QY 632 DSETLKPDNFEESGYTFIAPRDYCN-DLAKSDNNTFELNFEIDRKTNPNSCNADLI 690
DB 635 IEELG--HDLEHPDVSADSEWYCNITDLHPEHRHLSQLEAIKLYLKGRKP-LLOCDKELI 691
QY 691 NRVLLDAGFTNELVQYWS-----KQKNIKGVKARFVVTDDGITRYP----- 733
DB 692 QEVLFDA-VVSAPIEAYTWSLAINKSENKSGKGVFAFLGTRTGLSLRINLFVGAELTNQD 750
QY 734 -KEAGENWOENPETYEDSFYKRSLDN--DNYVFTAPY----FNKSGFGAYESGIMVSKAV 786
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RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,  
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,  
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,  
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,  
RA Celnikier S., Rubin G.M.,  
RT "An exploration of the sequence of a 2.9-Mb region of the genome of  
RT Drosophila melanogaster: the adh region.",  
RL Genetics 153:179-219(1999).  
RP [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Y, CN BW SP;  
RA Celnikier S.E., Agbayan A., Arcaina T.T., Baxter E., Blazej R.G.,  
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,  
RA Partan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,  
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,  
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,  
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,  
RA Sethi H., Snir E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,  
RA Zieran L.L., Rubin G.M.,  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF003415; RAP44988.1; -  
DR Flybase; FBgn0028859; BG:DS07473.1.  
DR InterPro; IPR002035; -  
KW Hypothetical protein.  
SQ SEQUENCE 2190 AA; 249754 MW; B8C657A2F80F226E CRC64;

Query Match 16.3%; Score 937; DB 5; Length 2190;  
Best Local Similarity 24.9%; Pred. No. 3.5e-51;  
Matches 289; Conservative 222; Mismatches 410; Indels 238; Gaps 47;

QY 29 SAYTIKSWDKQEDIVLAKTAGSNQVLDVIEKYQDLYTYEPNNAROLVETIARDIEK 88  
DB 13 SKATVGNWATQFGDELFAQAQIKTSQETKEIKYKN--ARVELKNGTELIKSIKNVGR 70  
QY 89 LLSNRKALVSLALEAEKYQAQHQWREDFASNEVYVY-----NAKDDLDPEKNDSE 139  
DB 71 MLARKWDVRCIOERAENYENEFNLTALQNTFYFSSKYSTFNCSSELEP--NEAE 128  
QY 140 PG-----SORIKPVIEDANF-GRQISYQAHAHVPDIDYEGSTIVLNELNWTSDALDEVPK 194  
DB 129 FAWMYRNMELNP----DTHFYNTPTVTEHSSVHVPSNIWDRSERVLKTTMWEHLEDEVR 184  
QY 195 KNEEPSLIMQVSGATGLARYPASPVDNSRTNPKDLDYDVRPPVYIOGAASPKDM 254  
DB 185 QNYQSPALSWQVFGSDTGLRHYPAAQWTDTRPNRDDADTDYCRKRSWITETATCSKDI 244  
QY 255 LILVDVSGVSGLTLLKRTSVSEMLETISDDDFVNVASFNSNAQD-VSCFO-HLVQANV 312  
DB 245 VILLDHSGMTGFRHHVAKFTIRSIIDTFSNDDFFILAYSSEVNDIIPCFNGALVQATP 304  
QY 313 RNKKVLKDAVNNI-TAKGTDYKGFSAFEQQLNTNVS-----ANCNKIIMLFTDGE 366  
DB 305 ENIEVFNOQIEQLDDPEGYANLFLAYETAFQLRKLYDRHCVNTGNCQAINLVTGVA 364  
QY 367 ERAQEIFNKNY-----KDKKVRVRESVGHNYERGPIONMACENKGYEIPISGA 418  
DB 365 GNTVEFQKTNWNGENGSTQMDTRFTYLLGKVTQVREIQWACLNGYVSHVOTLDE 424  
QY 419 IRTQBYLDVLRPMVLAGDKAKQVQWNTNVDLAL-----ELGLVITGTLPVFN 469  
DB 425 VHEVLKVDVIATPLVLQNEQHPPT-WTHAFTDKYDPKTSNEKRPRLMISVGVPAFDR 483  
QY 470 TGFENKTNKQLILGMVGVDSLEDKLTPRFLPCNPGYVFAIDPQVLLHNPLOP 529  
DB 484 FYRHANSTNPRAL-LGVAGTDVPVEDIDKLTLPYLGNGYGVYVSNNGYVLLHDPDR 542  
QY 530 -----KNPKSQEPVTLDFDAE-LENDIK-----VEIRKNMIDGSGE-KTERTLV 573  
DB 543 IGNGKNKNPNY---SIDFTEVHEHLEFQSPRPGSGILHINAMVHNEAFKSIKVF 599  
QY 574 KSQDERVIDKGRNTYWTVPNGVDYSIALVLP-LT-YSFYIKAKLEETITQARSKGMKD 632

DB 600 HYDKMRVRSEKQDYFFAPLPNTFTLGIVMPSYKGTWIKVGEVD-----KNHKMKINI 655  
QY 633 SETLKPDPNFEE-----SGYTIAP-----RDYC-----NDLKISDNTNTEFLNFI 672  
DB 656 SDFIGENKWKHPDWYKYHYHLEGEHEKTPAEALREFLAKMNDKWKSEQYAEDESMD 715  
QY 673 EFID-----RKTNNPNS--CNADLNRVLDDAGFTNELYQNYW-----SKQNKNIKVKA-- 719  
DB 716 DKDDLNCGRKTLGDDAYYCNKELVNLILFDKAVTNS-SYGVWRFSDEDEQLIERFADL 774  
QY 720 RPVVDGGITRVYKPEAGENWQ-----ENPTYEDSYKRSL-----D 757  
DB 775 RFVATMSGLTR-----WQIFGEVEVTDREFGDYHTAIDETWYKSAILQHHEDR 825  
QY 758 NDNVVETAPYENKSGPGAGESIMVSKAVEIYIOCKLLKPAVVGKIDVNSWNIENFTKTS 817  
DB 826 AESFYISVYKYVD-----DPMEDSE 844  
QY 818 IRDPCAGPVCDCRNSDMOCVILDDGGFLLMANHDDYTNQIGRFFGIDPFLMRHLVNI 877  
DB 845 VKCNHCLPIC-----TDDVDVCVVIDNNAYIVIGON---INTTGKFFGFGHGDVMTAMVER 897  
QY 878 SVYAFNKSYDQSVQV--EPGAAPKQAGHRSAYVPSVAD-ILQIGWATAAASWILQOFL 934  
DB 898 GIFLSIEVDYQEQCKEKPAYME-----YTDEIEDEVYAVVAGDGGKSSA----- 941  
QY 935 LSLTPRLLEAVEMEDDDFTASLSK-----QSCITEQTOYFFDNDKSKFSGLVDC--G 985  
DB 942 -----SKPKDSDSDENAMFDEPDPIYKACDKKSTLYAL--QPSALVGINDFVEA 990  
QY 986 NCSRTIFHGEKLMNTNLIPTMVE---SKGTCPCDTRLLIQABQTS-DGPNPCDMYKQRPY 1040  
DB 991 PSTREFLVKKIPNSNLVNVVNLMPSR-----SVRLTTEPQRMEDYKFEPCYKLNMSFY 1045  
QY 1041 -RKGPDVCFDNNVLEDTYD 1058  
DB 1046 ERRRIECCY--TVHEDLSD 1062  
  
RESULT 15  
Q9VJMO PRELIMINARY; PRT: 2172 AA.  
AC Q9VJMO;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)  
DE CG12455 PROTEIN.  
GN BG:DS07473.1 OR CG12455.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_taxid=7227;  
RP [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RX MEDLINE-20196006; PubMed-10731132;  
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards M.D., Zhang Q., Chen L.X.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayan A., An H.-J., Andrews-Pfannkoch C., Basley E.M.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Botchan P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchko M.R., Bouck J., Brokstein P., Brottner P.,  
RA Burtis J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,



RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpkins M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).  
DR EMBL; AE003650; AAF53505.1; -  
DR FlyBase; FBgn0028859; BG:DS07473.1.  
DR InterPro; IPR002035; -  
SQ SEQUENCE 2172 AA; 247574 MW; 39AA7BCB470D1A39 CRC64;

Query Match 16.0%; Score 920; DB 5; Length 2172;  
Best Local Similarity 25.0%; Pred. No. 4.3e-50;  
Matches 288; Conservative 216; Mismatches 406; Indels 242; Gaps 47;

QY 29 SAVTIKSWDKQEDLVILAKTAGVQNLVDIYKQDLYTTPENARQLVIAARDIEK 88  
Db 13 SKATVGNATQGDLEFALAAQIKTSQETKEKYKN--ARVELKNGTELKISITKNVGR 70  
QY 89 LLSNRKALVSLALEAKYQAAHQWREDA--SNEVYVNAKDDLDPEKNDSPEG---S 142  
Db 71 ML-----ARKMDAVRCIOEHFTYFFSKYSFNGNSSELEPNEAEFAWYRN 117  
QY 143 QRIKPVFIEDANF-QRQISYQHAHVHPTDIYEGTVILNELNWTSDALDEPKKNEEDP 201  
Db 118 MELNP---DTHFYNTVPDTEHSSVHPVSNIDRSERVLKTIWSEHLDEVERQNTQSDP 173  
QY 202 SLLWQVFGATGLARYYPASPHVDSRPNKIDLYDVRPRPHYIOGAASPKDKMLILVDVS 261  
Db 174 ALSWQIFGSDTGILRHYPAAQWTDTRPNRDDADTDYDKRRSWIETATCSKDIVILLDS 233  
QY 262 GSVGLTLKLRITSVSEMLETISDDDFVNAFNSNAQD-VSCFO-HLVQANVRNKKVLK 319  
Db 234 GSWTGRHHVAKFTIRSLDFTSNDFITILYSEVNDIIFCFNGALVQATPENIEVEN 293  
QY 320 DAVNNI-TAKGTTDYKGFSAFEOQLLNNVSR-----ANCKNIIMLFTDGEERAQEIF 373  
Db 294 QOIEQLDDPEGYANLTAYATAFQLLRKYIDSRHCVNSTCQALMLVTDGVAGNTTEVF 353  
QY 374 NKNY-----KDKKVRFRFVSGHVERGCPIDWACENKGYIYEIPSGAIRINTQE 425  
Db 354 QKYNNGENGTSQMDRTFTYLLGKEVTKVREIQIWMACLNRGYYSHVQTLDEVHEEVLK 413  
QY 426 YLDVLRGPVLAGDKAKQVQNTNVYLDAL-----ELGLVITGLTPVFNITQGFENK 476  
Db 414 YVDVATPLVLQNEQHPT-WTHATDXTYDPKTSNEKPRLMISVGVPAPDFRPHANS 472  
QY 477 TMLKNQILGVNGVDVSLIEDIKRLPRTPLCPNGYFAIDPNGYVLLHPNLQP-----K 530  
Db 473 TNPRARL-LGVAGTDVPVEDIDKLPYKLVGVNGYSFVVSNNGYVLLHPDLRPIGTNGKM 531  
QY 531 NPKSQEPVILDFLDAE-LENDIK-----VEINKMIDGESGE-KTFRTLVKSDERY 580  
Db 532 NPNYN---SIDFTEVHEHLEFQSPREGESILHIRNAMYRHEANEFKSIKSVKHFYDKMR 588  
QY 581 IDKGNRTVTWTPVNGTDYSIALVLPF-YSFYIKAKLEETITQARSKKGMKDSLETKPD 639

Search completed: July 23, 2001, 07:46:48

Job time: 574 sec

Db 589 VSEERQDYFAFLPNTPTFTLGIWMPSEYCKTWIKVGEVD---KNKHKMINISDFICE 644  
QY 640 NFE-----SGYTFIAP-----RDYC-----NDLKISDNNTFFLLNNEFTD--- 676  
Db 645 NKKVHPDWYCKYHYLGEHFEFTPEAELREFLAKMQNDKWSEQYAEDESMDKDDKDLNC 704  
QY 677 -RKTNNPS--CNADLINRVLDAGTNELVQNYW-----SKOKNIKGYKA--RFVVTG 726  
Db 705 GKRTGGDDAYCNKELVNLIIIDAKVTNS-SGVWRFESDERQOLIERFRADLRFVATNS 763  
QY 727 GTRVYVPEAGENWQ-----ENPTYEDSFYKRSI-----DNDNYVFT 764  
Db 764 GLTR-----WQFIFGEVEVDTDRFGDYHTTATIDETWYKSAILOHHEDRAESEFVS 814  
QY 765 ADFYFNKSGPGAYESGIMVSKAVEIYIQGLKLPVAVGIVKIDVNSWTENTKTSIRDPGAG 824  
Db 815 VKYYD-----DPMEDSEVCKNHCL 833  
QY 825 PYCDCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPDSILMRHLVNIYAFNK 884  
Db 834 PIC-----TDDVDVGVVDDNNAIVIGQN---INTTKFFGEFHGDVMTAWERGIPLSIE 886  
QY 885 SYDYQSVK--EPGAAPKQAGHRSAYVPSVAD--ILQIGWATAAAMSILQQFLLSLTFFR 941  
Db 887 VDYQEOCKEKPAYME-----YTDEIEEYVAVGGGKSSA----- 923  
QY 942 LLEAVEMEDDDFTASLSK-----QSCITEQTQYFFDNDKSFSGVLDC--GNCSRIHF 992  
Db 924 --SKPKDDSDDENAMFDEPEPDPIYKACDKRSTLYAL--OPSALVGINDFVEAPSTRPEL 979  
QY 993 GEKLMNTNLIFTWVE-----SKGTCPCDTELLIQAEQTS--DGNPNCDMVKQPRY-RKGPDV 1046  
Db 980 VKKIPNSNLVLVVVNVLMPSR-----SVRLTEPQRMEDYKFEPCYKLNMSFERRRIE 1034  
QY 1047 CFDDNNVLEDYTD 1058  
Db 1035 CY--TVHEDLSD 1044

